

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

File: nucleic search, using sw model

June 12, 2006, 07:37:54 ; Search time 5 Seconds  
(without alignments)  
3.589 Million cell updates/sec

US-09-930-503a-6

1766

1 aatcagagccacccgcggc.....cgagtcctcatcagatg 1766

Identity: NUC

Gap: 10.0, Gapext 0.5

264 seqs, 5081 residues

number of hits satisfying chosen parameters: 528

DB seq length: 8  
DB seq length: 30

processing: Minimum Match 0%

Maximum Match 100%

Listing first 272 summaries

us-09-930-503a-6.sl.rn14.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Score	Query Match	Length	ID	Description
30	1.7	30	1	US-08-513-974B-133
25.2	1.4	25	1	US-08-513-974B-132
25	1.4	25	1	US-09-396-196G-67915
25	1.4	25	1	US-09-396-196G-67925
24.8	1.4	30	1	US-08-444-581B-6
24.8	1.4	30	1	US-08-446-088A-6
24.8	1.4	30	1	US-08-513-974B-139
24.2	1.4	30	1	US-08-513-974B-232
24	1.4	24	1	PCT-US92-06532-6
24	1.4	29	1	US-08-513-974B-61
24	1.4	29	1	US-08-776-971-32
24	1.4	29	1	US-09-461-436B-61
24	1.4	29	1	US-09-576-290-32
24	1.4	29	1	US-09-716-147-32
23.8	1.3	27	1	US-08-513-974B-85
23.4	1.3	25	1	US-09-396-196G-67914
23.4	1.3	25	1	US-09-396-196G-67926
23	1.3	24	1	US-07-701-935-4
23	1.3	24	1	US-08-117-965-4
22.4	1.3	24	1	US-07-701-935-5
22.4	1.3	24	1	US-08-117-965-5
22.2	1.3	27	1	US-08-513-974B-82
22.2	1.3	27	1	US-08-513-974B-84
22	1.2	25	1	US-09-396-196G-67908
21.8	1.2	25	1	US-09-396-196G-67912
21.8	1.2	27	1	US-08-513-974B-2
21.8	1.2	27	1	US-08-513-974B-76
21.8	1.2	27	1	US-08-776-971-30
21.8	1.2	27	1	US-08-540-650B-8
21.8	1.2	27	1	US-09-255-518C-6
21.8	1.2	27	1	US-09-461-436B-2

34	21.8	1.2	27	1	US-09-576-290-30	Sequence 30, App1
35	21.8	1.2	27	1	US-09-716-147-30	Sequence 30, App1
36	21	1.2	21	1	US-07-701-935-10	Sequence 13, App1
37	21	1.2	21	1	US-07-701-935-13	Sequence 13, App1
38	21	1.2	21	1	US-07-701-935-15	Sequence 15, App1
39	21	1.2	21	1	US-07-701-935-17	Sequence 17, App1
40	21	1.2	21	1	US-07-701-935-18	Sequence 18, App1
41	21	1.2	21	1	US-08-117-965-10	Sequence 10, App1
42	21	1.2	21	1	US-08-117-965-13	Sequence 13, App1
43	21	1.2	21	1	US-08-117-965-15	Sequence 15, App1
44	21	1.2	21	1	US-08-117-965-17	Sequence 17, App1
45	21	1.2	21	1	US-08-117-965-18	Sequence 18, App1
46	21	1.2	21	1	US-08-117-965-22	Sequence 22, App1
47	21	1.2	21	1	US-08-513-974B-263	Sequence 263, App
48	21	1.2	21	1	US-08-513-974B-264	Sequence 264, App
49	21	1.2	21	1	PCT-US92-06532-5	Sequence 6, App1
50	20.8	1.2	24	1	US-07-701-935-6	Sequence 6, App1
51	20.8	1.2	24	1	US-08-117-965-6	Sequence 231, App
52	20.8	1.2	24	1	US-08-513-974B-231	Sequence 231, App
53	20.8	1.2	24	1	US-08-513-974B-233	Sequence 237, App
54	20.8	1.2	24	1	US-08-513-974B-237	Sequence 237, App
55	20.8	1.2	25	1	US-09-396-196G-67919	Sequence 17919, A
56	20.6	1.2	24	1	US-08-513-974B-15	Sequence 15, App1
57	20.6	1.2	24	1	US-08-513-974B-230	Sequence 230, App
58	20.6	1.2	24	1	US-09-461-436B-15	Sequence 15, App1
59	20.4	1.2	23	1	US-08-513-974B-235	Sequence 235, App
60	20.2	1.1	25	1	US-09-396-196G-67918	Sequence 67918, A
61	20.2	1.1	25	1	US-09-396-196G-67927	Sequence 67927, A
62	20.2	1.1	25	1	US-09-396-196G-67930	Sequence 67930, A
63	20.2	1.1	25	1	US-09-396-196G-67931	Sequence 67931, A
64	20	1.1	20	1	US-07-701-935-11	Sequence 11, App1
65	20	1.1	20	1	US-07-701-935-12	Sequence 12, App1
66	20	1.1	20	1	US-07-701-935-14	Sequence 14, App1
67	20	1.1	20	1	US-07-701-935-16	Sequence 16, App1
68	20	1.1	20	1	US-07-701-935-19	Sequence 19, App1
69	20	1.1	20	1	US-07-701-935-20	Sequence 20, App1
70	20	1.1	20	1	US-08-117-965-11	Sequence 11, App1
71	20	1.1	20	1	US-08-117-965-12	Sequence 12, App1
72	20	1.1	20	1	US-08-117-965-14	Sequence 14, App1
73	20	1.1	20	1	US-08-117-965-16	Sequence 16, App1
74	20	1.1	20	1	US-08-117-965-19	Sequence 19, App1
75	20	1.1	20	1	US-08-117-965-20	Sequence 20, App1
76	20	1.1	21	1	US-07-701-935-9	Sequence 9, App1
77	20	1.1	21	1	US-08-117-965-9	Sequence 9, App1
78	19.8	1.1	23	1	US-08-513-974B-240	Sequence 240, App
79	19.4	1.1	21	1	US-08-513-974B-257	Sequence 257, App
80	19.2	1.1	24	1	US-08-125-012-7	Sequence 7, App1
81	19.2	1.1	24	1	US-08-221-579A-7	Sequence 7, App1
82	19.2	1.1	24	1	US-08-783-818-7	Sequence 7, App1
83	19.2	1.1	24	1	US-08-453-349-7	Sequence 7, App1
84	19.2	1.1	24	1	US-08-704-701-7	Sequence 7, App1
85	19.2	1.1	24	1	US-08-979-385B-7	Sequence 7, App1
86	19.2	1.1	24	1	US-09-321-461-7	Sequence 7, App1
87	19.2	1.1	24	1	US-09-011-922A-13	Sequence 13, App1
88	19.2	1.1	24	1	US-08-880-576-7	Sequence 7, App1
89	19.2	1.1	24	1	US-09-359-975-7	Sequence 25, App1
90	19	1.1	19	1	US-07-701-935-25	Sequence 23, App1
91	19	1.1	19	1	US-08-117-965-25	Sequence 25, App1
92	19	1.1	19	1	US-08-117-965-25	Sequence 23, App
93	18.8	1.1	22	1	US-08-513-974B-223	Sequence 9, App1
94	18.4	1.0	20	1	US-08-287-075-9	Sequence 12, App1
95	18.2	1.0	20	1	US-07-915-966C-12	Sequence 12, App1
96	18.2	1.0	20	1	US-08-771-182-12	Sequence 12, App1
97	18.2	1.0	20	1	US-08-853-194-12	Sequence 21, App1
98	18	1.0	18	1	US-07-701-935-21	Sequence 21, App1
99	18	1.0	18	1	US-08-117-965-21	Sequence 1372, Ap
100	18	1.0	18	1	US-09-543-679A-1372	Sequence 256, App
101	17.8	1.0	21	1	US-08-513-974B-267	Sequence 267, App
102	17.8	1.0	21	1	US-08-513-974B-269	Sequence 269, App
103	17.8	1.0	21	1	US-08-513-974B-270	Sequence 270, App
104	17.8	1.0	22	1	US-08-513-974B-270	Sequence 5, App1
105	17.8	1.0	22	1	US-07-974-409C-5	Sequence 17, App1
106	17	1.0	21	1	US-08-182-175A-17	Sequence 17, App1

17	1.0	21	1	US-08-182-175A-19	Sequence 19, Appl	c 180	13.8	0.8	17	1	US-09-401-063-243	Sequence 243, App
17	1.0	21	1	US-08-182-175A-21	Sequence 21, Appl	c 181	13.8	0.8	17	1	US-09-866-108A-2756	Sequence 2756, Ap
17	1.0	21	1	US-08-474-633A-25	Sequence 25, Appl	c 182	13.8	0.8	17	1	US-09-866-108A-1764	Sequence 1764, Ap
17	1.0	21	1	US-08-474-633A-41	Sequence 41, Appl	c 183	13.8	0.8	17	1	US-09-685-664B-1774	Sequence 1774, Ap
17	1.0	21	1	US-08-474-633A-43	Sequence 43, Appl	c 184	13.8	0.8	17	1	US-09-685-664B-1886	Sequence 1886, Ap
17	1.0	21	1	US-08-823-771-25	Sequence 25, Appl	c 185	13.8	0.8	17	1	US-10-156-306B-6951	Sequence 6951, Ap
17	1.0	21	1	US-08-823-771-41	Sequence 41, Appl	c 186	13.8	0.8	17	1	US-10-138-674B-1714	Sequence 1714, Ap
17	1.0	21	1	US-08-823-771-43	Sequence 43, Appl	c 187	13.8	0.8	17	1	US-10-138-674B-1866	Sequence 1866, Ap
17	1.0	21	1	PCT-US92-06412-17	Sequence 17, Appl	c 188	13.8	0.8	17	1	US-10-138-674B-6345	Sequence 6345, Ap
17	1.0	21	1	PCT-US92-06412-19	Sequence 19, Appl	c 189	13.6	0.8	23	1	US-08-513-974B-240	Sequence 240, App
17	1.0	21	1	PCT-US92-06412-21	Sequence 21, Appl	c 190	13.4	0.8	15	1	US-08-585-664B-2100	Sequence 2100, Ap
16.8	1.0	21	1	US-08-431-080-7	Sequence 7, Appli	c 191	13.4	0.8	15	1	US-08-585-664B-2101	Sequence 2101, Ap
16.8	1.0	21	1	US-08-936-534-7	Sequence 7, Appli	c 192	13.4	0.8	15	1	US-09-038-073-2100	Sequence 2100, Ap
16.8	1.0	21	1	US-09-345-294-7	Sequence 7, Appli	c 193	13.4	0.8	15	1	US-09-038-073-2101	Sequence 2101, Ap
16.4	0.9	18	1	US-07-701-935-2	Sequence 2, Appli	c 194	13	0.7	15	1	US-08-502-185-16	Sequence 16, Appl
16.4	0.9	18	1	US-08-117-965-2	Sequence 2, Appli	c 195	13	0.7	15	1	US-08-388-945-16	Sequence 16, Appl
16.4	0.9	18	1	US-08-584-040-6209	Sequence 6209, Ap	c 196	13	0.7	15	1	US-08-501-779-16	Sequence 16, Appl
16.4	0.9	18	1	US-09-371-772B-2971	Sequence 2971, Ap	c 197	13	0.7	15	1	US-08-501-713-16	Sequence 16, Appl
16.4	0.9	18	1	US-09-685-664B-2971	Sequence 2971, Ap	c 198	13	0.7	15	1	US-08-378-860-16	Sequence 16, Appl
16.4	0.9	18	1	US-10-138-674B-2971	Sequence 2971, Ap	c 199	13	0.7	15	1	US-08-501-626-16	Sequence 16, Appl
16.4	0.9	20	1	US-09-967-669-87	Sequence 87, Appl	c 200	13	0.7	15	1	US-08-501-356-16	Sequence 16, Appl
15.4	0.9	17	1	US-08-584-040-5544	Sequence 5544, Ap	c 201	12.8	0.7	16	1	US-09-034-205-66	Sequence 66, Appl
15.4	0.9	17	1	US-09-371-772B-2435	Sequence 2435, Ap	c 202	12.8	0.7	16	1	US-09-677-218B-66	Sequence 66, Appl
15.4	0.9	17	1	US-09-685-664B-2435	Sequence 2435, Ap	c 203	12.8	0.7	16	1	US-09-677-192-66	Sequence 66, Appl
15.4	0.9	17	1	US-10-138-674B-2435	Sequence 2435, Ap	c 204	12.8	0.7	16	1	US-09-270-933-9	Sequence 9, Appli
15.4	0.9	18	1	US-08-513-974B-243	Sequence 243, App	c 205	12.8	0.7	16	1	US-09-060-289-412	Sequence 412, App
15.4	0.9	18	1	US-09-850-948-19	Sequence 19, Appl	c 206	12.8	0.7	16	1	US-09-402-923A-412	Sequence 412, App
15	0.8	15	1	US-09-543-679A-1373	Sequence 1373, Ap	c 207	12.8	0.7	16	1	US-09-371-772B-5850	Sequence 5850, Ap
15	0.8	17	1	US-09-543-679A-1374	Sequence 1374, Ap	c 208	12.8	0.7	16	1	US-09-371-772B-5863	Sequence 5863, Ap
15	0.8	17	1	US-09-866-108A-6966	Sequence 6966, Ap	c 209	12.8	0.7	16	1	US-09-479-005A-50	Sequence 50, Appl
15	0.8	17	1	US-09-866-108A-6967	Sequence 6967, Ap	c 210	12.8	0.7	16	1	US-09-402-618B-66	Sequence 66, Appl
15	0.8	17	1	US-09-866-108A-6968	Sequence 6968, Ap	c 211	12.8	0.7	16	1	US-09-720-435A-410	Sequence 410, App
15	0.8	18	1	US-08-475-742-5	Sequence 5, Appli	c 212	12.8	0.7	16	1	US-09-543-679A-1408	Sequence 1408, Ap
15	0.8	18	1	US-08-261-293-5	Sequence 5, Appli	c 213	12.8	0.7	16	1	US-09-543-679A-1453	Sequence 1453, Ap
14.8	0.8	18	1	US-08-210-762B-45	Sequence 45, Appl	c 214	12.8	0.7	16	1	US-09-543-679A-1454	Sequence 1454, Ap
14.8	0.8	18	1	US-09-071-433-50	Sequence 50, Appl	c 215	12.8	0.7	16	1	US-10-138-674B-5850	Sequence 5850, Ap
14.8	0.8	18	1	US-09-106-075A-45	Sequence 45, Appl	c 216	12.8	0.7	16	1	US-10-138-674B-5863	Sequence 5863, Ap
14.8	0.8	18	1	US-09-341-587-9	Sequence 9, Appli	c 217	12.6	0.7	20	1	US-07-701-935-14	Sequence 14, Appl
14.4	0.8	18	1	US-08-411-020-44	Sequence 44, Appl	c 218	12.6	0.7	20	1	US-08-117-965-14	Sequence 14, Appl
14.4	0.8	18	1	US-09-106-038A-9	Sequence 9, Appli	c 219	12.4	0.7	14	1	US-08-785-750-2	Sequence 2, Appli
14.4	0.8	18	1	US-09-289-376-17	Sequence 17, Appl	c 220	12.4	0.7	14	1	US-08-588-355-1	Sequence 1, Appli
14.4	0.8	18	1	US-09-344-520-9	Sequence 9, Appli	c 221	12.4	0.7	14	1	US-09-116-780-5	Sequence 5, Appli
14.4	0.8	18	1	US-08-584-040-6255	Sequence 6255, Ap	c 222	12.4	0.7	14	1	US-08-812-102-1	Sequence 1, Appli
14.4	0.8	18	1	US-09-422-978-10970	Sequence 10970, A	c 223	12.4	0.7	14	1	US-08-784-757-1	Sequence 1, Appli
14.4	0.8	18	1	US-09-371-772B-3013	Sequence 3013, Ap	c 224	12.4	0.7	14	1	US-08-745-957-1	Sequence 1, Appli
14.4	0.8	18	1	US-09-747-391-42	Sequence 42, Appl	c 225	12.4	0.7	14	1	US-08-765-340-124	Sequence 124, App
14.4	0.8	18	1	US-09-685-664B-3013	Sequence 3013, Ap	c 226	12.4	0.7	14	1	US-09-063-667-17	Sequence 17, Appli
14.4	0.8	18	1	US-10-138-674B-3013	Sequence 3013, Ap	c 227	12.4	0.7	14	1	US-09-205-337-2	Sequence 2, Appli
14	0.8	14	1	US-09-874-601-5	Sequence 5, Appli	c 228	12.4	0.7	14	1	US-09-406-362-1	Sequence 1, Appli
14	0.8	14	1	US-09-543-679A-1371	Sequence 1371, Ap	c 229	12.4	0.7	14	1	US-09-755-734-1	Sequence 1, Appli
14	0.8	16	1	US-08-588-821-84	Sequence 84, Appl	c 230	12.4	0.7	14	1	US-09-406-363-1	Sequence 1, Appli
14	0.8	16	1	US-08-915-214-84	Sequence 84, Appl	c 231	12.4	0.7	14	1	US-09-649-890-1	Sequence 1, Appli
14	0.8	16	1	US-09-005-532-84	Sequence 84, Appl	c 232	12.4	0.7	14	1	US-09-969-204A-1	Sequence 1, Appli
14	0.8	17	1	US-08-897-340-14	Sequence 14, Appl	c 233	12.4	0.7	14	1	US-09-874-601-6	Sequence 6, Appli
14	0.8	17	1	US-09-252-329-14	Sequence 14, Appl	c 234	12.4	0.7	14	1	US-10-177-871-1	Sequence 1, Appli
14	0.8	17	1	US-09-724-566A-22	Sequence 22, Appl	c 235	12.4	0.7	14	1	US-09-341-700A-1573	Sequence 1573, Ap
14	0.8	17	1	US-09-866-108A-6965	Sequence 6965, Ap	c 236	12.4	0.7	14	1	US-09-543-679A-1511	Sequence 1511, Ap
14	0.8	17	1	US-09-866-108A-6969	Sequence 6969, Ap	c 237	12.4	0.7	15	1	US-08-363-240A-619	Sequence 619, App
14	0.8	17	1	US-09-471-669A-22	Sequence 22, Appl	c 238	12.4	0.7	15	1	US-08-585-664B-797	Sequence 797, App
13.8	0.8	17	1	US-07-701-935-3	Sequence 3, Appli	c 239	12.4	0.7	15	1	US-08-585-664B-798	Sequence 798, App
13.8	0.8	17	1	US-08-117-965-3	Sequence 3, Appli	c 240	12.4	0.7	15	1	US-08-585-664B-2099	Sequence 2099, Ap
13.8	0.8	17	1	US-08-373-124A-1749	Sequence 1749, Ap	c 241	12.4	0.7	15	1	US-08-585-664B-2295	Sequence 2295, Ap
13.8	0.8	17	1	US-08-287-075-10	Sequence 10, Appl	c 242	12.4	0.7	15	1	US-08-588-664B-2296	Sequence 2296, Ap
13.8	0.8	17	1	US-08-435-628-1749	Sequence 1749, Ap	c 243	12.4	0.7	15	1	US-08-550-120-13	Sequence 13, Appl
13.8	0.8	17	1	US-08-985-162-243	Sequence 243, App	c 244	12.4	0.7	15	1	US-09-269-519A-2	Sequence 2, Appli
13.8	0.8	17	1	US-08-584-040-3947	Sequence 3947, Ap	c 245	12.4	0.7	15	1	US-09-038-073-797	Sequence 797, App
13.8	0.8	17	1	US-08-584-040-4119	Sequence 4119, Ap	c 246	12.4	0.7	15	1	US-09-038-073-798	Sequence 798, App
13.8	0.8	17	1	US-08-584-040-5545	Sequence 5545, Ap	c 247	12.4	0.7	15	1	US-09-038-073-2099	Sequence 2099, Ap
13.8	0.8	17	1	US-08-584-040-5694	Sequence 5694, Ap	c 248	12.4	0.7	15	1	US-09-038-073-2295	Sequence 2295, Ap
13.8	0.8	17	1	US-08-679-645-765	Sequence 765, App	c 249	12.4	0.7	15	1	US-09-038-073-2296	Sequence 2296, Ap
13.8	0.8	17	1	US-09-371-772B-1714	Sequence 1714, Ap	c 250	12.4	0.7	15	1	US-09-081-646-167	Sequence 167, App
13.8	0.8	17	1	US-09-371-772B-1886	Sequence 1886, Ap	c 251	12.4	0.7	15	1	US-09-856-662-4	Sequence 4, Appli
13.8	0.8	17	1	US-09-371-772B-6345	Sequence 6345, Ap	c 252	12.4	0.7	15	1		



12.4	0.7	15	1	US-09-341-700A-196	Sequence 196, App
12.4	0.7	15	1	US-10-156-306B-7875	Sequence 7875, App
12.4	0.7	15	1	PCT-US93-12600-15	Sequence 15, App
12.4	0.7	29	1	US-08-513-974B-61	Sequence 61, App
12.4	0.7	29	1	US-08-776-971-32	Sequence 32, App
12.4	0.7	29	1	US-09-461-436B-61	Sequence 61, App
12.4	0.7	29	1	US-09-576-290-32	Sequence 32, App
12.4	0.7	29	1	US-09-716-147-32	Sequence 32, App
12.4	0.7	29	1	US-08-173-489C-232	Sequence 232, App
12.4	0.7	13	1	US-09-724-857-30	Sequence 30, App
12.4	0.7	13	1	US-08-608-584-8	Sequence 8, App
12.4	0.7	14	1	US-09-720-435A-38	Sequence 38, App
12.4	0.7	15	1	US-08-588-595-1	Sequence 1, App
12.4	0.7	15	1	US-09-180-437-143	Sequence 143, App
12.4	0.7	15	1	US-09-275-850-31	Sequence 31, App
12.4	0.7	15	1	US-09-081-646-49	Sequence 49, App
12.4	0.7	15	1	US-09-081-646-560	Sequence 560, App
12.4	0.7	15	1	US-09-015-188-6	Sequence 6, App
12.4	0.7	15	1	US-09-720-435A-39	Sequence 39, App
12.4	0.7	15	1	US-09-907-111-31	Sequence 31, App

# ALIGNMENTS

513-974B-133  
 Invention 133, Application US/08513974B  
 Inventor: 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Onitaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Onogi, Kazuhiko  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 133:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-513-974B-133  
 Query Match 1.7%; Score 30; DB 1; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 979 TTGGCCATCTGCTGCTGCTGCTTCCACATC 1008  
 DB 1 TTGGCCATCTGCTGCTGCTTCCACATC 30  
 RESULT 2  
 US-08-513-974B-132  
 Sequence 132, Application US/08513974B  
 Inventor: 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Onitaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Onogi, Kazuhiko  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995

R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
R10R APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
513-974B-132

Y Match 1.4%; Score 25.2; DB 1; Length 30;  
Local Similarity 90.0%; Pred. No. 12;  
Indels 3; Mismatches 0; Gaps 0;  
hes 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATCTGCTGGCTGCGCTTCACATC 1008  
|||||  
1 TTGGCATCTGCTGGCTGCGCTTCACATC 30

3  
396-196G-67915  
ence 67915, Application US/09396196G  
nt No. 6821724  
RAL INFORMATION:  
LICANT: Michael Miltmann  
LICANT: David Mack  
LICANT: David Lockhart  
LICANT: Affimetrix, Inc.  
LE OF INVENTION: Methods of Genetic Analysis  
E REFERENCE: 3101.1  
RENT FILING DATE: 1999-09-15  
OR APPLICATION NUMBER: 60/100,678  
BER OF SEQ ID NOS: 127806  
TWARE: FastSeq for Windows Version 4.0  
ID NO 67915

LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-67915

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1261 GTGACCGCCTGGAGACCACCATCT 1285  
|||||  
Db 1 GTGACCGCCTGGAGACCACCATCT 25

RESULT 4  
US-09-396-196G-67925  
Sequence 67925, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affimetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 67925  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-67925

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1123 TACTGCTGCTCATGACAGGTTCC 1147  
|||||  
Db 1 TACTGCTGCTCATGACAGGTTCC 25

RESULT 5  
US-08-442-134A-6/C  
Sequence 6, Application US/08442134A  
Patent No. 5596088  
GENERAL INFORMATION:  
APPLICANT: Boucher, Richard C.  
APPLICANT: Weisman, Gary A.  
APPLICANT: Turner, John T.  
APPLICANT: Harden, Thomas K.  
APPLICANT: Parr, Claude E.  
APPLICANT: Sullivan, Daniel M.  
APPLICANT: Erb, Laura  
APPLICANT: Lustig, Kevin D.  
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and  
TITLE OF INVENTION: Null Cells Expressing P2U Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5596088th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/442,134A  
 FILING DATE: 16-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sibley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5470-71A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 FORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 -442-134A-6

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
 Local Similarity 76.7%; Pred. No. 14;  
 Cons 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGGCTGCTTCACATC 1008  
 30 TTGGCCCTCGCTKCTGCTTCACATC 1

1 6  
 -444-581B-6/c  
 Invention 6, Application US/08444581B  
 Int No. 5607836

GENERAL INFORMATION:  
 APPLICANT: Boucher, Richard C.  
 APPLICANT: Weisman, Gary A.  
 APPLICANT: Turner, John T.  
 APPLICANT: Harden, Thomas K.  
 APPLICANT: Parr, Claude E.  
 APPLICANT: Sullivan, Daniel M.  
 APPLICANT: Lustig, Kevin D.  
 TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and  
 TITLE OF INVENTION: Null Cells Expressing P2U Receptors  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bell, Seltzer, Park & Gibson  
 STREET: Post Office Drawer 34009  
 CITY: Charlotte  
 STATE: No. 5607836th Carolina  
 COUNTRY: USA  
 ZIP: 28234

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/444,581B  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/442,134  
 FILING DATE: 16-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sibley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5470-71A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 FORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-444-581B-6

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
 Best Local Similarity 76.7%; Pred. No. 14;  
 Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGGCTGCTTCACATC 1008  
 Db 30 TTGGCCCTCGCTKCTGCTTCACATC 1

RESULT 7  
 US-08-446-088A-6/c  
 Invention 6, Application US/08446088A  
 Patent No. 5691156

GENERAL INFORMATION:  
 APPLICANT: Boucher, Richard C.  
 APPLICANT: Weisman, Gary A.  
 APPLICANT: Turner, John T.  
 APPLICANT: Harden, Thomas K.  
 APPLICANT: Parr, Claude E.  
 APPLICANT: Sullivan, Daniel M.  
 APPLICANT: Exb, Laura  
 APPLICANT: Lustig, Kevin D.  
 TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and  
 TITLE OF INVENTION: Null Cells Expressing P2U Receptors  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bell, Seltzer, Park & Gibson  
 STREET: Post Office Drawer 34009  
 CITY: Charlotte  
 STATE: No. 5691156th Carolina  
 COUNTRY: USA  
 ZIP: 28234

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,088A  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kenneth D. Sibley  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5470-71C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-446-088A-6

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
 Best Local Similarity 76.7%; Pred. No. 14;  
 Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGGCTGCTTCACATC 1008  
 Db 30 TTGGCCCTCGCTKCTGCTTCACATC 1

8  
513-974B-139  
ence 139, Application US/08513974B  
te No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hosoya, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohnaki, Tetsuya  
PLICANT: Fukusumi, Shoji  
PLICANT: Ohgi, Kazuhito  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
UMBER OF SEQUENCES: 380  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
OMPUTER READABLE FORM:  
EDIUM TYPE: Floppy disk  
OMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
ILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
ILING DATE: 10-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
ILING DATE: 19-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
ILING DATE: 16-MAR-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
ILING DATE: 20-JAN-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
ILING DATE: 28-DEC-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
ILING DATE: 02-NOV-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
ILING DATE: 11-AUG-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
ILING DATE: 11-AUG-1945  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
ILING DATE: 11-AUG-1994  
TTORENEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
ELCOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
ORMATION FOR SEQ ID NO: 139:  
SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-513-974B-139  
  
Query Match 1.4%; Score 24.2; DB 1; Length 30;  
Best local Similarity 89.7%; Pred. No. 17;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 979 TTGGCATCTGCTGCTGCCTTCCACAT 1007  
Db 1 TTGGCATCTGCTGCTGCCTTCCACAT 29  
  
RESULT 9  
US-08-513-974B-232  
Sequence 232, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohnaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhito  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
EDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
ILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
ILING DATE: 10-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
ILING DATE: 19-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
ILING DATE: 16-MAR-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
ILING DATE: 20-JAN-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
ILING DATE: 28-DEC-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
ILING DATE: 02-NOV-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
ILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1945  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 FORMATION FOR SEQ ID NO: 232:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 513-974B-232

cy Match 1.4%; Score 24; DB 1; Length 24;  
 Local Similarity 100.0%; Pred. No. 12;  
 ches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

979 TTGGCATTGCTGGCTGCGCTTC 1002  
 1 TTGGCATTGCTGGCTGCGCTTC 24

10  
 392-06532-6/C  
 jence 6; Application PC/TUS9206532  
 NERAL INFORMATION:  
 APPLICANT: Krause, James E.  
 TITLE OF INVENTION: Human Substance P Receptor  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Scott J. Meyer, Monsanto Co., ASD  
 STREET: 800 N. Lindbergh Blvd.  
 CITY: St. Louis  
 STATE: Missouri  
 COUNTRY: U.S.A.  
 ZIP: 63167

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06532  
 FILING DATE: 19920805  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyer, Scott J.  
 REGISTRATION NUMBER: 25,275  
 REFERENCE/DOCKET NUMBER: 07-24(776)A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314)694-3117  
 FORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ANTI-SENSE: YES  
 392-06532-6

cy Match 1.4%; Score 24; DB 1; Length 24;  
 Local Similarity 100.0%; Pred. No. 12;  
 ches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 TTCTCTCCATGCTGCTCTCTAG 1434  
 DB 24 TTCTCTCCATGCTGCTCTCTAG 1

RESULT 11  
 US-08-513-974B-61/C  
 Sequence 61, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ohtaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiro  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1945  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753

```

SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-08-776-971-32

Query Match 1.4% Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 17;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 979 TTGCACATCTGCTGGCTGCCCTTCACAT 1007
Db 29 TTCTSYNTCTGCTGGCTGCCCTTWTGMT 1

RESULT 13
US-09-461-436B-61/c
Sequence 61, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasunaki Ito
Ryo Fujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angell, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-033989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.

```

REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4444  
TELEFAX: 617-439-4170  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
FEATURE:  
OTHER INFORMATION: /note= N is inosine; S is G or C; W is A or T;  
R is A or G; K is G or T; Y is C or T."  
SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
-461-436B-61  
Query Match 1.4%; Score 24; DB 1; Length 29;  
c Local Similarity 72.4%; Pred. No. 17;  
ches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
979 TTCGCCATCTGCTGCTGCCCTTCCACAT 1007  
||||:|||||||||||||||||:  
29 TTCRYSNCTGCTGCTGCCCTTCCATCMT 1  
r 14  
-576-290-32/c  
Jence 32, Application US/09576290  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Habata, Yugo  
APPLICANT: Kawamata, Yuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Kitada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/576,290  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/776,971  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Conlin, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 47176  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-576-290-32  
Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 17;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
979 TTCGCCATCTGCTGCTGCCCTTCCACAT 1007  
||||:|||||||||||||||||:  
29 TTCRYSNCTGCTGCTGCCCTTCCATCMT 1  
Db  
Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 17;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
979 TTCGCCATCTGCTGCTGCCCTTCCACAT 1007  
||||:|||||||||||||||||:  
29 TTCRYSNCTGCTGCTGCCCTTCCATCMT 1  
RESULT 15  
US-09-716-147-32/c  
Jence 32, Application US/09716147  
Patent No. 6881545  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Habata, Yugo  
APPLICANT: Kawamata, Yuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Kitada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/716,147  
FILING DATE: 17-NOV-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,971B  
FILING DATE: 06-FEB-1997  
APPLICATION NUMBER: PCT/JP96/03821  
FILING DATE: 28-DEC-1996  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-AUG-1996  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Conlin, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 47176





ent No. 6821724  
 SERIAL INFORMATION:  
 APPLICANT: Michael Miltmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 FOR APPLICATION NUMBER: 60/100,678  
 FOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSeq for Windows Version 4.0  
 ID NO: 67926  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: mus musculus  
 -396-196G-67926

cy Match 1.3%; Score 23.4; DB 1; Length 25;  
 Local Similarity 96.0%; Pred. No. 15;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1147 CGCTGGGCTTCAGCATGCTTCC 1171  
 1 CGCTGGGCTTCAGCATGCTTTC 25

19  
 -701-935-4/c  
 ent No. 5336595  
 SERIAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/701,935  
 FILING DATE: 19910517  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 FORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 -701-935-4

cy Match 1.3%; Score 23; DB 1; Length 24;  
 Local Similarity 100.0%; Pred. No. 16;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACACCCCATCATCTACTG 1127  
 Db 24 ATGTACACCCCATCATCTACTG 2

RESULT 20  
 US-08-117-965-4/c  
 Sequence 4, Application US/08117965  
 Patent No. 5484886  
 GENERAL INFORMATION:  
 APPLICANT: Tung, Fong M.  
 APPLICANT: Cathrine, Strader D.  
 TITLE OF INVENTION: Human Neurokinin-1 Receptor  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/117,965  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 691,197  
 FILING DATE: 25-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18387  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 US-08-117-965-4

Query Match 1.3%; Score 23; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACACCCCATCATCTACTG 1127  
 Db 24 ATGTACACCCCATCATCTACTG 2

RESULT 21  
 US-07-701-935-5/c  
 Sequence 5, Application US/07701935  
 Patent No. 5336595  
 GENERAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000

CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
701-935-5  
Y Match 1.3%; Score 22.4; DB 1; Length 24;  
Local Similarity 95.8%; Pred. No. 19;  
has 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGCTCTACTG 1074  
24 AAGTTCATCCAGCAGGCTCTACTG 1

22  
117-965-5/c  
ence 5, Application US/08117965  
nt No. 5484886  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P. O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-5  
Query Match 1.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 19;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGCTCTACTG 1074  
DB 24 AAGTTCATCCAGCAGGCTCTACTG 1

RESULT 23  
US-08-513-974B-82  
Sequence 82, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 FORMATION FOR SEQ ID NO: 82:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 -513-974B-82

Query Match 1.3%; Score 22.2; DB 1; Length 27;  
 Local Similarity 88.9%; Pred. No. 26;  
 Cons 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 1 TTGGCATTCTGCTGGCTGCCCTTCAC 27

1 24  
 -513-974B-84  
 ence 84, Application US/08513974B  
 ant No. 6114139  
 ERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ontaka, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiro  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 516  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 84:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-513-974B-84

Query Match 1.3%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 26;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 Db 1 TTGGCATTCTGCTGGCTGCCCTTCAC 27

RESULT 25  
 US-09-396-196G-67908  
 Sequence 67908, Application US/09396196G  
 Patent No. 6821724  
 GENERAL INFORMATION:  
 APPLICANT: Michael Miltmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 67908  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: mus musculus  
 US-09-396-196G-67908

Query Match 1.2%; Score 22; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 24;

hes 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGTCTACC 1072  
|||||  
4 AAGTTATCCAGCAGGTCTACC 25

26  
396-196G-67912  
ence 67912, Application US/09396196G  
nt No. 6821724  
RAL INFORMATION:  
LICANT: Michael Miltmann  
LICANT: David Mack  
LICANT: David Lockhart  
LICANT: Affymetrix, Inc.  
LE OF INVENTION: Methods of Genetic Analysis  
E REFERENCE: 3101.1  
RENT APPLICATION NUMBER: US/09/396,196G  
RENT FILING DATE: 1999-09-15  
OR APPLICATION NUMBER: 60/100,678  
OR FILING DATE: 1998-09-17  
BER OF SEQ ID NOS: 127806  
TWARE: FastSeq for Windows Version 4.0  
ID NO 67912  
NGTH: 25  
PE: DNA  
GANISM: mus musculus  
396-196G-67912

Y March 1.2%; Score 21.8; DB 1; Length 25;  
Local Similarity 92.0%; Pred. No. 25;  
hes 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

907 TCTGACCGCTACCGAGCAGCAAGTCT 931  
|||||  
1 TCTGACCGCTACCGAGCAGCAAGTCT 25

27  
396-196G-67913  
ence 67913, Application US/09396196G  
nt No. 6821724  
RAL INFORMATION:  
LICANT: Michael Miltmann  
LICANT: David Mack  
LICANT: David Lockhart  
LICANT: Affymetrix, Inc.  
LE OF INVENTION: Methods of Genetic Analysis  
E REFERENCE: 3101.1  
RENT APPLICATION NUMBER: US/09/396,196G  
RENT FILING DATE: 1999-09-15  
OR APPLICATION NUMBER: 60/100,678  
OR FILING DATE: 1998-09-17  
BER OF SEQ ID NOS: 127806  
TWARE: FastSeq for Windows Version 4.0  
ID NO 67913  
NGTH: 25  
PE: DNA  
GANISM: mus musculus  
396-196G-67913

Y Match 1.2%; Score 21.8; DB 1; Length 25;  
Local Similarity 92.0%; Pred. No. 25;  
hes 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

913 CGTACCGAGCAGCAAGTCTCGCCA 937  
|||||  
1 CGTACCGAGCAGCAAGTCTCGCCA 25

Sequence 2, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Maeki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single



REFERENCE/DOCKET NUMBER: 47176  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
FORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
776-971-30

1.2%; Score 21.8; DB 1; Length 27;  
Local Similarity 74.1%; Pred. No. 30;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATCTGCTGAGTGCCTTCAC 1005  
|||:|||||:|||||:|||||:|||||:  
27 TTGGCMTCTGCTGAGTGCCTTCAC 1

31  
540-650B-8/c  
ence 8, Application US/08540650B  
nt No. 6399325  
ERAL INFORMATION:  
.APPLICANT: HINDMA, Shuji  
.APPLICANT: FUJII, Ryo  
.APPLICANT: FUKUSUMI, Shoji  
.APPLICANT: OHTAKI, Tetsuya  
.APPLICANT: HOSOYA, Masaki  
.APPLICANT: OHGI, Kazuhiro  
.APPLICANT: ONDA, Haruo  
TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF  
UMBER OF SEQUENCES: 17  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,650B  
ILING DATE: 11-OCT-1995  
CLASSIFICATION: 435  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 7-134412  
ILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 6-326610  
ILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-247599  
ILING DATE: 13-OCT-1994  
TTORENEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45901  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
FORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single

TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid  
MOLECULE TYPE: Synthetic DNA  
FEATURE: N is A, G, C, or T  
US-08-540-650B-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 30;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGAGTGCCTTCAC 1005  
|||:|||||:|||||:|||||:|||||:  
Db 27 TTGGCMTCTGCTGAGTGCCTTCAC 1

RESULT 32  
US-09-255-518C-6/c  
Sequence 6, Application US/09255518C  
Patent No. 6492324  
GENERAL INFORMATION:  
.APPLICANT: HINDMA, SHUJI  
.APPLICANT: TATEMOTO, KAZUHIKO  
.APPLICANT: HOSOYA, MASAKI  
.APPLICANT: HABATA, YUO  
.APPLICANT: FUJII, RYO  
.APPLICANT: KITADA, CHIEKO  
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE  
FILE REFERENCE: 48970(342)  
CURRENT APPLICATION NUMBER: US/09/255,518C  
CURRENT FILING DATE: 1999-02-22  
PRIOR APPLICATION NUMBER: PCT/JP98/05805  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 9-353955  
PRIOR FILING DATE: 1997-12-24  
PRIOR APPLICATION NUMBER: 10-032577  
PRIOR FILING DATE: 1998-02-16  
PRIOR APPLICATION NUMBER: 10-220853  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 10-271645  
PRIOR FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
NAME/KEY: modified base  
LOCATION: (1)..(27)  
OTHER INFORMATION: "n" may be a, t, c, g  
US-09-255-518C-6

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 30;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATCTGCTGAGTGCCTTCAC 1005  
|||:|||||:|||||:|||||:|||||:  
Db 27 TTGGCMTCTGCTGAGTGCCTTCAC 1

RESULT 33  
US-09-461-436B-2/c  
Sequence 2, Application US/09461436B  
Patent No. 6538107  
GENERAL INFORMATION:  
.APPLICANT: Shuji Hinuma  
Yasuki Ito  
Ryo Fujii  
TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof  
NUMBER OF SEQUENCES: 61



CORRESPONDENCE ADDRESS:

ADDRESSEE: Edwards & Angell, LLP  
STREET: 101 Federal Street  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/461,436B  
FILING DATE: 14-Dec-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513,974  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: 7-093989  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: 7-057186  
FILING DATE: 16-MAR-1995  
APPLICATION NUMBER: 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189272  
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, DAVID G.  
REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4170  
TELEFAX: 617-439-4444

SEQUENCE CHARACTERISTICS:

LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
FEATURE:  
OTHER INFORMATION: /note= N is A, G, C, or T; W is A or T;  
R is A or G; K is G or T."

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

-461-436B-2

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 30;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

979 TTGGCATTCTGCTGCTGCTTCCAC 1005  
|||:|||||:|||||:|||||:|||||:  
27 TTGGCATTCTGCTGCTGCTTCCAC 1

1 34  
-576-290-30/C

; Sequence 30, Application US/09576290

; Patent No. 6794491

; GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji  
APPLICANT: Habata, Yugo  
APPLICANT: Kawamata, Yuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Fukusumi, Shoji  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/576,290  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/776,971  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-DEC-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-MAR-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-AUG-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.  
REGISTRATION NUMBER: 27, 026  
REFERENCE/DOCKET NUMBER: 47176  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-09-576-290-30

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 30;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTCTGCTGCTGCTTCCAC 1005  
|||:|||||:|||||:|||||:|||||:  
Db 27 TTGGCATTCTGCTGCTGCTTCCAC 1

RESULT 35

US-09-716-147-30/C

; Sequence 30, Application US/09716147

; Patent No. 6881545



URGENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORIGINATOR FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
701-935-18

Y Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTGCA 976  
|||||  
1 TGATGATTGTCGTGTGCA 21

117-965-10/c  
ence 10, Application US/08117965  
nt No. 548486  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
URGENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORIGINATOR FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
117-965-10

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 TTGGCAGTATCTATCTCATG 579  
|||||  
DB 21 TTGGCAGTATCTATCTCATG 1

## RESULT 42

US-08-117-965-13/c  
Sequence 13, Application US/08117965  
Patent No. 548486  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORIGINATOR FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-13

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 836 TGCTGTGATTGCTATGCAT 856  
|||||  
DB 21 TGCTGTGATTGCTATGCAT 1

## RESULT 43

US-08-117-965-15/c  
Sequence 15, Application US/08117965  
Patent No. 548486  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.

REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-701-935-13

cy Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

836 TGCTGTGATTGGCTATGTCAT 856  
|||||  
21 TGCTGTGATTGGCTATGTCAT 1

38  
-701-935-15/c  
ence 15, Application US/07701935  
ant No. 5336595  
GENERAL INFORMATION:  
APPLICANT: Strader, C. D.  
APPLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-701-935-15

cy Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGATGCA 976  
|||||  
21 TGATGATTGTCGTGATGCA 1

RESULT 39  
US-07-701-935-17  
Sequence 17, Application US/07701935  
Patent No. 5336595  
GENERAL INFORMATION:  
APPLICANT: Strader, C. D.  
APPLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-07-701-935-17

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTCTGCCAGCGCA 944  
|||||  
Db 1 GCAAGTCTCTGCCAGCGCA 21

RESULT 40  
US-07-701-935-18  
Sequence 18, Application US/07701935  
Patent No. 5336595  
GENERAL INFORMATION:  
APPLICANT: Strader, C. D.  
APPLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-117-965-15

Query Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976  
|||||  
21 TGATGATTGTCGTGTCGCA 1

117-965-17  
ence 17, Application US/08117965  
ent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976  
|||||  
21 TGATGATTGTCGTGTCGCA 1

117-965-17  
ence 17, Application US/08117965  
ent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976  
|||||  
21 TGATGATTGTCGTGTCGCA 1

REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-17

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

924 GCAAGTCCTGCGCAAGCGCA 944  
|||||  
1 GCAAGTCCTGCGCAAGCGCA 21

RESULT 45  
US-08-117-965-18  
Sequence 18, Application US/08117965  
Patent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-18

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976  
|||||  
21 TGATGATTGTCGTGTCGCA 1

117-965-17  
ence 17, Application US/08117965  
ent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-18

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976  
|||||  
21 TGATGATTGTCGTGTCGCA 1

46  
117-965-22/c  
ence 22, Application US/08117965  
nt No. 548486  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESS: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
OMPUTER READABLE FORM:  
EDIUM TYPE: Floppy disk  
OMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TTOBNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
OMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
117-965-22  
Y Match 1.2%; Score 21; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 23;  
hes 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1567 AGGAAACATTCATCTTG 1587  
21 AGGAAACATTCATCTTG 1  
47  
513-974B-263  
ence 263, Application US/08513974B  
nt No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hosoya, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohtaki, Tetsuya  
PLICANT: Fukusumi, Shoji  
PLICANT: Ohgi, Kazuhito  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
UMBER OF SEQUENCES: 380  
ORRESPONDENCE ADDRESS:  
ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
EDIUM TYPE: Floppy disk  
OMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
ILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
ILING DATE: 10-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
ILING DATE: 19-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
ILING DATE: 16-MAR-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
ILING DATE: 20-JAN-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
ILING DATE: 28-DEC-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
ILING DATE: 02-NOV-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
ILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
ILING DATE: 11-AUG-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
ILING DATE: 11-AUG-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
ILING DATE: 11-AUG-1994  
TTOBNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
FORMATION FOR SEQ ID NO: 263:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
OLECULE TYPE: CDNA  
US-08-513-974B-263  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
979 TTGCGCATCTGCTGCTGCC 999  
1 TTGCGCATCTGCTGCTGCC 21  
RESULT 48  
US-08-513-974B-264  
; Sequence 264, Application US/08513974B

```

VENT NO. 6114139
VERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukushima, Shoji
APPLICANT: Ohgi, Kazuhito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
FORMATION FOR SEQ ID NO: 264:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

```

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```



STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
URGENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
701-935-6

Y Match 1.2%; Score 20.8; DB 1; Length 24;  
Local Similarity 91.7%; Pred. No. 32;  
hes 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGCTGACTG 1074  
|||||  
24 AAGTTCATCCAGCAGGCTGACTG 1

51  
117-965-6/c  
ence 6, Application US/08117965  
nt No. 5484886  
BRAL INFORMATION:  
PLICANT: Tung, Pong M.  
PLICANT: Cathline, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
URGENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
TTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-6

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 32;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGCTGACTG 1074  
|||||  
Db 24 AAGTTCATCCAGCAGGCTGACTG 1

RESULT 52  
US-08-513-974B-231  
Sequence 231, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhito  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/jp95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274

FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 FORMATION FOR SEQ ID NO: 231:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 513-974B-231

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
 Local Similarity 91.7%; Pred. No. 32;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGGCTGCCCTTC 1002  
 1 TTGGCCATCTGCTGGCTGCCCTAC 24

53  
 513-974B-233  
 Invention 233, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ontaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiro  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 233:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 513-974B-233

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 32;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

979 TTGGCCATCTGCTGGCTGCCCTTC 1002  
 1 TTGGCCATCTGCTGGCTGCCCTAC 24

54  
 US-08-513-974B-237  
 Invention 237, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ontaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiro  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513, 974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
RJOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
ORAMATION FOR SEQ ID NO: 237:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
OLBECUR TYPE: CDNA  
513-974B-237

Y Match 1.2%; Score 20.8; DB 1; Length 24;  
Local Similarity 91.7%; Pred. No. 32;  
hes 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

979 TTGCGCATCTGCTGCTGCCCTTC 1002  
|||||  
1 TTCACCCCTCTGCTGCTGCCCTTC 24

55  
396-196G-67919  
ence 67919, Application US/09396196G  
nt No. 6821724  
RAL INFORMATION:  
LICANT: Michael Miltmann  
LICANT: David Mack  
LICANT: David Lockhart  
LICANT: Affymetrix, Inc.  
LE OF INVENTION: Methods of Genetic Analysis  
E REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396, 196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100, 678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 67919  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-67919

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 35;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1382 ACTCGAAGACCATGACGAGAGCT 1405  
|||||  
Db 2 ACTCGAAGACCATGACGAGAGCT 25

RESULT 56  
US-08-513-974B-15/c  
Sequence 15, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513, 974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-226356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "synthetic DNA"  
 FEATURE: OTHER INFORMATION: N = inosine  
 -513-974B-15

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
 Local Similarity 70.8%; Pred. No. 34;  
 Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

979 TTGCGCATCTGCTGCTGCTTC 1002  
 ||:||||:||||:||||:||||:  
 24 TTYGCGNTSTGCTGCTGCTSCCWWC 1

57  
 -513-974B-230  
 Invention 230, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ohtaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhiko  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-226357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-226356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 230:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 -US-08-513-974B-230

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
 Best Local Similarity 70.8%; Pred. No. 34;  
 Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCTTC 1002  
 ||:||||:||||:||||:||||:  
 Db 1 TTYGCGNTSTGCTGCTGCTSCCWWC 24

RESULT 58  
 US-09-461-436B-15/c  
 Sequence 15, Application US/09461436B  
 Patent No. 6538107  
 GENERAL INFORMATION:  
 APPLICANT: Shuji Hinuma  
 APPLICANT: Yasuaki Ito  
 APPLICANT: Ryo Fujii  
 TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
 PRODUCTION, And Use Thereof  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Edwards & Angell, LLP  
 STREET: 101 Federal Street  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02209  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/461,436B  
FILING DATE: 14-Dec-1999  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/513,974  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: 7-093989  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: 7-057186  
FILING DATE: 16-MAR-1995  
APPLICATION NUMBER: 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CONLIN, DAVID G.  
REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4444  
TELEFAX: 617-439-4170  
FORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
FEATURE:  
OTHER INFORMATION: /note= N is inosine; W is A or T;  
S is G or C; K is G or T; R is A or G."  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
461-436B-15  
v Match 1.2%; Score 20.6; DB 1; Length 24;  
Local Similarity 70.8%; Pred. No. 34;  
hes 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
979 TTGCGCATCTGCTGGCTGCCTTC 1002  
|||||:|||||:|||||:  
24 TTGCGCNTSTGCTGMTSCCWC 1  
59  
513-974B-235  
ence 235, Application US/08513974B  
nt No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hosoya, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohtaki, Tetsuya  
PLICANT: Fukusumi, Shoji

APPLICANT: Ohgi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
FORMATION FOR SEQ ID NO: 235:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-513-974B-235  
Query Match 1.2%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 33;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCATCTGCTGCTGCCCT 1000  
 |||||  
 1 TTGGCATCTGCTGCTGCCCT 22

60  
 -396-196G-67918  
 ence 67918, Application US/09396196G  
 nt No. 6821724  
 ERAL INFORMATION:  
 PLICANT: Michael Miltmann  
 PLICANT: David Mack  
 PLICANT: David Lockhart  
 PLICANT: Affymetrix, Inc.  
 FILE OF INVENTION: Methods of Genetic Analysis  
 JE REFERENCE: 3101.1  
 RENT APPLICATION NUMBER: US/09/396,196G  
 RENT FILING DATE: 1999-09-15  
 OR APPLICATION NUMBER: 60/100,678  
 OR FILING DATE: 1998-09-17  
 ABER OF SEQ ID NOS: 127806  
 TWARE: FastSeq for Windows Version 4.0  
 ID NO 67918  
 LENGTH: 25  
 YPE: DNA  
 ORGANISM: mus musculus  
 -396-196G-67918

Match 1.1%; Score 20.2; DB 1; Length 25;  
 Local Similarity 88.0%; Pred. No. 42;  
 hes 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1375 CGAAGTACTCCAGACCATGACAG 1399  
 |||||  
 1 CGAAGCACTCGAAGCATGACAG 25

61  
 -396-196G-67927  
 ence 67927, Application US/09396196G  
 nt No. 6821724  
 ERAL INFORMATION:  
 PLICANT: Michael Miltmann  
 PLICANT: David Mack  
 PLICANT: David Lockhart  
 PLICANT: Affymetrix, Inc.  
 FILE OF INVENTION: Methods of Genetic Analysis  
 JE REFERENCE: 3101.1  
 RENT APPLICATION NUMBER: US/09/396,196G  
 RENT FILING DATE: 1999-09-15  
 OR APPLICATION NUMBER: 60/100,678  
 OR FILING DATE: 1998-09-17  
 ABER OF SEQ ID NOS: 127806  
 TWARE: FastSeq for Windows Version 4.0  
 ID NO 67927  
 LENGTH: 25  
 YPE: DNA  
 ORGANISM: mus musculus  
 -396-196G-67927

Match 1.1%; Score 20.2; DB 1; Length 25;  
 Local Similarity 88.0%; Pred. No. 42;  
 hes 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1165 GCCTTCGGTGTGCCCCCTTCATCA 1189  
 |||||  
 1 GCCTTCGGTGTGCCCCCTTCATCA 25

62  
 -396-196G-67930  
 ence 67930, Application US/09396196G  
 nt No. 6821724

GENERAL INFORMATION:  
 APPLICANT: Michael Miltmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 67930  
 LENGTH: 25  
 YPE: DNA  
 ORGANISM: mus musculus  
 US-09-396-196G-67930

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 42;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1231 TATCTCCAGACCCGCGAGTGTG 1255  
 |||||  
 Db 1 TACTCCAGACCCGCGAGTGTG 25

RESULT 63  
 US-09-396-196G-67931  
 Sequence 67931, Application US/09396196G  
 Patent No. 6821724  
 GENERAL INFORMATION:  
 APPLICANT: Michael Miltmann  
 APPLICANT: David Mack  
 APPLICANT: David Lockhart  
 APPLICANT: Affymetrix, Inc.  
 TITLE OF INVENTION: Methods of Genetic Analysis  
 FILE REFERENCE: 3101.1  
 CURRENT APPLICATION NUMBER: US/09/396,196G  
 CURRENT FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: 60/100,678  
 PRIOR FILING DATE: 1998-09-17  
 NUMBER OF SEQ ID NOS: 127806  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 67931  
 LENGTH: 25  
 YPE: DNA  
 ORGANISM: mus musculus  
 US-09-396-196G-67931

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 42;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1237 CAGACCCAGGCGAGTGTACAAAG 1261  
 |||||  
 Db 1 CAGACCCAGGCGAGTGTACAAAG 25

RESULT 64  
 US-07-701-935-11/C  
 Sequence 11, Application US/07701935  
 Patent No. 5336595  
 GENERAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P.O. Box 2000

CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/07/701,935  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELEPHONE: (908) 594-4720  
TELEFAX: (908) 594-5315  
ORAMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
701-935-11

y Match 1.1%; Score 20; DB 1; Length 20;  
Local Similarity 100.0%; Pred. No. 29;  
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

601 TACATGCCATCATCATCC 620  
20 TACATGCCATCATCATCC 1

701-935-12/c  
ence 12, Application US/07701935  
nt No. 5336595  
ERAL INFORMATION:  
PLICANT: Strader, C. D.  
PLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELEPHONE: (908) 594-4720  
TELEFAX: (908) 594-5315  
ORAMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-07-701-935-12

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 637 TCAGCCACAGCCCAAGT 656  
Db 20 TCAGCCACAGCCCAAGT 1

RESULT 66  
US-07-701-935-14/c  
Sequence 14, Application US/07701935  
Patent No. 5336595  
GENERAL INFORMATION:  
APPLICANT: Strader, C. D.  
APPLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-07-701-935-14

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 GTAGTGGAAATCAGCTATG 881  
Db 20 GTAGTGGAAATCAGCTATG 1

RESULT 67  
US-07-701-935-16/c  
Sequence 16, Application US/07701935  
Patent No. 5336595  
GENERAL INFORMATION:  
APPLICANT: Strader, C. D.



APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P. O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/701,935  
 FILING DATE: 19910517  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 -701-935-16  
 Local Similarity 1.1%; Score 20; DB 1; Length 20;  
 Cons 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1012 TTCCTCTGCGCTTACATCAA 1031  
 |||||  
 20 TTCCTCTGCGCTTACATCAA 1  
 1 68  
 -701-935-19  
 ence 19, Application US/07701935  
 ent No. 5336595  
 VERAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P. O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/701,935  
 FILING DATE: 19910517  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.

REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 US-07-701-935-19  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1000 TTCACATCTTCTCTCTCT 1019  
 |||||  
 Db 1 TTCACATCTTCTCTCTCT 20  
 RESULT 69  
 US-07-701-935-20  
 Sequence 20, Application US/07701935  
 Patent No. 5336595  
 GENERAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 TITLE OF INVENTION: Receptor Short Form  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P. O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/701,935  
 FILING DATE: 19910517  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 US-07-701-935-20  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1023 CTACATCAACCCGATCTCT 1042  
 |||||  
 Db 1 CTACATCAACCCGATCTCT 20

70  
117-965-11/c  
ence 11, Application US/08117965  
nt No. 548486  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TTORENEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
117-965-11  
Y Match 1.1%; Score 20; DB 1; Length 20;  
Local Similarity 100.0%; Pred. No. 29;  
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
601 TACATGGCCATCATACATCC 620  
|||||  
20 TACATGGCCATCATACATCC 1  
71  
117-965-12/c  
ence 12, Application US/08117965  
nt No. 548486  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TTORENEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
US-08-117-965-12  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 637 TCAGCCACAGCCACCAAGT 656  
|||||  
Db 20 TCAGCCACAGCCACCAAGT 1  
RESULT 72  
US-08-117-965-14/c  
Sequence 14, Application US/08117965  
Patent No. 548486  
GENERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TTORENEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-117-965-14

Query Match 1.1%; Score 20; DB 1; Length 20;  
Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

862 GTACGTGGATTCACACTATG 881  
|||||  
20 GTAGTGGATTCACACTATG 1

117-965-16/C  
ence 16, Application US/08117965  
ent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
-117-965-16

Query Match 1.1%; Score 20; DB 1; Length 20;  
Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1012 TTCCTCTGCGCTACATCAA 1031  
|||||  
20 TTCCTCTGCGCTACATCAA 1

117-965-19  
ence 19, Application US/08117965  
ent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.

APPLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-19

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCT 1019  
|||||  
Db 1 TTCACATCTTCTCTCT 20

RESULT 75  
US-08-117-965-20  
Sequence 20, Application US/08117965  
Patent No. 5484886  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
ELECTRONIC/DOCKET NUMBER: 18387  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORAMION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
117-965-20

Y Match 1.1%; Score 20; DB 1; Length 20;  
Local Similarity 100.0%; Pred. No. 29;  
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1023 CTACATCAACCCAGACTTCT 1042  
|||||  
1 CTACATCAACCCAGACTTCT 20

76  
701-935-9/c  
since 9, Application US/07701935  
nt No. 5336595  
ERAL INFORMATION:  
PLICANT: Strader, C. D.  
PLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
ELECTRONIC/DOCKET NUMBER:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORAMION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
701-935-9

Y Match 1.1%; Score 20; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 32;  
hes 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAAGTTCACAACTTCTT 542  
|||||  
Db 21 TGCAAGTTCACAACTTCTT 2

RESULT 77  
US-08-117-965-9/c  
Sequence 9, Application US/08117965  
Patent No. 548486  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
APPLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC/DOCKET NUMBER:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-9

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAAGTTCACAACTTCTT 542  
|||||  
Db 21 TGCAAGTTCACAACTTCTT 2

RESULT 78  
US-08-513-974B-240  
Sequence 240, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
513-974B-240

979 TTGGCCTGCTGCTGCTGCTT 1001  
|||||  
1 TTGGCCTGCTGCTGCTGCTT 23

979 Match 1.1%; Score 19.8; DB 1; Length 23;  
: Local Similarity 91.3%; Pred. No. 40;  
:hes 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 79  
US-08-513-974B-257  
; Sequence 257, Application US/08513974B  
; Patent No. 6114139  
; GENERAL INFORMATION:  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Hosoya, Masaki  
; APPLICANT: Fujii, Ryo  
; APPLICANT: Ohtaki, Tetsuya  
; APPLICANT: Fukushima, Shoji  
; APPLICANT: Ohgi, Kazuhiro  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
; NUMBER OF SEQUENCES: 380  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,974B  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP95/01599  
; FILING DATE: 10-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-093989  
; FILING DATE: 19-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-057186  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-270017  
; FILING DATE: 02-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236357  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-236356  
; FILING DATE: 30-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189274  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189273  
; FILING DATE: 11-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-189272  
; FILING DATE: 11-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Resnick, David S.  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 45753  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 257:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
VECTUE TYPE: CDNA  
513-974B-257

Y Match 1.1%; Score 19.4; DB 1; Length 21;  
Local Similarity 95.2%; Pred. No. 38;  
hes 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCATTCTGCTGCTGCC 999

1 TTGGCATTCTGCTGCTGCC 21

80  
125-012-7  
ence 7, Application US/08125012  
nt No. 5593972

ERAL INFORMATION:  
PLICANT: Weiner, David B.  
PLICANT: Williams, William V.  
PLICANT: Wang, Bin  
PLICANT: Coney, Leslie R.  
TITLE OF INVENTION: Genetic Immunization  
UMBER OF SEQUENCES: 34  
ORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5593972ris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103

OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,012  
ILING DATE:

CLASSIFICATION: 435  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/029,336  
ILING DATE: 11-MAR-1993

NAME:  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008,342  
ILING DATE: 26-JAN-1993

NAME:  
TORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0013  
ELCOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEPHONE: 215-568-3429  
ORMATION FOR SEQ ID NO: 7:  
BOUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECUE TYPE: DNA  
125-012-7

Y Match 1.1%; Score 19.2; DB 1; Length 24;  
Local Similarity 87.5%; Pred. No. 52;  
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAGATCCCGGAGACTCCTC 908

1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 81  
US-08-221-579A-7  
Sequence 7, Application US/08221579A  
Patent No. 5739118

GENERAL INFORMATION:  
APPLICANT: Carrano, Richard A.  
TITLE OF INVENTION: Compositions and Methods for  
TITLE OF INVENTION: Delivery of Genetic Material  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
ADDRESSEE: and No. 573918ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 720 Kb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,579A  
ILING DATE: 01-APR-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

ILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0186  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEPHONE: 215-568-3429  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-221-579A-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 52;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCCTC 908  
DB 1 CAGTGATATCCCGGAGACTCCTC 24

RESULT 82  
US-08-783-818-7  
Sequence 7, Application US/08783818  
Patent No. 5817637  
GENERAL INFORMATION:  
APPLICANT: Weiner, David B.  
APPLICANT: Williams, William V.  
APPLICANT: Wang, Bin  
APPLICANT: Coney, Leslie R.  
TITLE OF INVENTION: Genetic Immunization  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5817637ris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/783,818  
FILING DATE: 13-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/125,012  
FILING DATE: 21-SEP-1993  
APPLICATION NUMBER: 08/029,336  
FILING DATE: 11-MAR-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008,342  
FILING DATE: 26-JAN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3429  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
-783-818-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Local Similarity 87.5%; Pred. No. 52;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAGATCCCGGAGACTCTC 908  
|||||  
1 CAGTGATATCCCGGAGACTCTC 24

83  
-453-349-7  
ence 7, Application US/08453349  
nt No. 5830876  
ERAL INFORMATION:  
PLICANT: Weiner, David B.  
PLICANT: Williams, William V.  
PLICANT: Wang, Bin  
TTL OF INVENTION: Genetic Immunization  
NUMBER OF SEQUENCES: 34  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5830876ris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,349  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/029,336  
FILING DATE: March 11, 1993

APPLICATION NUMBER: 08/008,342  
FILING DATE: January 26, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3429  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-453-349-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 52;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908  
|||||  
Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 84  
US-08-704-701-7  
Sequence 7, Application US/08704701  
Patent No. 5962428  
GENERAL INFORMATION:  
APPLICANT: Carrano, Richard A.  
TITLE OF INVENTION: Compositions and Methods for  
TITLE OF INVENTION: Delivery of Genetic Material  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
STREET: and No. 5962428ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 720 Kb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,701  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,579  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0186  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-701-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Local Similarity 87.5%; Pred. No. 52;  
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAGATCCCGGAGACTCTC 908

|||||  
1 CAGTGATATCCCGGAGACTCTC 24

85

979-385B-7

ence 7, Application US/08979385B  
nt No. 5981505

ERAL INFORMATION:

PLICANT: Weiner, David B.  
PLICANT: Williams, William V.

PLE OF INVENTION: Compositions and Methods for Delivery of

NUMBER OF SEQUENCES: 52

ORRESPONDENCE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5981505ris  
STREET: One Liberty Place 46th Floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF

URRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,385B

FILING DATE: 26-NOV-1997

CLASSIFICATION: 514

RIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/495,684

FILING DATE: 28-SEP-1995

RIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/00899

FILING DATE: 26-JAN-1994

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/125,012

FILING DATE: 21-SEP-1993

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/124,962

FILING DATE: 21-SEP-1993

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/093,235

FILING DATE: 15-JUL-1993

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/029,336

FILING DATE: 11-MAR-1993

RIOR APPLICATION DATA:

APPLICATION NUMBER: 08/008,342

FILING DATE: 26-JAN-1993

ITORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: UPAW-0253

ELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3429

ORMATION FOR SEQ ID NO: 7:

QUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

OLECULE TYPE: DNA

979-385B-7

Y Match 1.1%; Score 19.2; DB 1; Length 24;

Local Similarity 87.5%; Pred. No. 52;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908

|||||  
Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 86

US-09-321-461-7

; Sequence 7, Application US/09321461

; Patent No. 6197755

GENERAL INFORMATION:

APPLICANT: Carrano, Richard A.

PLE OF INVENTION: Compositions and Methods for

Delivery of Genetic Material

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz  
and No. 6197755ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 KB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/321,461

FILING DATE: 27-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,701

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: APOL-0186

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-321-461-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 52;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 885 CAGTGAGATCCCGGAGACTCTC 908

|||||  
Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 87

US-09-011-922A-13/C

; Sequence 13, Application US/09011922A

; Patent No. 6320022

GENERAL INFORMATION:

APPLICANT: Cuttitta, Frank; Martinez,

APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward

APPLICANT: U.; Hook, William; Walsh, Thomas; Grey,

APPLICANT: Karen; Macri, Charles

PLE OF INVENTION: Functional Role of

ADRENOMEDULLIN (AM) and the Gene-Related

PRODUCT (PAMP) in Human Pathology and



TITLE OF INVENTION: Physiology  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS WORD 97  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,922A  
FILING DATE: 17-Feb-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/60/002,514  
FILING DATE: 18-Aug-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/60/002,936  
FILING DATE: 30-Aug-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/60/013,172  
FILING DATE: 12-Mar-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/13286  
FILING DATE: 16-Aug-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Leslie A. Serunian  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-4202US3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 758-4800  
FORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
HYPOTHETICAL: No  
ANTI-SENSE: Yes  
FEATURE:  
NAME/KEY: AM-R(788-811)  
OTHER INFORMATION: AM-R antisense probe  
-011-922A-13  
Match 1.1%; Score 19.2; DB 1; Length 24;  
Local Similarity 87.5%; Pred. No. 52;  
Indels 3; Mismatches 0; Gaps 0;  
Conservative 0; Indels 0; Gaps 0;  
980 TCGCATCTGCTGCTGCTGCTTCC 1003  
24 TTGTGATATCCCGGAGACTCTC 24  
1 88  
-880-576-7  
ence 7, Application US/08880576  
nt No. 6468982  
GENERAL INFORMATION:  
APPLICANT: Weiner, David B.  
APPLICANT: Williams, William V.  
APPLICANT: Wang, Bin  
APPLICANT: Coney, Leslie R.  
TITLE OF INVENTION: Genetic Immunization  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6468982ris  
STREET: One Liberty Place 46th Floor

CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,576  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/125,012  
FILING DATE: 21-SEP-1993  
APPLICATION NUMBER: 08/029,336  
FILING DATE: 11-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008,342  
FILING DATE: 26-JAN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: APOL-0013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3429  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-880-576-7

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 52;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 885 CAGTGAGATCCCGGAGACTCTC 908  
Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 89  
US-09-359-975-7  
Sequence 7, Application US/09359975  
Patent No. 7001759  
GENERAL INFORMATION:  
APPLICANT: Weiner, David B.  
APPLICANT: Williams, William V.  
APPLICANT: Wang, Bin  
TITLE OF INVENTION: Compositions and Methods for Delivery of  
Genetic Material  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 7001759ris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 mb-MD/JAF  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/359,975  
FILING DATE: 23-JUN-1999

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,385B  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 08/495,684  
FILING DATE: 28-SEP-1995  
APPLICATION NUMBER: PCT/US94/00899  
FILING DATE: 26-JUN-1994  
APPLICATION NUMBER: 08/125,012  
FILING DATE: 21-SEP-1993  
APPLICATION NUMBER: 08/124,962  
FILING DATE: 21-SEP-1993  
APPLICATION NUMBER: 08/093,235  
FILING DATE: 15-JUL-1993  
APPLICATION NUMBER: 08/029,336  
FILING DATE: 11-MAR-1993  
APPLICATION NUMBER: 08/008,342  
FILING DATE: 26-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPAP-0253  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3429  
FORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
359-975-7  
Y Match 1.1%; Score 19.2; DB 1; Length 24;  
Local Similarity 87.5%; Pred. No. 52;  
hes 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
885 CAGTGAGATCCCCGGGAGACTCTC 908  
|||||  
1 CAGTATATCCCGGAGACTCTC 24  
701-935-25  
90  
ence 25, Application US/07701935  
nt No. 5336595  
ERAL INFORMATION:  
PLICANT: Strader, C. D.  
PLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor short form  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
TTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147

REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-07-701-935-25  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 GTGTACGATGATGAGGCTT 194  
|||||  
Db 1 GTGTACGATGATGAGGCTT 19  
RESULT 91  
US-08-117-965-23/C  
Sequence 23, Application US/08117965  
Patent No. 548486  
GENERAL INFORMATION:  
APPLICANT: Tung, Fong M.  
APPLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
US-08-117-965-23  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1548 AAAAGGTCAGTATGCGTT 1566  
|||||  
Db 19 AAAAGGTCAGTATGCGTT 1

92  
117-965-25  
ence 25, Application US/08117965  
nt No. 548486  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
PLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
NUMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
FORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
117-965-25

Match 1.1%; Score 19; DB 1; Length 19;  
Local Similarity 100.0%; Pred. No. 35;  
hes 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

176 GTGTACAGATAGTGGCTT 194  
|||||  
1 GTGTACAGATAGTGGCTT 19

93  
513-974B-223  
ence 223, Application US/08513974B  
nt No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hongo, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohnaki, Tetsuya  
PLICANT: Fukusumi, Shoji  
PLICANT: Ohgi, Kazuhito  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
FORMATION FOR SEQ ID NO: 223:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-513-974B-223

Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 587 TGGCCTTGATGATGATGCG 608  
|||||  
Db 1 TGGCCTTGATGATGATGCG 22

RESULT 94  
US-08-287-075-9  
Sequence 9, Application US/08287075

nt No. 5656462  
BRAL INFORMATION:  
APPLICANT: Keller, Cylla  
APPLICANT: Mitsuhashi, Masato  
APPLICANT: Akitaya, Tatsuo  
TITLE OF INVENTION: POLYNUCLEOTIDE IMMOBILIZED SUPPORT  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KNOBBE, MARTENS, OLSON, AND BEAR  
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
CITY: NEWPORT BEACH  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/287,075  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/827,975  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: HITACHI.002A  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
CREATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: TAC-S OLIGONUCLEOTIDE PRIMER  
287-075-9

Y Match 1.0%; Score 18.4; DB 1; Length 20;  
Local Similarity 95.0%; Pred. No. 47;  
hes 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

562 GCCAGTATCTACTCCATGAC 581  
1 GCCAGCATCTACTCCATGAC 20

95  
915-966C-12  
ence 12, Application US/07915966C  
nt No. 5668006  
BRAL INFORMATION:  
APPLICANT: Hadcock Dr., John R.  
APPLICANT: Ozenberger Dr., Bradley A.  
APPLICANT: Pausch Dr., Mark H.  
TITLE OF INVENTION: Receptor Identification Method  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07054  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/915,966C  
FILING DATE: 17-JUL-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthews, Gale M.  
REGISTRATION NUMBER: 32,269  
REFERENCE/DOCKET NUMBER: 31,829-00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-4117  
TELEFAX: 201-683-2134  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Synthetic  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 16  
PUBLICATION INFORMATION:  
AUTHORS: Hadcock Dr., John R.  
AUTHORS: Dr. Ozenberger, Bradley A.  
AUTHORS: Dr. Pausch, Mark H.  
TITLE: Receptor Identification Method  
DATE: 17-JUL-1992  
US-07-915-966C-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 50;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGGCAGTCTGCTGCTGCC 998  
Db 1 TTGGCAGTCTGCTGCTGCC 20

RESULT 96  
US-08-771-182-12  
Sequence 12, Application US/08771182  
Patent No. 5929209  
GENERAL INFORMATION:  
APPLICANT: Hadcock Dr., John R.  
APPLICANT: Ozenberger Dr., Bradley A.  
APPLICANT: Pausch Dr., Mark H.  
TITLE OF INVENTION: Receptor Identification Method  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/771,182  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Matchewe, Gale F.  
 REGISTRATION NUMBER: 32,269  
 REFERENCE/DOCKET NUMBER: 31,829-D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-683-2134  
 TELEFAX: 201-683-4117  
 FORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Synthetic  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: 16  
 PUBLICATION INFORMATION:  
 AUTHORS: Hadcock Dr., John R.  
 AUTHORS: Dr. Ozenberger, Bradley A.  
 AUTHORS: Dr. Pausch, Mark H.  
 TITLE: Receptor Identification Method  
 DATE: 20-DEC-1996  
 -771-182-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
 : Local Similarity 85.0%; Pred. No. 50;  
 : Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

979 TTGGCATCTGCTGCTGCC 998  
 ||:|||||||||  
 1 TTGYCATCTGCTGANTGCC 20

-853-194-12  
 ence 12, Application US/08853194  
 ent No. 6077666  
 GENERAL INFORMATION:  
 APPLICANT: Hadcock Dr., John R.  
 APPLICANT: Ozenberger Dr., Bradley A.  
 APPLICANT: Pausch Dr., Mark H.  
 TITLE OF INVENTION: Receptor Identification Method  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Cyanamid Company  
 STREET: One Cyanamid Plaza  
 CITY: Wayne  
 STATE: NJ  
 COUNTRY: United States of America  
 ZIP: 06904-0060  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/853,194  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/915,966  
 FILING DATE: 17-JUL-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Tsevdos Dr., Estelle J.  
 REGISTRATION NUMBER: 31,145  
 REFERENCE/DOCKET NUMBER: 31829-00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 203-321-2361  
 TELEFAX: 203-321-2971

TELEX: 710-474-4059  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Synthetic  
 FEATURE:  
 NAME/KEY: modified\_base  
 LOCATION: 16  
 OTHER INFORMATION: /mod\_base=1  
 PUBLICATION INFORMATION:  
 AUTHORS: Hadcock Dr., John R.  
 AUTHORS: Dr. Ozenberger, Bradley A.  
 AUTHORS: Dr. Pausch, Mark  
 TITLE: Receptor Identification Method  
 DATE: 17-JUL-1992  
 US-08-853-194-12

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 50;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGCTGCC 998  
 ||:|||||||||  
 Db 1 TTGYCATCTGCTGANTGCC 20

RESULT 98  
 US-07-701-935-21  
 Sequence 21, Application US/07701935  
 Patent No. 5336595  
 GENERAL INFORMATION:  
 APPLICANT: Strader, C. D.  
 APPLICANT: Fong, T. M.  
 TITLE OF INVENTION: Method of Using Human Neurokinin-1  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P. O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: US  
 ZIP: 07065-0907  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/701,935  
 FILING DATE: 19910517  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholson, William H.  
 REGISTRATION NUMBER: 25,147  
 REFERENCE/DOCKET NUMBER: 18409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-5315  
 TELEFAX: (908) 594-4720  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE:

701-935-21  
Y March 1.0%; Score 18; DB 1; Length 18;  
Local Similarity 100.0%; Pred. No. 43;  
hes 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1038 TCTCTACTGAAGAAGTT 1055  
|||||  
1 TCTCTACTGAAGAAGTT 18  
99  
117-965-21  
ence 21, Application US/08117965  
nt No. 548486  
ERAL INFORMATION:  
PPICANT: Tung, Fong M.  
PPLICANT: Cathrine, Strader D.  
TITLE OF INVENTION: Human Neutrokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TJORNERY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
RMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
117-965-21  
Y Match 1.0%; Score 18; DB 1; Length 18;  
Local Similarity 100.0%; Pred. No. 43;  
hes 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1038 TCTCTACTGAAGAAGTT 1055  
|||||  
1 TCTCTACTGAAGAAGTT 18  
100  
543-679A-1372/C  
ence 1372, Application US/09543679A  
nt No. 7034007  
ERAL INFORMATION:  
PPICANT: NYCE, Jonathan W.  
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
COMPOSITIONS, KIT & METHOD FOR TREATMENT  
OF AIRWAY DISORDERS ASSOCIATED WITH  
BRONCHOCONSTRICITION, LUNG INFLAMMATION,  
NUMBER OF SEQUENCES: 3111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIDEMISIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: NJ  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-R  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: N/A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/543,679A  
ILING DATE: 13-APR-2000  
CLASSIFICATION: UNKNOWN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/127,958  
ILING DATE: 1998-08-03  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-0067191b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <unknown>  
INFORMATION FOR SEQ ID NO: 1372:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1372:  
US-09-543-679A-1372  
Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
638 CAGCCACAGCCACCAAG 655  
|||||  
Db 18 CAGCCACAGCCACCAAG 1  
RESULT 101  
US-08-513-974B-256  
Sequence 256, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukushima, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
NUMBER OF SEQUENCES: 380  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 256:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
513-974B-256

25 Match 1.0%; Score 17.8; DB 1; Length 21;
Local Similarity 90.5%; Pred. No. 62;
Indels 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

979 TTCGCCATCTGCTGCGTCC 999
|||||
1 TTCACCCCTGCTGCGTCC 21

```

```

1  TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
2  NUMBER OF INVENTION:  PRODUCTION, AND USE THEREOF
3  NUMBER OF SEQUENCES:  380
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
6  STREET:  130 Water Street
7  City:  Boston
8  STATE:  MA
9  COUNTRY:  USA
10 ZIP:  02109
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Floppy disk
14 OPERATING SYSTEM:  IBM PC compatible
15 SOFTWARE:  PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/513,974B
18 FILING DATE:  14-SEP-1995
19 CLASSIFICATION:  536
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:  PCT/JP95/01599
23 FILING DATE:  10-AUG-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  JP 7-093989
26 FILING DATE:  19-AUG-1995
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER:  JP 7-057186
29 FILING DATE:  16-MAR-1995
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER:  JP 7-007177
32 FILING DATE:  20-JAN-1995
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER:  JP 6-326611
35 FILING DATE:  28-DEC-1994
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER:  JP 6-270017
38 FILING DATE:  02-NOV-1994
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER:  JP 6-236357
41 FILING DATE:  30-SEP-1994
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER:  JP 6-236356
44 FILING DATE:  30-SEP-1994
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER:  JP 6-189274
47 FILING DATE:  11-AUG-1994
48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER:  JP 6-189273
50 FILING DATE:  11-AUG-1994
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER:  JP 6-189272
53 FILING DATE:  11-AUG-1994
54 ATTORNEY/AGENT INFORMATION:
55 NAME:  Reenick, David S.
56 REGISTRATION NUMBER:  34,235
57 REFERENCE/DOCKET NUMBER:  45753
58 TELECOMMUNICATION INFORMATION:
59 TELEPHONE:  617-523-3400
60 TELEFAX:  617-523-6440
61 INFORMATION FOR SEQ ID NO:  267:
62 SEQUENCE CHARACTERISTICS:
63 LENGTH:  21 base pairs
64 TYPE:  nucleic acid
65 STRANDEDNESS:  double
66 TOPOLOGY:  linear
67 MOLECULE TYPE:  cDNA
68
69 US-08-513-974B-267
70
71 Query Match 1.0%; Score 17.8; DB 1; Length 21;
72 Best Local Similarity 90.5%; Pred. No. 62;
73 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

1 TTTCATCTCTGCTGCTGCC 21

103  
513-974B-269  
ence 269, Application US/08513974B  
nt No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hosoya, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohtaki, Tetsuya  
PLICANT: Fukusumi, Shoji  
PLICANT: Ohgi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
UMBER OF SEQUENCES: 380  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
TORN/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 269:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-513-974B-269

Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 62;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCC 999  
Db 1 TTTCCTCTGCTGCTGCC 21

RESULT 104  
US-08-513-974B-270  
Sequence 270, Application US/08513974B  
Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1945  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 270:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 513-974B-270  
 Match 1.0%; Score 17.8; DB 1; Length 21;  
 Local Similarity 90.5%; Pred. No. 62;  
 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 979 TTGCGCATCTGCTGCTGCC 999  
 1 TTGATCATCTGCTGCTGCC 21  
 105  
 974-409C-5  
 ence 5, Application US/07974409C  
 ent No. 6300058  
 VERAL INFORMATION:  
 APPLICANT: Akitaya, Tatsu  
 APPLICANT: Mitsuhashi, Masato  
 APPLICANT: Cooper, Allan  
 TITLE OF INVENTION: METHOD AND REAGENT  
 TITLE OF INVENTION: FOR MEASURING MESSENGER RNA  
 NUMBER OF SEQUENCES: 457  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson, and Bear  
 STREET: 620 Newport Center Dr. Sixteenth Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/974,409C  
 FILING DATE: 12-NOV-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E.  
 REGISTRATION NUMBER: 34,115  
 REFERENCE/DOCKET NUMBER: HITACHI. 006CP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 714-760-0404  
 TELEFAX: 714-760-9502  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: CDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: SUBSTANCE P RECEPTOR mRNA PROBE  
 US-07-974-409C-5  
 Query Match 1.0%; Score 17.8; DB 1; Length 22;  
 Best Local Similarity 90.5%; Pred. No. 68;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 780 GATTATGAGAAAGTGTCACCA 800  
 DB 2 GACTTATGAGAAAGGCTACCA 22  
 RESULT 106  
 US-08-182-175A-17/C  
 Sequence 17, Application US/08182175A  
 Patent No. 5559223  
 GENERAL INFORMATION:  
 APPLICANT: Saverio Carl Falco  
 APPLICANT: Sharon J. Keeler  
 APPLICANT: Janet A. Rice  
 TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E.I. du Pont de Nemours and Company  
 STREET: 1007 Market Street  
 CITY: Wilmington  
 STATE: Delaware  
 COUNTRY: USA  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: Macintosh System, 6.0  
 SOFTWARE: Microsoft Word, 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/182,175A  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/743,006  
 FILING DATE: 9 August 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Linda Axemethy Floyd  
 REGISTRATION NUMBER: 33,692  
 REFERENCE/DOCKET NUMBER: BB-1031  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (302) 992-4929  
 TELEFAX: (302) 892-7949  
 TELEX: 835420  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1..21  
 OTHER INFORMATION: /product= "synthetic oligonucleotide"  
 OTHER INFORMATION: /strand\_name= "SM 82"  
 US-08-182-175A-17  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1404 CTTGAGCTTCTCTCCA 1420

|||||  
19 CTTGAGCTTCTCTCCA 3

107  
182-175A-19/c  
ence 19, Application US/08182175A  
nt No. 5559223  
ERAL INFORMATION:  
PLICANT: Saverio Carl Falco  
PLICANT: Sharon J. Keeler  
PLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,175A  
FILING DATE:  
CLASSIFICATION: 800  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda Akamehy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
ORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLUCULE TYPE: DNA (genomic)  
ATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic oligonucleotide"  
OTHER INFORMATION: /standard\_name= "SM 86"  
182-175A-19

Y Match 1.0%; Score 17; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 79;  
hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCA 1420  
|||||  
19 CTTGAGCTTCTCTCCA 3

108  
182-175A-21/c  
ence 21, Application US/08182175A  
nt No. 5559223  
ERAL INFORMATION:  
PLICANT: Saverio Carl Falco  
PLICANT: Sharon J. Keeler  
PLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,175A  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda Akamehy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic oligonucleotide"  
OTHER INFORMATION: /standard\_name= "SM 88"  
US-08-182-175A-21

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
|||||  
DB 19 CTTGAGCTTCTCTCCA 3

RESULT 109  
US-08-474-633A-25/c  
Sequence 25, Application US/08474633A  
Patent No. 5773691  
GENERAL INFORMATION:  
APPLICANT: E. I. DU PONT DE NEMOURS AND  
APPLICANT: COMPANY  
TITLE OF INVENTION: CHIMERIC GENES AND  
TITLE OF INVENTION: METHODS FOR INCREASING  
TITLE OF INVENTION: INCREASING THE LYSINE  
TITLE OF INVENTION: AND THREONINE CONTENT  
TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
ADDRESSEE: AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,633A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
FORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product="synthetic"  
OTHER INFORMATION: oligonucleotide  
OTHER INFORMATION: /standard\_name="SM"  
OTHER INFORMATION: 82"  
-474-633A-25

Query Match 1.0%; Score 17; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 79;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCCA 1420  
|||||  
19 CTTGAGCTTCTCTCCCA 3

110  
-474-633A-41/c  
ence 41, Application US/08474633A  
nt No. 5773691  
ERAL INFORMATION:  
APPLICANT: E. I. DU PONT DE NEMOURS AND  
APPLICANT: COMPANY  
TITLE OF INVENTION: CHIMERIC GENES AND  
TITLE OF INVENTION: METHODS FOR INCREASING  
TITLE OF INVENTION: INCREASING THE LYSINE  
TITLE OF INVENTION: AND THREONINE CONTENT  
TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
ADDRESSEE: AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,633A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL

REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
FORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product="synthetic"  
OTHER INFORMATION: oligonucleotide  
OTHER INFORMATION: /standard\_name="SM"  
OTHER INFORMATION: 86"  
US-08-474-633A-41

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCCA 1420  
|||||  
Db 19 CTTGAGCTTCTCTCCCA 3

RESULT 111  
US-08-474-633A-43/c  
Sequence 43, Application US/08474633A  
Patent No. 5773691  
GENERAL INFORMATION:  
APPLICANT: E. I. DU PONT DE NEMOURS AND  
APPLICANT: COMPANY  
TITLE OF INVENTION: CHIMERIC GENES AND  
TITLE OF INVENTION: METHODS FOR INCREASING  
TITLE OF INVENTION: INCREASING THE LYSINE  
TITLE OF INVENTION: AND THREONINE CONTENT  
TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
ADDRESSEE: AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,633A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
FORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..21  
 OTHER INFORMATION: /product= "synthetic  
 OTHER INFORMATION: /standard\_name= "SM  
 OTHER INFORMATION: /standard\_name= "SM  
 OTHER INFORMATION: 88"  
 474-633A-43

Y Match 1.0%; Score 17; DB 1; Length 21;  
 Local Similarity 100.0%; Pred. No. 79;  
 hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCA 1420  
 |||||  
 19 CTTGAGCTTCTCTCCA 3

112  
 823-771-25/c  
 ence 25, Application US/08823771  
 nt No. 6459019  
 NERAL INFORMATION:  
 APPLICANT: E. I. DU PONT DE NEMOURS AND  
 COMPANY  
 TITLE OF INVENTION: CHIMERIC GENES AND  
 METHODS FOR INCREASING  
 INCREASING THE LYSINE  
 AND THREONINE CONTENT  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E. I. DU PONT DE NEMOURS  
 AND COMPANY  
 STREET: 1007 MARKET STREET  
 CITY: WILMINGTON  
 STATE: DELAWARE  
 COUNTRY: U.S.A.  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MICROSOFT WORD VERSION 2.0C  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/823,771  
 FILING DATE: 24-Mar-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/474,633  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BARBARA C. SIEGEL  
 REGISTRATION NUMBER: 30,684  
 REFERENCE/DOCKET NUMBER: BB-1037-C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 302-992-4931  
 TELEFAX: 302-773-0164  
 TELEX: 835420  
 FORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..21  
 OTHER INFORMATION: /product= "synthetic  
 oligonucleotide"

; /standard\_name= "SM  
 ; 82"  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
 US-08-823-771-25  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
 |||||  
 Db 19 CTTGAGCTTCTCTCCA 3

RESULT 113  
 US-08-823-771-41/c  
 ; Sequence 41, Application US/08823771  
 ; Patent No. 6459019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E. I. DU PONT DE NEMOURS AND  
 ; COMPANY  
 ; TITLE OF INVENTION: CHIMERIC GENES AND  
 ; METHODS FOR INCREASING  
 ; INCREASING THE LYSINE  
 ; AND THREONINE CONTENT  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: E. I. DU PONT DE NEMOURS  
 ; AND COMPANY  
 ; STREET: 1007 MARKET STREET  
 ; CITY: WILMINGTON  
 ; STATE: DELAWARE  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19898  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY DISK  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: MICROSOFT WORD VERSION 2.0C  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/823,771  
 ; FILING DATE: 24-Mar-1997  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/474,633  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BARBARA C. SIEGEL  
 ; REGISTRATION NUMBER: 30,684  
 ; REFERENCE/DOCKET NUMBER: BB-1037-C  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 302-992-4931  
 ; TELEFAX: 302-773-0164  
 ; TELEX: 835420  
 ; INFORMATION FOR SEQ ID NO: 41:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 21 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 1..21  
 ; OTHER INFORMATION: /product= "synthetic  
 ; oligonucleotide"  
 ; /standard\_name= "SM  
 ; 86"  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
 ; US-08-823-771-41  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 79;

hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCTCA 1420  
19 CTTGAGCTTCTCTCCTCA 3

114  
-823-771-43/c  
ence 43, Application US/08823771  
nt No. 6459019  
GENERAL INFORMATION:  
APPLICANT: E. I. DU PONT DE NEMOURS AND  
COMPANY  
TITLE OF INVENTION: CHIMERIC GENES AND  
METHODS FOR INCREASING  
INCREASING THE LYSINE  
AND THREONINE CONTENT

NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/823,771  
FILING DATE: 24-Mar-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/474,633  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420

FORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
88"

SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
-823-771-43

Match 1.0%; Score 17; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 79;  
hes 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1404 CTTGAGCTTCTCTCCTCA 1420  
19 CTTGAGCTTCTCTCCTCA 3

RESULT 115  
PCT-US92-06412-17/c  
Sequence 17, Application PC/TUS9206412  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda Mxamethy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420

FORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic oligonucleotide"  
/standard\_name= "SM 82"

PCT-US92-06412-17

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCTCA 1420  
Db 19 CTTGAGCTTCTCTCCTCA 3

RESULT 116  
PCT-US92-06412-19/c  
Sequence 19, Application PC/TUS9206412  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware

COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991  
TORNEY/AGENT INFORMATION:  
NAME: Linda Axamechy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
ELECTRONIC INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
ORAMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE: DNA (genomic)  
EATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..21  
OTHER INFORMATION: /product="synthetic oligonucleotide"  
OTHER INFORMATION: /standard\_name="SM 86"  
92-06412-19  
Y Match 1.0%; Score 17; DB 1; Length 21;  
Local Similarity 100.0%; Pred. No. 79;  
has 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1404 CTTGAGCTTCTCTCCA 1420  
19 CTTGAGCTTCTCTCCA 3  
117  
92-06412-21/c  
since 21, Application PC/TUS9206412  
ERAL INFORMATION:  
PLICANT: Saverio Carl Falco  
PLICANT: Sharon J. Keeleer  
PLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F  
NUMBER OF SEQUENCES: 113  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Linda Axamechy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..21  
OTHER INFORMATION: /product="synthetic oligonucleotide"  
OTHER INFORMATION: /standard\_name="SM 88"  
PCT-US92-06412-21  
Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1404 CTTGAGCTTCTCTCCA 1420  
Db 19 CTTGAGCTTCTCTCCA 3  
RESULT 118  
US-08-431-080-7/c  
Sequence 7, Application US/08431080  
Patent No. 5698686  
GENERAL INFORMATION:  
APPLICANT: Gottschling, Daniel E.  
APPLICANT: Singer, Miriam S.  
TITLE OF INVENTION: Telomerase Compositions and Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,080  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SN 08/326,781  
FILING DATE: October 20, 1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear

938-534-7/c  
ence 7, Application US/08938534  
nt No. 5316752  
GENERAL INFORMATION:  
APPLICANT: Gottschling, Daniel E.  
APPLICANT: Singer, Miriam S.  
TITLE OF INVENTION: Telomerase Compositions and Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210

921 CGAGCAAGTCTGTGCCAAGC 940  
|||||  
21 CGAGCAAGTCTGTGCCAAGC 2

938-534-7/c  
ence 7, Application US/08938534  
nt No. 5316752  
GENERAL INFORMATION:  
APPLICANT: Gottschling, Daniel E.  
APPLICANT: Singer, Miriam S.  
TITLE OF INVENTION: Telomerase Compositions and Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,534  
FILING DATE: 26-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/431,080  
FILING DATE:  
APPLICATION NUMBER: SN 08/326,781  
FILING DATE: October 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/345,294  
FILING DATE: 30-Jun-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/431,080  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517

921 CGAGCAAGTCTGTGCCAAGC 940  
|||||  
21 CGAGCAAGTCTGTGCCAAGC 2

921 CGAGCAAGTCTGTGCCAAGC 940  
|||||  
21 CGAGCAAGTCTGTGCCAAGC 2

921 CGAGCAAGTCTGTGCCAAGC 940  
|||||  
21 CGAGCAAGTCTGTGCCAAGC 2

921 CGAGCAAGTCTGTGCCAAGC 940  
|||||  
21 CGAGCAAGTCTGTGCCAAGC 2

CLASSIFICATION: 435  
TTOURNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORIGIN FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
701-935-2

Y Match 0.9%; Score 16.4; DB 1; Length 18;  
Local Similarity 94.4%; Pred. No. 71;  
hes 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

448 TCGATGCTGCATTCAT 465  
1 TCGATGCTGCATTCAT 18

122  
117-965-2  
ence 2, Application US/08117965  
nt No. 5484886  
ERAL INFORMATION:  
PLICANT: Tung, Fong M.  
TITLE OF INVENTION: Human Neurokinin-1 Receptor  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,965  
ILING DATE:  
CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: US 691,197  
ILING DATE: 25-APR-1991  
TTOURNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18387  
ELECTRONIC INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
ORIGIN FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECULE TYPE:  
117-965-2

Y Match 0.9%; Score 16.4; DB 1; Length 18;  
Local Similarity 94.4%; Pred. No. 71;  
hes 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 448 TCGATGCTGCATTCAT 465  
Db 1 TCGATGCTGCATTCAT 18

RESULT 123  
US-08-584-040-6209/C  
Sequence 6209, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
ELECTRONIC INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6209:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-6209

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCGGCTGTACG 641  
Db 18 CCAGCCCGGCTGTACG 1

RESULT 124  
US-09-371-772B-2971/C  
Sequence 2971, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.



STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

URRANT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995

TORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
ELECTRONIC INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

ORAMATION FOR SEQ ID NO: 5544:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
584-040-5544

Y March 0.9%; Score 15.4; DB 1; Length 17;  
Local Similarity 94.1%; Pred. No. 86;  
hes 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

716 CAACCAAGAGAGCCATG 732  
17 CAACCAAGAGAGCCATG 1

129  
371-772B-2435/C  
ence 2435, Application US/09371772B  
nt No. 6566127

GENERAL INFORMATION:  
LICANT: Ribozyme Pharmaceuticals, Inc.  
LICANT: Pavco, Pam  
LICANT: McSwigen, Jim  
LICANT: Stinchcomb, Dan  
LICANT: Escobedo, Jaime  
LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
E REFERENCE: MBH00, 876-J (237/198)  
RENT APPLICATION NUMBER: US/09/371,772B  
RENT FILING DATE: 1999-08-10  
OR APPLICATION NUMBER: US 60/005,974  
OR FILING DATE: 1995-10-26  
OR APPLICATION NUMBER: US 08/584,040  
OR FILING DATE: 1996-01-08  
BER OF SEQ ID NOS: 14225  
TWARE: PatentIn version 3.0  
ID NO 2435  
NGTH: 17  
PE: RNA  
GANISM: Mus sp.  
371-772B-2435

Y March 0.9%; Score 15.4; DB 1; Length 17;  
Local Similarity 94.1%; Pred. No. 86;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 716 CAACCAAGAGAGCCATG 732  
Db 17 CAACCAAGAGAGCCATG 1

RESULT 130  
US-09-685-664B-2435/C  
; Sequence 2435, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2435  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-09-685-664B-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 86;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCAAGAGAGCCATG 732  
Db 17 CAACCAAGAGAGCCATG 1

RESULT 131  
US-10-138-674B-2435/C  
; Sequence 2435, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674B  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2435  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-138-674B-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 86;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 716 CAACCAAGAGAGCCATG 732

APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
REFERENCE: MBH00,876-J (237/198)  
CURRENT FILING DATE: 1995-08-10  
FOR FILING DATE: 1995-10-26  
FOR APPLICATION NUMBER: US 08/584,040  
FOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
ID NO: 2971  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Mus sp.  
-371-772B-2971

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641  
18 CCAGCCCGGCTGTGACG 1

125  
-685-664B-2971/C  
Sequence 2971, Application US/09685664B  
Pat No. 681847  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
REFERENCE: MBH00-876-K (400/021)  
CURRENT FILING DATE: 2000-10-10  
FOR FILING DATE: 1995-10-26  
FOR APPLICATION NUMBER: US 06/005,974  
FOR FILING DATE: 1996-01-08  
FOR APPLICATION NUMBER: US 09/371,772  
FOR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8231  
SOFTWARE: PatentIn version 3.0  
ID NO: 2971  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Mus musculus  
-685-664B-2971

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

624 CCAGCCCGGCTGTGACG 641  
18 CCAGCCCGGCTGTGACG 1

126  
-138-674B-2971/C  
Sequence 2971, Application US/10138674B  
Pat No. 7034009  
GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
REFERENCE: MBH00-876-N (400/049)  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20829  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2971  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Mus musculus  
US-10-138-674B-2971

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCGGCTGTGACG 641  
DB 18 CCAGCCCGGCTGTGACG 1

RESULT 127  
US-09-967-669-87/C  
Sequence 87, Application US/09967669  
Patent No. 6692960  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freiler  
TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION  
FILE REFERENCE: RTS-0259  
CURRENT FILING DATE: 2001-09-28  
NUMBER OF SEQ ID NOS: 90  
SEQ ID NO: 87  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-967-669-87

Query Match 0.9%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 86;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 963 TGTGTGTGTGTGACCTT 980  
DB 18 TGTGTGTGTGTGACCTT 1

RESULT 128  
US-08-584-040-5544/C  
Sequence 5544, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

|||||  
17 CAACGAGAGAGCATG 1

1 132  
-513-974B-243  
ence 243, Application US/08513974B  
nt No. 6114139  
REAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ogi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Reenick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 243:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-513-974B-243

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 427 AACCTGGCCTTGGCGGA 443  
|||||  
DB 1 AACCTGGCCTTGGCGGA 17

RESULT 133  
US-09-850-948-19/C  
Sequence 19, Application US/09850948  
Patent No. 6919176

GENERAL INFORMATION:  
APPLICANT: Yang, Jianxin  
APPLICANT: An, Songzhu  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer  
FILE REFERENCE: 018781-008300US  
CURRENT APPLICATION NUMBER: US/09/850,948  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:quantitative  
OTHER INFORMATION: RT-PCR primer OGR1 reverse  
US-09-850-948-19

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGCTGCTTC 1002  
|||||  
DB 18 TCTGCTGCTGCTTC 2

RESULT 134  
US-09-543-679A-1373/C  
Sequence 1373, Application US/09543679A  
Patent No. 7034007  
GENERAL INFORMATION:  
APPLICANT: NYCE, Jonathan W.  
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
COMPOSITIONS, KIT & METHOD FOR TREATMENT  
OF AIRWAY DISORDERS ASSOCIATED WITH  
BRONCHOCONSTRICITION, LUNG INFLAMMATION,  
NUMBER OF SEQUENCES: 3111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: NJ  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-R  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: N/A  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/543,679A  
 FILING DATE: 13-Apr-2000  
 CLASSIFICATION: UNKNOWN  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/127,958  
 FILING DATE: 1998-08-03  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amzel, Viviana  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: EPI-0067191b  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-409-3035  
 TELEFAX: 413-254-9245  
 TELEX: <Unknown>  
 FORMATION FOR SEQ ID NO: 1373:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1373:  
 543-679A-1373  
 Y Match 0.8%; Score 15; DB 1; Length 15;  
 Local Similarity 100.0%; Pred. No. 77;  
 hes 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 716 CAACCAAGAGACCA 730  
 |||||  
 15 CAACCAAGAGACCA 1  
 135  
 543-679A-1374/C  
 ence 1374, Application US/09543679A  
 nt No. 7034007  
 NERAL INFORMATION:  
 APPLICANT: NNC, Jonathan W.  
 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
 COMPOSITIONS, KIT & METHOD FOR TREATMENT  
 OF AIRWAY DISORDERS ASSOCIATED WITH  
 BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
 NUMBER OF SEQUENCES: 3111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EPIDEMIS PHARMACEUTICALS, INC.  
 STREET: 7 Clarke Drive  
 CITY: Cranbury  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08512  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-R  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: N/A  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/543,679A  
 FILING DATE: 13-Apr-2000  
 CLASSIFICATION: UNKNOWN  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/127,958  
 FILING DATE: 1998-08-03  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amzel, Viviana  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: EPI-0067191b  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-409-3035  
 TELEFAX: 413-254-9245  
 TELEX: <Unknown>  
 FORMATION FOR SEQ ID NO: 1374:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1374:  
 US-09-543-679A-1374  
 Query Match 0.8%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1236 CCAGACCCAGGCGAG 1250  
 |||||  
 Db 15 CCAGACCCAGGCGAG 1  
 RESULT 136  
 US-09-866-108A-6966  
 ; Sequence 6966, Application US/09866108A  
 ; Patent No. 6686188  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: PENN, Shatton G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: ABOMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108A  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; Remaining Prior Application data removed - See file wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1575  
 ; SOFTWARE: Acemica Sequence Listing Engine  
 ; Patent No. 6686188  
 ; SEQ ID NO 6966  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-866-108A-6966  
 Query Match 0.8%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 CAGTCATCCAGAG 42  
 |||||  
 Db 3 CAGTCATCCAGAG 17  
 RESULT 137

```

-866-108A-6967
ence 6967, Application US/09866108A
nt No. 6686188
RAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharron G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
LE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
E REFERENCE: AEOMICA-7
RENT FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: GB 24263.6
OR FILING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
aining Prior Application data removed - See File Wrapper or PALM.
BER OF SEQ ID NOS: 15755
TWARE: Aeomica Sequence Listing Engine
nt No. 6686188
NGTH: 17
PE: DNA
GANISM: Homo sapiens
-866-108A-6967

0.8%; Score 15; DB 1; Length 17;
Local Similarity 100.0%; Pred. No. 97;
nes 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

28 CAGTGCATCCAGAG 42
|||||
2 CAGTGCATCCAGAG 16

r 138
-866-108A-6968
ence 6968, Application US/09866108A
nt No. 6686188
RAL INFORMATION:
PLICANT: GU, Yizhong
PLICANT: JI, Yonggang
PLICANT: PENN, Sharron G.
PLICANT: HANZEL, David K.
PLICANT: RANK, David R.
PLICANT: CHEN, Wensheng
PLICANT: SHANNON, Mark
LE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
E REFERENCE: AEOMICA-7
RENT FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US/09/866,108A
OR FILING DATE: 2001-05-25
OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: GB 24263.6

```

```

PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent NO. 668618
SEQ ID NO. 6968
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-6968

Query Match          0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY          28 CAGTCATCCGAG 42
          |||||
          1 CAGTCATCCGAG 15

RESULT 139
US-08-475-742-5
Sequence 5, Application US/08475742
Patent No. 6121015
GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475, 742
CURRENT FILING DATE: 1995-06-07
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1993-01-28
EARLIER APPLICATION NUMBER: US 08/014,013
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer- TM
PUBLICATION INFORMATION:
TITLE: The rat dopamine D4 receptor: sequence, gene structure
TITLE: and demonstration of expression in the cardiovascular
TITLE: system
JOURNAL: New Biol.
VOLUME: 4
PAGES: 1-9
DATE: 1992
US-08-475-742-5

Query Match          0.8%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

988 TGCTGCTGCCCTTC 1002  
 |||||  
 1 TGCTGCTGCCCTTC 15

140  
 261-293-5  
 ence 5, Application US/08261293  
 nt No. 6486310  
 RRAL INFORMATION:  
 PPLICANT: O'Malley, Karen L.  
 PPLICANT: Todd, Richard D.  
 TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4  
 TITLE OF INVENTION: Receptor  
 UMBER OF SEQUENCES: 16  
 ORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kilpatrick & Cody  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: U.S.  
 ZIP: 30309-4530  
 OMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 URRNT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/261,293  
 FILING DATE:  
 CLASSIFICATION: 435  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/014,013  
 FILING DATE:  
 TTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: WU 102  
 ELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 815-6524  
 TELEFAX: (404) 815-6555  
 ORAMATION FOR SEQ ID NO: 5:  
 EQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 OLECULE TYPE: CDNA  
 YPOTHEICAL: NO  
 NTI-SENSE: NO  
 EATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..18  
 OTHER INFORMATION: /note="Synthetic oligonucleotide  
 OTHER INFORMATION: primer - Tm VI/VII primer set otd-403"  
 UBICATION INFORMATION:  
 AUTHORS: O'Malley, K. L.  
 AUTHORS: Harmon, S.  
 AUTHORS: Tang, L.  
 AUTHORS: Todd, R. D.  
 TITLE: The rat dopamine D4 receptor: sequence, gene  
 TITLE: structure and demonstration of expression in the  
 TITLE: cardiovascular system.  
 JOURNAL: New Biol.  
 VOLUME: 4  
 PAGES: 1-9  
 DATE: 1992  
 RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 18  
 261-293-5  
 Y Match 0.8%; Score 15; DB 1; length 18;  
 Local Similarity 100.0%; Pred. NO. 1.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 988 TGCTGCTGCCCTTC 1002  
 |||||  
 Db 1 TGCTGCTGCCCTTC 15  
 RESULT 141  
 US-08-210-762E-45/C  
 ; Sequence 45, Application US/08210762E  
 ; Patent No. 5837441  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hjelte, Brian  
 ; APPLICANT: Jensen, Steve  
 ; TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of  
 ; TITLE OF INVENTION: the HARDS Virus.  
 ; NUMBER OF SEQUENCES: 85  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffman, Wason & Gitler  
 ; STREET: 2361 Jefferson Davis Highway  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 500 Kb storage  
 ; COMPUTER: Accel 486  
 ; OPERATING SYSTEM: Windows 3.1  
 ; SOFTWARE: Wordperfect 6.1 for Windows  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/210,762E  
 ; FILING DATE: 22-MAR-94  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/141,035  
 ; FILING DATE: 26-OCT-93  
 ; APPLICATION NUMBER: 08/120,096  
 ; FILING DATE: 13-SEP-93  
 ; APPLICATION NUMBER: 08/111,519  
 ; FILING DATE: 25-AUG-93  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Buttm, Jean A.  
 ; REGISTRATION NUMBER: 24,236  
 ; REFERENCE/DOCKET NUMBER: A4710CIP3.SL3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)418-2768  
 ; TELEFAX: (703)418-2768  
 ; INFORMATION FOR SEQ ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: CDNA viral  
 ; HYPOTHETICAL: no  
 ; ANTI-SENSE: no  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Four Corners Hantavirus  
 ; INDIVIDUAL ISOLATE: 3H226  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY:  
 ; CLONE:  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Hjelte, Brian  
 ; AUTHORS: Jensen, Steven  
 ; AUTHORS: Torres-Martinez, No. 5837441ah  
 ; AUTHORS: Yamada, Takashi  
 ; AUTHORS: No. 5837441te, Kurt  
 ; AUTHORS: Zumwalt, Ross  
 ; AUTHORS: MacInnes, Kersti  
 ; AUTHORS: Myers, Gerald  
 ; TITLE: A No. 5837441el Hantavirus Associated with an Outbreak of Fatal Respirato  
 ; TITLE: Disease in the Southwestern United States: Evolutionary Relationships to

TITLE: Hantaviruses-Running Title: Hantavirus-associated ARDS  
JOURNAL: Journal of Virology  
VOLUME: 68  
PAGES: in press  
DATE: 1994  
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 18  
210-762E-45

Match 0.8%; Score 14.8; DB 1; Length 18;  
Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

129 CCTGAGCCCGAGCGCCA 146  
18 CCTGAGCCCGAGCGCCA 1

142  
-071-433-50/c  
ence 50, Application US/09071433A  
ent No. 6197584  
GENERAL INFORMATION:  
PLICANT: Bennett, C. Frank  
PLICANT: Cowsett, Lex M  
FILE OF INVENTION: Antisense Modulation of CD40 Expression  
E REFERENCE: RTS-0002  
CURRENT APPLICATION NUMBER: US/09/071,433A  
CURRENT FILING DATE: 1998-05-01  
BER OF SEQ ID NOS: 91  
FTWARE: Patent In Ver. 2.0  
ID NO 50  
NGTH: 18  
YPE: DNA  
GANISM: Artificial Sequence  
ATURE:  
HER INFORMATION: Description of Artificial Sequence: Synthetic  
-071-433-50

Match 0.8%; Score 14.8; DB 1; Length 18;  
Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1406 TCAGCTTCTCTCCATG 1423  
18 TCGGCTTCTCTCCATG 1

143  
-106-075A-45/c  
ence 45, Application US/09106075A  
ent No. 6316250  
GENERAL INFORMATION:  
LICANT: Hjelle MD, Brian  
LICANT: Jensen, Steve  
FILE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of  
E OF INVENTION: the HARDS Virus.  
E REFERENCE: 10312-8U1, Hjelle et al. (210312.0009)  
CURRENT APPLICATION NUMBER: US/09/106,075A  
CURRENT FILING DATE: 1998-06-29  
CURRENT APPLICATION NUMBER: 08/210,762  
FOR FILING DATE: 1994-03-22  
FOR APPLICATION NUMBER: 08/141,035  
FOR FILING DATE: 1993-10-26  
FOR APPLICATION NUMBER: 08/120,096  
FOR FILING DATE: 1993-09-13  
FOR APPLICATION NUMBER: 08/111,519  
FOR FILING DATE: 1993-08-25  
BER OF SEQ ID NOS: 90  
FTWARE: Patent In Ver. 2.1  
ID NO 45  
NGTH: 18  
YPE: DNA  
GANISM: Prospect Hill Virus

US-09-106-075A-45

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 CCTGAGCCCGAGCGCCA 146  
DB 18 CCTGAGCCCGAGCGCCA 1

RESULT 144  
US-09-341-587-9/c  
Sequence 9, Application US/09341587  
Patent No. 6346606  
GENERAL INFORMATION:  
APPLICANT: Mollenhauer, Jan  
TITLE OF INVENTION: Protein Containing an SRCR Domain  
FILE REFERENCE: 4121-108  
CURRENT APPLICATION NUMBER: US/09/341,587  
CURRENT FILING DATE: 1999-08-31  
EARLIER APPLICATION NUMBER: PCT/DE98/00096  
EARLIER FILING DATE: 1998-01-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 9  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-341-587-9

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CAGCCGCTGAGACAC 1280  
DB 18 CAGCTGCTGAGACAC 1

RESULT 145  
US-08-411-020-44  
Sequence 44, Application US/08411020  
Patent No. 5712094  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
APPLICANT: CHAN, SHIN-SHAY TIAN  
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
CITY: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675

TELEFAX: (619) 535-3906  
 ORAMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 OLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
 DESCRIPTION: SYNTHETIC DNA"  
 411-020-44

Y Match 0.8%; Score 14.4; DB 1; Length 18;  
 Local Similarity 93.8%; Pred. No. 1.3e+02;  
 hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1717 TCCATTTCGAGACG 1732  
 |||||  
 3 TCCATTTCGAAATG 18

146  
 106-038A-9  
 ence 9, Application US/09106038A  
 nt No. 6007995  
 ERAL INFORMATION:  
 PPLICANT: Brenda F. Baker and Lex M. Cowser  
 TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1  
 TITLE OF INVENTION: EXPRESSION  
 UMBER OF SEQUENCES: 91  
 ORRESPONDENCE ADDRESS:  
 ADDRESS: Isis Pharmaceuticals, Inc.  
 STREET: 2292 Faraday Avenue  
 CITY: Carlebad  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92008

OMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows NT  
 SOFTWARE: Microsoft Word 97  
 URRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/106,038A  
 FILING DATE: June 26, 1998  
 CLASSIFICATION: 514  
 TTORNEY/AGENT INFORMATION:  
 NAME: Laurel Spear Bernstein  
 REGISTRATION NUMBER: 37,280  
 REFERENCE/DOCKET NUMBER: RTS-0004  
 ELECOMMUNICATION INFORMATION:  
 TELEPHONE: (760) 931-9200  
 TELEFAX: (760) 603-3820  
 ORAMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 18  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 106-038A-9

Y Match 0.8%; Score 14.4; DB 1; Length 18;  
 Local Similarity 93.8%; Pred. No. 1.3e+02;  
 hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

105 CCCTCTGCTGCTT 120  
 |||||  
 3 CCCTCTCTGCTT 18

147  
 289-376-17/c  
 ence 17, Application US/09289376

; Patent No. 6013788  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Lex M. Cowser  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD3 EXPRESSION  
 ; FILE REFERENCE: RTS-0043  
 ; CURRENT APPLICATION NUMBER: US/09/289,376  
 ; CURRENT FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 17  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-289-376-17

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1118 TCATCTACTGCTGCTT 1133  
 |||||  
 Db 18 TCATCTACTGCCGCT 3

RESULT 148  
 US-09-344-520-9/c  
 ; Sequence 9, Application US/09344520  
 ; Patent No. 6037176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank Bennett  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF Integrin beta 3 EXPRESSION  
 ; FILE REFERENCE: RTS-0070  
 ; CURRENT APPLICATION NUMBER: US/09/344,520  
 ; CURRENT FILING DATE: 1999-06-25  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 9  
 ; TYPE: DNA  
 ; LENGTH: 18  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-344-520-9

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 804 CTGTGTGACTGTGCTG 819  
 |||||  
 Db 18 CTGGGTGACTGTGCTG 3

RESULT 149  
 US-08-584-040-6255/c  
 ; Sequence 6255, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
 ; GROWTH FACTOR  
 ; NUMBER OF SEQUENCES: 8502  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Lyon & Lyon



STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6255:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

-584-040-6255

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677  
18 TCTGTGTCATCTGAGT 3

F 150

422-978-10970  
ence 10970, Application US/09422978  
ent No. 6537751

GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marla

APPLICANT: Chumakov, Ilya

FILE OF INVENTION: Biallelic markers for use in constructing a high density...

REFERENCE: GENEST.020CPI  
CURRENT APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20  
CURRENT APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: 1999-04-21  
CURRENT APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: 1998-11-23  
CURRENT APPLICATION NUMBER: US 60/082,614

PRIOR FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796

ID NO 10970

TYPE: DNA  
ORGANISM: Homo sapiens

NAME/KEY: primer\_bind  
CATION: 1..18  
HER INFORMATION: downstream amplification primer 99-23427 for SEQ 3105, in complement  
422-978-10970

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCCTCC 1419  
Db 2 CTTGATCTTCCTCC 17

RESULT 151  
US-09-371-772B-3013/C

Sequence 3013, Application US/09371772B  
Patent No. 6566127

GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

FILE REFERENCE: MBBH00,876-J (237/198)

CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1995-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3013

LENGTH: 18

TYPE: RNA

ORGANISM: Mus sp.

US-09-371-772B-3013

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 662 TCTGTGTCATCTGGGT 677  
Db 18 TCTGTGTCATCTGAGT 3

RESULT 152  
US-09-747-391-42/C

Sequence 42, Application US/09747391  
Patent No. 6670124

GENERAL INFORMATION:  
APPLICANT: Chow, Robert

APPLICANT: Tonal, Richard

APPLICANT: StemCyle, Inc.

TITLE OF INVENTION: High Throughput Methods of HLA Typing

FILE REFERENCE: 020035-000210US  
CURRENT APPLICATION NUMBER: US/09/747,391

PRIOR FILING DATE: 2001-07-13  
CURRENT APPLICATION NUMBER: US 60/172,768

PRIOR FILING DATE: 1999-12-20  
NUMBER OF SEQ ID NOS: 278

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 42

LENGTH: 18  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-747-391-42

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CCGGAGCGCTCATG 453  
18 CCGGAGCGCTCATG 453

18 CGCGAGGACCTTCATG 3

153

685-664B-3013/c  
ence 3013, Application US/09685664B  
nt No. 6818447

RAL INFORMATION:

LICANT: Ribozyme Pharmaceuticals, Inc.

LICANT: Pavco, Pam

LICANT: McSwiggen, Jim

LICANT: Stinchcomb, Dan

LICANT: Escobedo, Jaime

LE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor

E REFERENCE: MHB00-876-K (400/021)

RENT APPLICATION NUMBER: US/09/685,664B

RENT FILING DATE: 2000-10-10

OR APPLICATION NUMBER: US 60/005,974

OR FILING DATE: 1995-10-26

OR APPLICATION NUMBER: US 08/584,040

OR FILING DATE: 1996-01-08

OR APPLICATION NUMBER: US 09/371,772

OR FILING DATE: 1999-08-10

BER OF SEQ ID NOS: 8231

TWARE: PatentIn version 3.0

ID NO 3013

NGTH: 18

PE: RNA

GANISM: Mus musculus

685-664B-3013

Y Match 0.8%; Score 14.4; DB 1; Length 18;  
Local Similarity 93.8%; Pred. No. 1.3e+02;  
hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677

18 TCTGTGTCATCTGAGT 3

154

138-674B-3013/c  
ence 3013, Application US/10138674B  
nt No. 7034009

RAL INFORMATION:

LICANT: Sirna Therapeutics, Inc.

LICANT: Pavco, Pam

LICANT: McSwiggen, James

LICANT: Stinchcomb, Dan

LICANT: Escobedo, Jaime

LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor

E REFERENCE: MHB00-876-N (400/049)

RENT APPLICATION NUMBER: US/10/138,674B

RENT FILING DATE: 2002-05-03

BER OF SEQ ID NOS: 20829

TWARE: PatentIn version 3.0

ID NO 3013

NGTH: 18

PE: RNA

GANISM: Mus musculus

138-674B-3013

Y Match 0.8%; Score 14.4; DB 1; Length 18;  
Local Similarity 93.8%; Pred. No. 1.3e+02;  
hes 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

662 TCTGTGTCATCTGGGT 677

18 TCTGTGTCATCTGAGT 3

RESULT 155  
US-09-874-601-5  
; Sequence 5, Application US/09874601  
; Patent No. 6632057

GENERAL INFORMATION:

APPLICANT: LEWIN, ALFRED S.

APPLICANT: SHAW, LYNN C.

APPLICANT: GRANT, MARIA B.

TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD

TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

FILE REFERENCE: 4300.014100

CURRENT APPLICATION NUMBER: US/09/874,601

CURRENT FILING DATE: 2001-05-01

PRIOR APPLICATION NUMBER: 09/063,667

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/046,147

PRIOR FILING DATE: 1997-05-09

PRIOR APPLICATION NUMBER: 60/044,492

PRIOR FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 182

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 14

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

LOCATION: ( )..( )

OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-874-601-5

Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 92;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 689 TGCTGGCCTTCCCC 702

Db 1 UGCGGCCUCC 14

RESULT 156

US-09-543-679A-1371/c  
; Sequence 1371, Application US/09543679A  
; Patent No. 7034007

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245

TELEX: <Unknown>  
SEQUENCE FOR SEQ ID NO: 1371:  
SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1371:  
-543-679A-1371

Match 0.8%; Score 14; DB 1; Length 14;  
Local Similarity 100.0%; Pred. No. 92;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

384 AGCCCAAAAGAA 397  
14 AGCCCAAAAGAA 1

157  
-588-821-84  
ence 84, Application US/08588821  
nt No. 5712097

GENERAL INFORMATION:  
APPLICANT: Kern, Scott E.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,821  
FILING DATE: 19-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/079001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5070  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
-588-821-84

Match 0.8%; Score 14; DB 1; Length 16;  
Local Similarity 100.0%; Pred. No. 1.2e+02;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

730 ATGCCAGCAGT 743  
2 ATGCCAGCAGT 15

RESULT 158  
US-08-915-214-84  
Sequence 84, Application US/08915214  
Patent No. 5814457

GENERAL INFORMATION:  
APPLICANT: Kern, Scott E.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,214  
FILING DATE: 20-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/588,821  
FILING DATE: 19-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/079001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-915-214-84

Query Match 0.8%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 ATGCCAGCAGT 743  
Db 2 ATGCCAGCAGT 15

RESULT 159  
US-09-005-532-84  
Sequence 84, Application US/09005532  
Patent No. 5955292  
GENERAL INFORMATION:  
APPLICANT: Kern, Scott E.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
 URGENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/005,532  
 FILING DATE:  
 CLASSIFICATION:  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/588,821  
 FILING DATE: 19-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haile, Lisa A.  
 REGISTRATION NUMBER: 38,347  
 REFERENCE/DOCKET NUMBER: 07265/079001  
 ELECTRONIC COMMUNICATION INFORMATION:  
 TELEPHONE: 619/678-5070  
 TELEFAX: 619/678-5099  
 ORAMATION FOR SEQ ID NO: 84:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 005-532-84  
 Y Match 0.8%; Score 14; DB 1; Length 16;  
 Local Similarity 100.0%; Pred. No. 1.2e+02;  
 hes 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 730 ATGCCGACGAGGT 743  
 2 ATGCCGACGAGGT 15  
 160  
 897-340-14  
 ence 14, Application US/08897340  
 nt No. 5955306  
 ERAL INFORMATION:  
 PPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
 TITLE OF INVENTION: Therefor  
 UMBER OF SEQUENCES: 36  
 ORRESPONDENCE ADDRESS:  
 ADDRESSSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 OMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 URGENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/897,340  
 FILING DATE:  
 CLASSIFICATION: 435  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/715,032  
 FILING DATE: 17-SEP-1996  
 TTORNEY/AGENT INFORMATION:  
 NAME: Silveri, Jean M.  
 REGISTRATION NUMBER: 39,030  
 REFERENCE/DOCKET NUMBER: MNI-005CP  
 ELECTRONIC COMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 ORAMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: single

TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-897-340-14  
 Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 571 TACTCCATGACGGC 584  
 Db 3 TACTCCATGACGGC 16  
 RESULT 161  
 US-09-252-329-14  
 Sequence 14, Application US/09252329  
 Patent No. 6147192  
 GENERAL INFORMATION:  
 APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
 TITLE OF INVENTION: Therefor  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/252,329  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/897,340  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silveri, Jean M.  
 REGISTRATION NUMBER: 39,030  
 REFERENCE/DOCKET NUMBER: MNI-005CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-09-252-329-14  
 Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 571 TACTCCATGACGGC 584  
 Db 3 TACTCCATGACGGC 16  
 RESULT 162  
 US-09-724-566A-22  
 Sequence 22, Application US/09724566A  
 Patent No. 6627739  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, John P.  
 APPLICANT: Basi, Gurigbal

PLICANT: Doane, Minh Tam  
PLICANT: Frigon, No. 6627739mand  
PLICANT: John, Varghese  
PLICANT: Power, Michael  
PLICANT: Sinha, Sukanto  
PLICANT: Tatsuno, Gwen  
PLICANT: Tung, Jay  
PLICANT: Wang, Shuwen  
PLICANT: McConlogue, Lisa  
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
METHOD OF INVENTION: Methods  
REFERENCE: 228-US-NEWC2  
CURRENT APPLICATION NUMBER: US/09/724,566A  
PARENT FILING DATE: 2000-11-28  
FOR APPLICATION NUMBER: US 09/501,708  
FOR FILING DATE: 2000-02-10  
FOR APPLICATION NUMBER: 60/119,571  
FOR FILING DATE: 1999-02-10  
FOR APPLICATION NUMBER: 60/139,172  
FOR FILING DATE: 1999-06-15  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: FastSeq for Windows Version 4.0  
ID NO: 22  
LENGTH: 17  
SPECIES: DNA  
ORGANISM: Artificial Sequence  
NATURE: Degenerate oligonucleotide primer  
FEATURE: misc\_feature  
LOCATION: (1)...(17)  
OTHER INFORMATION: n = A,T,C or G  
-724-566A-22  
Match 0.8%; Score 14; DB 1; Length 17;  
Local Similarity 82.4%; Pred. No. 1.3e+02;  
Indels 1; Mismatches 2; Gaps 0;  
1306 GAGGAGGAGCCAGAGGA 1322  
1 GAYGAGGAGCCAGAGGA 17  
-866-108A-6965  
Patent No. 6686188  
GENERAL INFORMATION:  
PLICANT: GU, Yizhong  
PLICANT: JI, Yonggang  
PLICANT: PENN, Sharon G.  
PLICANT: HANZEL, David K.  
PLICANT: RANK, David R.  
PLICANT: CHEN, Wensheng  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
REFERENCE: AECOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
PARENT FILING DATE: 2001-05-25  
FOR APPLICATION NUMBER: US 60/207,456  
FOR FILING DATE: 2000-05-26  
FOR APPLICATION NUMBER: GB 24263.6  
FOR FILING DATE: 2000-10-04  
FOR APPLICATION NUMBER: US 60/236,359  
FOR FILING DATE: 2000-09-27  
FOR APPLICATION NUMBER: PCT/US01/00666  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00667  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00664  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00669  
FOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecmica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO: 6965  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-6965  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
28 CAGTGATCCAGAA 41  
4 CAGTGATCCAGAA 17  
Db  
RESULT 164  
US-09-866-108A-6969  
Sequence 6969, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
PLICANT: GU, Yizhong  
PLICANT: JI, Yonggang  
PLICANT: PENN, Sharon G.  
PLICANT: HANZEL, David K.  
PLICANT: RANK, David R.  
PLICANT: CHEN, Wensheng  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
REFERENCE: AECOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
PARENT FILING DATE: 2001-05-25  
FOR APPLICATION NUMBER: US 60/207,456  
FOR FILING DATE: 2000-05-26  
FOR APPLICATION NUMBER: GB 24263.6  
FOR FILING DATE: 2000-10-04  
FOR APPLICATION NUMBER: US 60/236,359  
FOR FILING DATE: 2000-09-27  
FOR APPLICATION NUMBER: PCT/US01/00666  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00667  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00664  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00669  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00665  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00668  
FOR FILING DATE: 2001-01-30  
FOR APPLICATION NUMBER: PCT/US01/00663  
FOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecmica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO: 6969  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-6969  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

hes 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

29 AGTGCATCCAGAG 42  
|||||  
1 AGTGCATCCAGAG 14

165  
471-669A-22  
ence 22, Application US/09471669A  
nt No. 6830918  
RAL INFORMATION:  
LICANT: Anderson, John P.  
LICANT: Basl, Guribai  
LICANT: Doane, Minh Tam  
LICANT: Frigon, No. 6830918mand  
LICANT: John, Varghese  
LICANT: Power, Michael  
LICANT: Sinha, Sukanto  
LICANT: Tatsuno, Gwen  
LICANT: Tung, Jay  
LICANT: Wang, Shuwen  
LICANT: McConlogue, Lisa  
LE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS  
E REFERENCE: 015270-006430US  
RENT APPLICATION NUMBER: US/09/471,669A  
RENT FILING DATE: 1999-12-24  
OR APPLICATION NUMBER: US 60/114,408  
OR FILING DATE: 1998-12-31  
OR APPLICATION NUMBER: US 60/119,571  
OR FILING DATE: 1999-02-10  
OR APPLICATION NUMBER: US 60/139,172  
OR FILING DATE: 1999-06-15  
BER OF SEQ ID NOS: 108  
TWARE: PatentIn Ver. 2.1  
ID NO 22  
NGTH: 17  
PE: DNA  
GANISM: Artificial Sequence  
ATURE:  
HER INFORMATION: Description of Artificial Sequence: Degenerate  
HER INFORMATION: Oligonucleotide primer  
ATURE:  
ME/KEY: misc feature  
CATION: (...)  
HER INFORMATION: n = a, c, g, or t.  
471-669A-22

Y Match 0.8%; Score 14; DB 1; Length 17;  
Local Similarity 82.4%; Pred. No. 1.3e+02;  
hes 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1306 GAGGAGGAGCCAGAGGA 1322  
|||:|||||  
1 GAYGARAGAGCCAGAGGA 17

166  
701-935-3  
ence 3, Application US/07701935  
nt No. 5336595  
ERAL INFORMATION:  
PLICANT: Strader, C. D.  
PLICANT: Fong, T. M.  
TITLE OF INVENTION: Method of Using Human Neurokinin-1  
TITLE OF INVENTION: Receptor Short Form  
UMBER OF SEQUENCES: 27  
ORRESPONDENCE ADDRESS:  
ADDRESSER: Merck & Co., Inc.  
STREET: P. O. Box 2000  
CITY: Rahway  
STATE: New Jersey

COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/701,935  
FILING DATE: 19910517  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nicholson, William H.  
REGISTRATION NUMBER: 25,147  
REFERENCE/DOCKET NUMBER: 18409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5315  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
MOLECULE TYPE:  
TOPOLOGY: linear  
US-07-701-935-3

Query March 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 448 TCCATGCTGCATTCAA 464  
|||||  
Db 1 TGCATGCTGCCTTCAA 17

RESULT 167  
US-08-117-965-3  
; Sequence 3, Application US/08117965  
; Patent No. 548486  
; GENERAL INFORMATION:  
; APPLICANT: Tung, Fong M.  
; APPLICANT: Cathrine, Strader D.  
; TITLE OF INVENTION: Human Neurokinin-1 Receptor  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P. O. Box 2000  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,965  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 691,197  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nicholson, William H.  
; REGISTRATION NUMBER: 25,147  
; REFERENCE/DOCKET NUMBER: 18387  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-5315  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
117-965-3

Query Match 0.8% Score 13.8; DB 1; Length 17;  
Local Similarity 88.2% Pred. No. 1.4e+02;  
Indels 15; Conservative 0; Mismatches 2; Gaps 0;

448 TCCATGCTGCTGCTCA 464  
1 TGCATGCTGCTGCTCA 17

168  
-373-124A-1749  
ence 1749, Application US/08373124A  
nt No. 5646042  
HERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/967,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

FORMATION FOR SEQ. ID NO: 1749:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
-373-124A-1749

Query Match 0.8% Score 13.8; DB 1; Length 17;  
Local Similarity 70.6% Pred. No. 1.4e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Query 441 GGAGGCTTCATGCTG 457  
DB 1 GGAGGCTTCATGCTG 17

RESULT 169

US-08-287-075-10/c  
Sequence 10, Application US/08287075  
Patent No. 5656462

GENERAL INFORMATION:

APPLICANT: Keller, Cy'ia  
APPLICANT: Mitsuhashi, Masato  
APPLICANT: Akitaya, Tatsuo  
TITLE OF INVENTION: POLYNUCLEOTIDE IMMOBILIZED SUPPORT  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KNOBBE, MARTENS, OLSON, AND BEAR  
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
CITY: NEWPORT BEACH  
STATE: CA  
COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/287,075  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/827,975  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: HITACHI.002A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: TRC-AS OLIGONUCLEOTIDE PRIMER  
US-08-287-075-10

Query Match

Best Local Similarity 0.8% Score 13.8; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 983 CCATCTGCTGCTGCTCC 999

DB 17 CCATCTGCTGCTGCTCC 1

RESULT 170

US-08-435-628-1749  
Sequence 1749, Application US/08435628  
Patent No. 5817796

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
 TREATMENT OF RESTENOSIS AND  
 CANCER USING RIBOZYMES  
 NUMBER OF SEQUENCES: 2627  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/435,628  
 FILING DATE: 05-MAY-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/373,124  
 FILING DATE: January 13, 1995  
 APPLICATION NUMBER: 08/245,466  
 FILING DATE: May 18, 1994  
 APPLICATION NUMBER: 08/192,943  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: 07/987,132  
 FILING DATE: December 7, 1992  
 APPLICATION NUMBER: 07/936,422  
 FILING DATE: August 26, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 209/035  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 ORAMATION FOR SEQ ID NO: 1749:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 435-628-1749  
 Y Match 0.8%; Score 13.8; DB 1; Length 17;  
 Local Similarity 70.6%; Pred. No. 1.4e+02;  
 hes 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 441 GGAGGCTTCATGCTG 457  
 1 GGAGGCTTCATGCTG 17  
 985-162-243/C  
 ence 243, Application US/08985162  
 nt No. 6057156  
 ERAL INFORMATION:  
 APPLICANT: Akhtar, Saghir  
 APPLICANT: Fell, Patricia  
 APPLICANT: McSwigen, James  
 TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT  
 OF DISEASES OR CONDITIONS RELATED  
 TO LEVELS OF EPIDERMAL GROWTH  
 TITLE OF INVENTION: FACTOR RECEPTORS  
 NUMBER OF SEQUENCES: 1877  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/985,162  
 FILING DATE: 04 December 1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/036,476  
 FILING DATE: 31 January 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/107  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 243:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-985-162-243  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1313 AGCCAGAGAGAGGCCCC 1329  
 17 AGCAAGAGAGAGGCCCC 1  
 RESULT 172  
 US-08-584-040-3947/C  
 ; Sequence 3947, Application US/08584040  
 ; Patent No. 6346398  
 ; GENERAL INFORMATION:  
 APPLICANT: Pavco, Pamela  
 APPLICANT: McSwigen, James  
 APPLICANT: Stinchcomb, Dan T.  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TREATMENT OF DISEASES OR  
 CONDITIONS RELATED TO LEVELS  
 OF VASCULAR ENDOTHELIAL  
 GROWTH FACTOR  
 TITLE OF INVENTION: GROWTH FACTOR  
 NUMBER OF SEQUENCES: 8502  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0



SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
FORMATION FOR SEQ ID NO: 3947:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
-584-040-3947

173  
-584-040-4119/c  
ence 4119, Application US/08584040  
nt No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
FORMATION FOR SEQ ID NO: 4119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-4119

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCACTGGACATCA 1521  
DB 17 TTCACTGGATCATGA 1

RESULT 174  
US-08-584-040-5545/c  
Sequence 5545, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
FORMATION FOR SEQ ID NO: 5545:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5545

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
Local Similarity 88.2%; Pred. No. 1.4e+02;  
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACACGACGACCA 730  
|||||  
17 CACACGACGACGACCA 1

175  
584-040-5694/C  
ence 5694, Application US/08584040  
nt No. 6346398

BRAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996

CLASSIFICATION: 514  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
TTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
ORINATION FOR SEQ ID NO: 5694:  
EQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
584-040-5694

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
Local Similarity 88.2%; Pred. No. 1.4e+02;  
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGGAACATCA 1521  
|||||  
17 TTCATCTGGAACATCA 1

176  
679-645-765/C  
ence 765, Application US/08679645

Patent No. 6350934  
GENERAL INFORMATION:  
APPLICANT: Zwick, Michael G.  
APPLICANT: Edington, Brent E.  
APPLICANT: McSwigen, James A.  
APPLICANT: Merlo, Patricia Ann Owens  
APPLICANT: Guo, Lining  
APPLICANT: Skokut, Thomas A.  
APPLICANT: Young, Scott A.  
APPLICANT: Folkerts, Otto  
APPLICANT: Merlo, Donald J.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,645  
FILING DATE: July 12, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
ELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 765:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-679-645-765  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 636 GTCAGCCAGACGACCA 652  
|||||  
Db 17 GTCAGCCAGACGACCA 1  
RESULT 177  
US-09-371-772B-1714/C  
Sequence 1714, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime

FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor  
 REFERENCE: MBH800, 876-J (237/198)  
 CURRENT APPLICATION NUMBER: US/09/371,772B  
 PRIOR FILING DATE: 1999-08-10  
 PRIOR APPLICATION NUMBER: US 60/005,974  
 PRIOR FILING DATE: 1995-10-26  
 PRIOR APPLICATION NUMBER: US 08/584,040  
 NUMBER OF SEQ ID NOS: 14225  
 SOFTWARE: PatentIn version 3.0  
 ID NO: 1714  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 371-772B-1714

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
 Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCAACCCAGAGACCA 730  
 17 CACAACCCAGAGACCA 1

178  
 371-772B-1886/C  
 REFERENCE: 1886, Application US/09371772B  
 Patent No. 6566127  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Pavo, Pam  
 APPLICANT: McSwigen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor  
 REFERENCE: MBH800, 876-J (237/198)  
 CURRENT APPLICATION NUMBER: US/09/371,772B  
 PRIOR FILING DATE: 1999-08-10  
 PRIOR APPLICATION NUMBER: US 60/005,974  
 PRIOR FILING DATE: 1995-10-26  
 PRIOR APPLICATION NUMBER: US 08/584,040  
 NUMBER OF SEQ ID NOS: 14225  
 SOFTWARE: PatentIn version 3.0  
 ID NO: 1886  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 371-772B-1886

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
 Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGACCATCA 1521  
 17 TTCATCTGATCATCA 1

179  
 371-772B-6345/C  
 REFERENCE: 6345, Application US/09371772B  
 Patent No. 6566127  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Pavo, Pam  
 APPLICANT: McSwigen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor

FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 REFERENCE: MBH800, 876-J (237/198)  
 CURRENT APPLICATION NUMBER: US/09/371,772B  
 PRIOR FILING DATE: 1999-08-10  
 PRIOR APPLICATION NUMBER: US 60/005,974  
 PRIOR FILING DATE: 1995-10-26  
 PRIOR APPLICATION NUMBER: US 08/584,040  
 PRIOR FILING DATE: 1996-01-08  
 NUMBER OF SEQ ID NOS: 14225  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 6345  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-09-371-772B-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 713 ACTCAACCCAGAGACC 729  
 Db 17 ACACAACCCAGAGACC 1

RESULT 180  
 US-09-401-063-243/C  
 Sequence 243, Application US/09401063  
 Patent No. 6623962  
 GENERAL INFORMATION:  
 APPLICANT: Akhtar, Saghir  
 APPLICANT: Fell, Patricia  
 APPLICANT: McSwigen, James  
 TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
 TITLE OF INVENTION: FACTOR RECEPTORS  
 NUMBER OF SEQUENCES: 1877  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/401,063  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/985,162  
 FILING DATE: 04 December 1997  
 APPLICATION NUMBER: 60/036,476  
 FILING DATE: 31 January 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 230/107  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 243:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
401-063-243

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
Local Similarity 88.2%; Pred. No. 1.4e+02;  
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1313 AGCAGAGGAGGAGGCCCC 1329  
17 AGCAGAGGAGGAGGCCCC 1

181  
866-108A-2756  
ence 2756, Application US/09866108A  
nt No. 6686188

RAL INFORMATION:  
LICANT: GU, Yizhong  
LICANT: JI, Yonggang  
LICANT: PENN, Sharon G.  
LICANT: HANZEL, David K.  
LICANT: RANK, David R.  
LICANT: CHEN, Wensheng  
LICANT: SHANNON, Mark  
LE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
E REFERENCE: AEOMICA-7  
RENT APPLICATION NUMBER: US/09/866,108A  
RENT FILING DATE: 2001-05-25  
OR APPLICATION NUMBER: US 60/207,456  
OR FILING DATE: 2000-05-26  
OR APPLICATION NUMBER: GB 24263.6  
OR FILING DATE: 2000-10-04  
OR APPLICATION NUMBER: US 60/236,359  
OR FILING DATE: 2000-09-27  
OR APPLICATION NUMBER: PCT/US01/00666  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00667  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00664  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00669  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00665  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00668  
OR FILING DATE: 2001-01-30  
OR APPLICATION NUMBER: PCT/US01/00663  
OR FILING DATE: 2001-01-30

aining Prior Application data removed - See File Wrapper or PALM.

BER OF SEQ ID NOS: 15755  
TWARE: Aeomica Sequence Listing Engine  
ID NO 2756  
NGTH: 17  
PE: DNA  
GANISM: Homo sapiens  
866-108A-2756

Y Match 0.8%; Score 13.8; DB 1; Length 17;  
Local Similarity 88.2%; Pred. No. 1.4e+02;  
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
1196 GCGACTATGAGGGGCTG 1212  
1 GCGAGTATGAGGAGCTG 17

182  
866-108A-7674/C  
ence 7674, Application US/09866108A  
nt No. 6686188  
RAL INFORMATION:

APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aeomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 7674  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 17 CTTGCTTCTCTCCA 1

RESULT 183  
US-09-685-664B-1714/C  
Sequence 1714, Application US/09685664B  
Patent No. 6818447  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBH00-876-K (400/021)  
CURRENT APPLICATION NUMBER: US/09/685,664B  
CURRENT FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
PRIOR APPLICATION NUMBER: US 09/371,772  
PRIOR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8231  
SOFTWARE: PatentIn version 3.0

ID NO 1714  
LENGTH: 17  
/PE: RNA  
ORGANISM: Homo sapiens  
-685-664B-1714

Query Match      0.8%; Score 13.8; DB 1; Length 17;  
: Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCCAGAGACCA 730  
|||||  
17 CACACCCAGAGACCA 1

184  
-685-664B-1886/C  
ence 1886, Application US/09685664B  
ent No. 6818447  
RAL INFORMATION:  
PLICANT: Ribozyme Pharmaceuticals, Inc.  
PLICANT: Pavco, Pam  
PLICANT: McSwiggen, Jim  
PLICANT: Stinchcomb, Dan  
PLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related  
TO OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
REFERENCE: MBH00-876-K (400/021)  
CURRENT APPLICATION NUMBER: US/09/685,664B  
CURRENT FILING DATE: 2000-10-10  
OR APPLICATION NUMBER: US 60/005,974  
OR FILING DATE: 1995-10-26  
OR APPLICATION NUMBER: US 08/584,040  
OR FILING DATE: 1996-01-08  
OR APPLICATION NUMBER: US 09/371,772  
OR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8231  
SOFTWARE: PatentIn version 3.0  
ID NO 1886  
LENGTH: 17  
/PE: RNA  
ORGANISM: Homo sapiens  
-685-664B-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;  
: Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGAGACCATCA 1521  
|||||  
17 TTCATCTGAGACCATCA 1

185  
-156-306B-6951/C  
ence 6951, Application US/10156306B  
ent No. 7022828  
RAL INFORMATION:  
PLICANT: Ribozyme Pharmaceuticals, Inc.  
PLICANT: McSwiggen, James  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
TO OF INVENTION: Levels of IKK-Gamma and PKR  
REFERENCE: MBH01-664-A (400/050)  
CURRENT APPLICATION NUMBER: US/10/156,306B  
CURRENT FILING DATE: 2002-05-28  
NUMBER OF SEQ ID NOS: 8014  
SOFTWARE: PatentIn version 3.0  
ID NO 6951  
LENGTH: 17  
/PE: RNA  
ORGANISM: Homo sapiens  
-156-306B-6951

Query Match      0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1402 AGCTTCAGCTTCCTC 1418  
|||||  
17 AGCTTCCTCTCTCTC 1

186  
US-10-138-674B-1714/C  
; Sequence 1714, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related  
; TO OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674B  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1714  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674B-1714

Query Match      0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

714 CTCACCCAGAGACCA 730  
|||||  
17 CACACCCAGAGACCA 1

187  
US-10-138-674B-1886/C  
; Sequence 1886, Application US/10138674B  
; Patent No. 7034009  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related  
; TO OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674B  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20829  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1886  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674B-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1505 TTCATCTGAGACCATCA 1521  
|||||  
17 TTCATCTGAGACCATCA 1

188  
138-674B-6345/c  
ence 6345, Application US/10138674B  
nt No. 7034009  
RAL INFORMATION:  
LICANT: Sirna Therapeutics, Inc.  
LICANT: Paveco, Pam  
LICANT: McSwiggen, James  
LICANT: Stinchcomb, Dan  
LICANT: Escobedo, Jaime  
LE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
E REFERENCE: MHB00-876-N (400/049)  
RENT FILING DATE: 2002-05-03  
BER OF SEQ ID NOS: 20829  
TWARE: Patentin version 3.0  
ID NO 6345  
NGTH: 17  
PR: RNA  
3ANISM: Homo sapiens  
138-674B-6345  
Y Match 0.8%; Score 13.8; DB 1; Length 17;  
Local Similarity 88.2%; Pred. No. 1.4e+02;  
hes 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
713 ACTCAACGACGAGACC 729  
17 ACACACGACGAGAGACC 1  
189  
513-974B-240/c  
ence 240, Application US/08513974B  
nt No. 6114139  
ERAL INFORMATION:  
PLICANT: Hinuma, Shuji  
PLICANT: Hosoya, Masaki  
PLICANT: Fujii, Ryo  
PLICANT: Ohnaki, Tetsuya  
PLICANT: Fukusumi, Shoji  
PLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
UMBER OF SEQUENCES: 380  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
URRANT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
RIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
RIOR APPLICATION DATA: JP 7-093389  
FILING DATE: 19-AUG-1995  
RIOR APPLICATION DATA: JP 7-057186  
FILING DATE: 16-MAR-1995  
RIOR APPLICATION DATA: JP 7-007177  
APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA: JP 6-189272  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: JP 6-189272  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-513-974B-240  
Query Match 0.8%; Score 13.6; DB 1; Length 23;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1307 AGGAGAGCCGACGAGCGC 1326  
Db 23 AGGAGAGCCGACGAGCGC 4  
RESULT 190  
US-08-585-684B-2100  
Sequence 2100, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ. ID NO.: 2100:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-585-684B-2100

CY Match          0.8%; Score 13.4; DB 1; Length 15;
Local Similarity 60.0%; Pred. No. 1.2e+02;
hes 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0

1409 GCTTCCTCCTCAATG 1423
||||:||||:|
1 GCUCUCUCUCAUG 15

r 191
-585-684B-2101
ence 2101, Application US/08585684B
ent No. 5877021
ERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ. ID NO.: 2101:
SEQUENCE CHARACTERISTICS:

```

```

: LENGTH: 15 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-08-585-684B-2101

Query Match
Best Local Similarity 53.3%; Score 13.4; DB 1; Length 15;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1411 TTCTCTCCCAATG 1425
:|:|:|:|:|:|
Db 1 tucucuccaauug 15

RESULT 192
US-09-038-073-2100
: Sequence 2100, Application US/09038073
: Patent No. 6194150
:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 80courage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038.073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2100:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-2100

Query Match
Best Local Similarity 60.0%; Score 13.4; DB 1; Length 15;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAATG 1423
|||:|:|:|:|:|
Db 1 gcucucuccaauug 15

RESULT 193

```

038-073-2101  
 since 2101, Application US/09038073  
 nt No. 6194150  
 ERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 APPLICANT: McSwiggen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Fast-Seq Version 1.5  
 URENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/038,073  
 FILING DATE:  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585,684  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEEX: 67-3510  
 ORAMTION FOR SEQ ID NO: 2101:  
 EQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 038-073-2101  
 Y Match 0.8%; Score 13.4; DB 1; Length 15;  
 Local Similarity 53.3%; Pred. No. 1.2e+02;  
 hes 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 1411 TTCTCCTCAATGTG 1425  
 :||:||||||:|  
 1 UUCUCUCCCAUGUG 15  
 194  
 502-185-16  
 since 16, Application US/08502185  
 nt No. 5639736  
 ERAL INFORMATION:  
 APPLICANT: Robinson, Gregory S.  
 APPLICANT: Robinson, Gregory S.  
 TITLE OF INVENTION: Human VEGF-Specific  
 TITLE OF INVENTION: Oligonucleotides  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lappin & Kusmer  
 STREET: 200 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/502,185  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kerner, Ann-Louise  
 REGISTRATION NUMBER: 33,523  
 REFERENCE/DOCKET NUMBER: HYZ-031CPDVI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-330-1300  
 TELEFAX: 617-330-1311  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: cdna  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-502-185-16  
 Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1011 CTTCTCTCTGCC 1023  
 Db 1 CTTCTCTCTGCC 13  
 RESULT 195  
 US-08-398-945-16  
 Sequence 16, Application US/08398945  
 Patent No. 5639872  
 GENERAL INFORMATION:  
 APPLICANT: Robinson, Gregory S.  
 TITLE OF INVENTION: Human VEGF-Specific  
 TITLE OF INVENTION: Oligonucleotides  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lappin & Kusmer  
 STREET: 200 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/398,945  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kerner, Ann-Louise  
 REGISTRATION NUMBER: 33,523  
 REFERENCE/DOCKET NUMBER: HYZ-031CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-330-1300  
 TELEFAX: 617-330-1311  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear



MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
398-945-16

Query Match 0.7%; Score 13; DB 1; Length 15;  
Local Similarity 100.0%; Pred. No. 1.4e+02;  
Indels 0; Mismatches 0; Gaps 0;

1011 CTTCCTCTGCCC 1023

1 CTTCCTCTGCCC 13

196  
501-779-16  
ence 16, Application US/08501779  
nt No. 5661135  
ERAL INFORMATION:  
PPICANT: Robinson, Gregory S.  
TITLE OF INVENTION: Human VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 53  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/501,779  
ILING DATE:  
CLASSIFICATION: 514  
TTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031CPDV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
FORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
501-779-16  
y Match 0.7%; Score 13; DB 1; Length 15;  
Local Similarity 100.0%; Pred. No. 1.4e+02;  
Indels 0; Mismatches 0; Gaps 0;  
1011 CTTCCTCTGCCC 1023  
1 CTTCCTCTGCCC 13  
197  
501-713-16  
ence 16, Application US/08501713  
nt No. 5710136  
ERAL INFORMATION:  
PPICANT: Robinson, Gregory S.  
PPICANT: Smith, Lois E.H.

TITLE OF INVENTION: Inhibition of  
TITLE OF INVENTION: Neovascularization Using  
TITLE OF INVENTION: VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/501,713  
ILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031DV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
FORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-501-713-16

Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023

Db 1 CTTCCTCTGCCC 13

RESULT 198  
US-08-378-860-16  
Sequence 16, Application US/08378860  
Patent No. 5731294  
GENERAL INFORMATION:  
APPLICANT: Robinson, Gregory S.  
APPLICANT: Smith, Lois E.H.  
TITLE OF INVENTION: Inhibition of  
TITLE OF INVENTION: Neovascularization Using  
TITLE OF INVENTION: VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,860  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031  
ELECTRONIC INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
ORAMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
YPOTHEICAL: NO  
NTI-SENSE: NO  
378-860-16  
Y Match 0.7%; Score 13; DB 1; Length 15;  
Local Similarity 100.0%; Pred. No. 1.4e+02;  
hes 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1011 CTTCCTCTGCCCC 1023  
1 CTTCCTCTGCCCC 13  
199  
501-626-16  
ence 16, Application US/08501626  
nt No. 580156  
ERAL INFORMATION:  
PLICANT: Robinson, Gregory S.  
TITLE OF INVENTION: Inhibition of  
TITLE OF INVENTION: Neovascularization Using  
TITLE OF INVENTION: VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
UMBER OF SEQUENCES: 53  
ORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
OMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
URRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/501,626  
ILING DATE:  
CLASSIFICATION: 435  
TTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031DV4  
ELECTRONIC INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
ORAMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
YPOTHEICAL: NO

ANTI-SENSE: NO  
US-08-501-626-16  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1011 CTTCCTCTGCCCC 1023  
1 CTTCCTCTGCCCC 13  
RESULT 200  
US-08-501-356-16  
Sequence 16, Application US/08501356  
Patent No. 5814620  
GENERAL INFORMATION:  
APPLICANT: Robinson, Gregory S.  
TITLE OF INVENTION: Inhibition of  
TITLE OF INVENTION: Neovascularization Using  
TITLE OF INVENTION: VEGF-Specific  
TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/501,356  
ILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-031DV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
ORAMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
YPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-501-356-16  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1011 CTTCCTCTGCCCC 1023  
1 CTTCCTCTGCCCC 13  
RESULT 201  
US-09-034-205-66/C  
Sequence 66, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.  
 APPLICANT: Fors, Lance P.  
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
 TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
 NUMBER OF SEQUENCES: 68  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MEDLEN & CARROLL, LLP  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/034,205  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MacKnight, Kamryn T.  
 REGISTRATION NUMBER: 38,230  
 REFERENCE/DOCKET NUMBER: FORS-03268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338  
 INFORMATION FOR SEQ ID NO: 66:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "DNA"  
 -034-205-66  
 Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 : Local Similarity 87.5%; Pred. No. 1.7e+02;  
 : Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1436 CCACAGGCGCTTGGC 1451  
 |||||  
 16 CCACAGGCGCTTGGC 1  
 : 202  
 : 677-218B-66/C  
 : ence 66, Application US/09677218B  
 : nt No. 635375  
 : NERAL INFORMATION:  
 : APPLICANT: Lyamichev, Victor I.  
 : Brow, Mary Ann D.  
 : Fors, Lance P.  
 : Neri, Bruce P.  
 : TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
 : STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
 : NUMBER OF SEQUENCES: 68  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: MEDLEN & CARROLL, LLP  
 : STREET: 220 Montgomery Street, Suite 2200  
 : CITY: San Francisco  
 : STATE: CA  
 : COUNTRY: USA  
 : ZIP: 94104  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B  
 FILING DATE: 02-Oct-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/034,205  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MacKnight, Kamryn T.  
 REGISTRATION NUMBER: 38,230  
 REFERENCE/DOCKET NUMBER: FORS-03268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 705-8410  
 TELEFAX: (415) 397-8338  
 INFORMATION FOR SEQ ID NO: 66:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "DNA"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
 US-09-677-218B-66  
 Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1436 CCACAGGCGCTTGGC 1451  
 |||||  
 16 CCACAGGCGCTTGGC 1  
 RESULT 203  
 US-09-677-192-66/C  
 : Sequence 66, Application US/09677192  
 : Patent No. 6358691  
 : GENERAL INFORMATION:  
 : APPLICANT: Lyamichev, Victor I.  
 : APPLICANT: Brow, Mary Ann D.  
 : APPLICANT: Fors, Lance P.  
 : APPLICANT: Neri, Bruce P.  
 : TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
 : FILE REFERENCE: OLIGONUCLEOTIDES  
 : FILE REFERENCE: FORS-04708  
 : CURRENT APPLICATION NUMBER: US/09/677,192  
 : PRIOR FILING DATE: 2000-10-02  
 : CURRENT APPLICATION NUMBER: 09/034,205  
 : PRIOR FILING DATE: 1998-03-03  
 : NUMBER OF SEQ ID NOS: 68  
 : SOFTWARE: Patentin Ver. 2.0  
 : SEQ ID NO 66  
 : LENGTH: 16  
 : TYPE: DNA  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 : US-09-677-192-66  
 Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1436 CCACAGGCGCTTGGC 1451  
 |||||  
 16 CCACAGGCGCTTGGC 1  
 RESULT 204  
 US-09-270-933-9/C  
 : Sequence 9, Application US/09270933  
 : Patent No. 6365375  
 : GENERAL INFORMATION:

LICANT: Dietmaier, Wolfgang  
 LICANT: Ruschoff, Josef  
 LE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION  
 LE OF INVENTION: PCR  
 E REFERENCE: 4802  
 RENT APPLICATION NUMBER: US/09/270,933  
 RENT FILING DATE: 1999-03-16  
 LER APPLICATION NUMBER: DE 198 13 317.0  
 LER FILING DATE: 1998-03-26  
 BER OF SEQ ID NOS: 17  
 TWARE: Patentin Ver. 2.0  
 ID NO 9  
 NGTH: 16  
 PE: DNA  
 GANISM: Artificial Sequence  
 ATURE:  
 HER INFORMATION: Description of Artificial Sequence: Primer for  
 HER INFORMATION: Human Genomic Sequence  
 270-933-9

Y Match 0.7%; Score 12.8; DB 1; Length 16;  
 Local Similarity 87.5%; Pred. No. 1.7e+02;  
 hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1061 AGCAGGCTACCTGGC 1076  
 16 ATCAGGCTACCTGTC 1

205  
 060-299-412  
 ence 412, Application US/09060299  
 nt No. 6545137

ERAL INFORMATION:  
 PPLICANT: Todd, John A  
 PPLICANT: Hess, John W  
 PPLICANT: Caskey, Charles T  
 PPLICANT: Cox, Roger D  
 PPLICANT: Gerhold, David  
 PPLICANT: Hammond, Holly  
 PPLICANT: Hey, Patricia  
 PPLICANT: Kawaguchi, Yoshiniko  
 PPLICANT: Merriman, Tony R  
 PPLICANT: Metzker, Michael L  
 TLE OF INVENTION: No. 6545137el Receptor  
 UMBER OF SEQUENCES: 455

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon and Vanderhye  
 STREET: 1100 No. 6545137ch Glebe Road, Eighth Floor  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: US

OMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 URRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/060,299  
 FILING DATE: 15-APR-1998  
 CLASSIFICATION: 435  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/043,553  
 FILING DATE: 15-APR-1997  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/048,740  
 FILING DATE: 05-JUN-1997  
 TORNEY/AGENT INFORMATION:  
 NAME: B.J.Sadoff  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/DOCKET NUMBER: 620-35  
 ELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)816-4091

TELEFAX: (703)816-4100  
 INFORMATION FOR SEQ ID NO: 412:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

US-09-060-299-412

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 13 CCGCGGGCAGCGCGGC 28  
 1 CCGCGGGTAGTGCGGC 16

RESULT 206  
 US-09-402-923A-412  
 Sequence 412, Application US/09402923A  
 Patent No. 6555654  
 GENERAL INFORMATION:  
 APPLICANT: Todd, John A  
 Hess, John W  
 Caskey, Charles T  
 Cox, Roger D  
 Gerhold, David  
 Hammond, Holly  
 Hey, Patricia  
 Kawaguchi, Yoshiniko  
 Merriman, Tony R  
 Metzker, Michael L  
 TITLE OF INVENTION: No. 6555654el LDL-Receptor  
 NUMBER OF SEQUENCES: 455  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon and Vanderhye  
 STREET: 1100 No. 6555654th Glebe Road, Eighth Floor  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: US  
 ZIP: VA 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/402,923A  
 FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB98/01102  
 FILING DATE: 15-APR-1998  
 APPLICATION NUMBER: US 60/043,553  
 FILING DATE: 15-APR-1997  
 APPLICATION NUMBER: US 60/048,740  
 FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: B.J.Sadoff  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/DOCKET NUMBER: 620-81  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)816-4091  
 TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 412:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 412:  
 US-09-402-923A-412

Y Match 0.7%; Score 12.8; DB 1; Length 16;  
Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

13 CCGCGGCGACGCGGCGC 28  
|||||  
1 CCGCGGCGTAGGTGGGC 16

207  
371-772B-5850/c  
ence 5850, Application US/09371772B  
ant No. 6566127  
RAL INFORMATION:  
PLICANT: Ribozyme Pharmaceuticals, Inc.  
PLICANT: Pavco, Pam  
PLICANT: MCSwigen, Jim  
PLICANT: Stinchcomb, Dan  
PLICANT: Escobedo, Jaime  
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
E REFERENCE: MBH00,876-J (237/198)  
RENT FILING DATE: 1999-08-10  
OR APPLICATION NUMBER: US 60/005,974  
OR FILING DATE: 1995-10-26  
OR APPLICATION NUMBER: US 08/584,040  
OR FILING DATE: 1996-01-08  
BER OF SEQ ID NOS: 14225  
TWARE: Patentin version 3.0  
ID NO 5850  
NGTH: 16  
PE: RNA  
GANISM: Homo sapiens  
371-772B-5850

Y Match 0.7%; Score 12.8; DB 1; Length 16;  
Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1594 AAAATCTCAATCTTC 1609  
|||||  
16 AAAATCACAATCTTC 1

208  
371-772B-5863  
ence 5863, Application US/09371772B  
ant No. 6566127  
RAL INFORMATION:  
PLICANT: Ribozyme Pharmaceuticals, Inc.  
PLICANT: Pavco, Pam  
PLICANT: MCSwigen, Jim  
PLICANT: Stinchcomb, Dan  
PLICANT: Escobedo, Jaime  
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
E REFERENCE: MBH00,876-J (237/198)  
RENT FILING DATE: 1999-08-10  
OR APPLICATION NUMBER: US 60/005,974  
OR FILING DATE: 1995-10-26  
OR APPLICATION NUMBER: US 08/584,040  
OR FILING DATE: 1996-01-08  
BER OF SEQ ID NOS: 14225  
TWARE: Patentin version 3.0  
ID NO 5863  
NGTH: 16  
PE: RNA  
GANISM: Homo sapiens  
371-772B-5863

Y Match 0.7%; Score 12.8; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.7e+02;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 389 ACAAAGATGAGGAC 404  
|||||  
DB 1 ACAAUGAUGAGGAC 16

RESULT 209  
US-09-479-005A-50/c  
Sequence 50, Application US/09479005A  
Patent No. 6656731  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
FILE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
E REFERENCE: MBH00-884-C  
CURRENT APPLICATION NUMBER: US/09/479,005A  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/444,209  
PRIOR FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: US 09/159,274  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: US 60/059,473  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 1208  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 50  
LENGTH: 16  
TYPE: RNA  
GANISM: Homo sapiens  
US-09-479-005A-50

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 527 AGTCCACAATCTTCTT 542  
|||||  
DB 16 AATTCATTAATCTTCTT 1

RESULT 210  
US-09-402-618B-66/c  
Sequence 66, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamchev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
FILE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
E REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 66  
LENGTH: 16  
TYPE: DNA  
GANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-402-618B-66

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1436 CCACAGGCGCTTGGC 1451  
 |||||  
 16 CCACAGGCGCTTGGC 1

211  
 720-435A-410/c  
 ence 410, Application US/09720435A  
 nt No. 6803187  
 RAL INFORMATION:

LICANT: Stuyver, Lieven  
 LE OF INVENTION: Method for detection of drug-selected mutations in the protease  
 LE OF INVENTION: gene  
 E REFERENCE: 11362.0030.PCUS00 INNS:030  
 RENT APPLICATION NUMBER: US/09/720,435A  
 RENT FILING DATE: 2001-06-25  
 CR APPLICATION NUMBER: PCT/EP99/04317  
 CR FILING DATE: 1999-06-22  
 CR APPLICATION NUMBER: 98870143.9  
 CR FILING DATE: 1998-06-24  
 BR OF SEQ ID NOS: 529  
 TWARE: PatentIn version 3.2  
 ID NO 410  
 NGTH: 16  
 PE: DNA  
 GANISM: Aids-associated retrovirus  
 720-435A-410

y Match 0.7%; Score 12.8; DB 1; Length 16;  
 Local Similarity 87.5%; Pred. No. 1.7e+02;  
 hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1586 TGAGTCACAAATCTC 1601  
 |||||  
 16 TGAGTCACAAATCTC 1

212  
 543-679A-1408/c  
 ence 1408, Application US/09543679A  
 nt No. 7034007  
 NERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.  
 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
 COMPOSITIONS, KIT & METHOD FOR TREATMENT  
 OF AIRWAY DISORDERS ASSOCIATED WITH  
 BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
 NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
 STREET: 7 Clarke Drive  
 CITY: Cranbury  
 STATE: NJ  
 COUNTRY: USA

ZIP: 08512  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-R  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: N/A

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/543,679A  
 FILING DATE: 13-Apr-2000  
 CLASSIFICATION: UNKNOWN  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amzel, Viviana  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: EPI-0067191b  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035  
 TELEFAX: 413-254-9245  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 1408:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1408:  
 US-09-543-679A-1408

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 636 GTGAGCCAGCGCAC 651  
 |||||  
 Db 16 GGCAGCCAGCGCAC 1

RESULT 213  
 US-09-543-679A-1453  
 Sequence 1453, Application US/09543679A  
 Patent No. 7034007  
 GENERAL INFORMATION:  
 APPLICANT: NYCE, Jonathan W.  
 TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
 COMPOSITIONS, KIT & METHOD FOR TREATMENT  
 OF AIRWAY DISORDERS ASSOCIATED WITH  
 BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
 NUMBER OF SEQUENCES: 3111  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
 STREET: 7 Clarke Drive  
 CITY: Cranbury  
 STATE: NJ  
 COUNTRY: USA

ZIP: 08512  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-R  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: N/A

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/543,679A  
 FILING DATE: 13-Apr-2000  
 CLASSIFICATION: UNKNOWN  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amzel, Viviana  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: EPI-0067191b  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035  
 TELEFAX: 413-254-9245  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 1453:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1453:  
 US-09-543-679A-1453

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 537 CTTCTTCCATCGCC 552

|||||  
1 CTTCTTCCGCTCTCC 16

214  
-543-679A-1454  
ence 1454, Application US/09543679A  
nt No. 7034007  
GENERAL INFORMATION:  
APPLICANT: NICE, Jonathan W.  
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
COMPOSITIONS, KIT & METHOD FOR TREATMENT  
OF AIRWAY DISORDERS ASSOCIATED WITH  
BRONCHOCONSTRICITION, LUNG INFLAMMATION,  
NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: NJ

COUNTRY: USA  
ZIP: 08512

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-R  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: N/A

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/543,679A  
FILING DATE: 13-Apr-2000  
CLASSIFICATION: UNKNOWN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/127,958  
FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-0067191b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245

TELEX: <Unknown>  
FORMATION FOR SEQ ID NO: 1454:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1454:  
-543-679A-1454

Y Match 0.7%; Score 12.8; DB 1; Length 16;  
Local Similarity 87.5%; Pred. No. 1.7e+02;  
hes 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

537 CTTCTTCCGCTCTCC 552  
1 CTTCTTCCGCTCTCC 16

215  
-138-674B-5850/c  
ence 5850, Application US/10138674B  
nt No. 7034009

GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
LE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
E REFERENCE: MBH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674B  
CURRENT FILING DATE: 2002-05-03  
NUMBER OF SEQ ID NOS: 20829  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 5850  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-138-674B-5850

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1594 AAAATCTCATTTCTTC 1609  
Db 16 AAAATCACAATCTTC 1

RESULT 216

US-10-138-674B-5863  
Sequence 5863, Application US/10138674B  
Patent No. 7034009

GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R

FILE REFERENCE: MBH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674B

NUMBER OF SEQ ID NOS: 20829

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5863

LENGTH: 16

TYPE: RNA

ORGANISM: Homo sapiens  
US-10-138-674B-5863

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 1.7e+02;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 389 ACAAAGATGAGGAC 404  
Db 1 ACAAUGAUGAGGAC 16

RESULT 217

US-07-701-935-14  
Sequence 14, Application US/07701935  
Patent No. 5336595

GENERAL INFORMATION:  
APPLICANT: Strader, C. D.

APPLICANT: Fong, T. M.

TITLE OF INVENTION: Method of Using Human Neurokinin-1

RECEPTOR SHORT FORM

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Releasee #1.0, Version #1.25

```

Query Match          0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      861 CGTAGTGGGAATCACACTA 879
      1 |||||
      1 CATAGTGTGATTCACACTA 19

RESULT 219
US-08-785-750-2
; Sequence 2, Application US/08785750
; Patent No. 5846528
;
GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,750
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 514
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,355
; FILING DATE: 18-JAN-1996
;
ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0009.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 325-7812
; TELEFAX: (415) 325-7823
;
INFORMATION FOR SEQ ID NO: 2:
;
SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-785-750-2

Query Match          0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      315 GGCACTGCTCTACA 328
      1 |||||
      1 GGCACTGCTCTGCA 14

RESULT 220
US-08-588-355-1
; Sequence 1, Application US/08588355
; Patent No. 5858351
;
GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KESSLER, PAUL D.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE

```



TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/588,355  
APPLICATION NUMBER: US/08/588,355  
FILING DATE: 18-JAN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
FORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
589-355-1  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
315 GGCAGCTGCTTACA 328  
|||||  
1 GGCAGCTGCTTACA 14  
116-780-5  
221  
ence 5, Application US/09116780  
ent No. 5945335  
RAL INFORMATION:  
LICANT: Colosi, Peter  
TITLE OF INVENTION: Adenovirus Helper-Free Systems for Producing  
LE OF INVENTION: Recombinant AAV Virions Lacking Oncogenic Sequences  
E REFERENCE: 2555.2.2  
CURRENT APPLICATION NUMBER: US/09/116,780  
CURRENT FILING DATE: 1998-07-16  
OTHER APPLICATION NUMBER: 08/745,957  
OTHER FILING DATE: 1996-11-07  
OTHER APPLICATION NUMBER: 60/006,402  
OTHER FILING DATE: 1995-11-09  
BER OF SEQ ID NOS: 11  
TMWARE: Patentin Ver. 2.0  
ID NO 5  
NGTH: 14  
PE: DNA  
GANISM: Artificial Sequence  
ATURE:  
HER INFORMATION: Description of Artificial Sequence: oligonucleotide  
116-780-5  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Query 315 GGCAGCTGCTTACA 328  
|||||  
Db 1 GGCAGCTGCTTACA 14  
RESULT 222  
US-08-812-102-1  
Sequence 1, Application US/08812102  
Patent No. 5952221  
GENERAL INFORMATION:  
APPLICANT: KURTZMAN, GARY J.  
APPLICANT: COLOSI, PETER C.  
APPLICANT: YOSHIDA, JUN  
APPLICANT: MIZUNO, MASAKI  
APPLICANT: OKADA, HIDEO  
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID  
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,102  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,209  
FILING DATE: 06-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415) 325-7823  
FORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-812-102-1  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Query 315 GGCAGCTGCTTACA 328  
|||||  
Db 1 GGCAGCTGCTTACA 14  
RESULT 223  
US-08-784-757-1  
Sequence 1, Application US/08784757  
Patent No. 5962313  
GENERAL INFORMATION:  
APPLICANT: PODSAKOFF, GREGORY M.  
APPLICANT: KESSLER, PAUL D.  
APPLICANT: BYRNE, BARRY J.  
APPLICANT: KURTZMAN, GARY J.

TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,757  
FILING DATE: 16-JAN-1997  
CLASSIFICATION: 514  
RITOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/588,355  
FILING DATE: 18-JAN-1996  
TITORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009.20  
ELECTRONIC COMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415) 325-7823  
ORINATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
784-757-1  
Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
315 GGCAGCTGCCTGCA 328  
|||||  
1 GGCAGCTGCCTGCA 14  
224  
745-957-1  
ence 1, Application US/08745957  
nt No. 6004797  
ERAL INFORMATION:  
PLICANT: COLOSI, PETER C.  
TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN  
TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED & ROBINS LLP  
STREET: 285 HAMILTON AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/745,957  
FILING DATE: 07-NOV-1996  
CLASSIFICATION: 530  
RITOR APPLICATION DATA:

APPLICATION NUMBER: US 60/006,402  
FILING DATE: 09-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 327-3231  
TELEFAX: (415) 327-3400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-745-957-1  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 315 GGCAGCTGCCTGCA 328  
|||||  
Db 1 GGCAGCTGCCTGCA 14  
RESULT 225  
US-08-765-340-124/C  
Sequence 124, Application US/08765340  
Patent No. 6150092  
GENERAL INFORMATION:  
APPLICANT: UCHIDA, K.,  
APPLICANT: UCHIDA, T.,  
APPLICANT: TANAKA, Y.,  
APPLICANT: MATSUDA, Y.,  
APPLICANT: KONDO, S.,  
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID  
NUMBER OF SEQUENCES: 185  
TITLE OF INVENTION: COMPOUND  
NUMBER OF SEQUENCES: 185  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version  
SOFTWARE: #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,340  
FILING DATE: 23-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 145146/94  
FILING DATE: 27-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 31130/94  
FILING DATE: 21-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SERUNIAN, LESLIE  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 1452-4005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
-765-340-124

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

468 AGTGTGAAGTTCA 481  
|||||  
14 AGTGTGAAGTTCA 1

226  
-309-042-1  
ence 1, Application US/09309042  
nt No. 621163  
ERAL INFORMATION:  
PPICANT: PODSAKOFF, GREGORY M.  
PPICANT: KESSLER, PAUL D.  
PPICANT: BYRNE, BARRY J.  
PPICANT: KURTZMAN, GARY J.  
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
TITLE OF INVENTION: CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
NUMBER OF SEQUENCES: 5  
ADDRESS: ADDRESS:  
CORRESPONDENCE ADDRESS:  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/309,042  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/588,355  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
FORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
-309-042-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCAGCTGCTTACA 328  
|||||  
1 GGCAGCTGCTTACA 14

227  
-063-667-17/c

Sequence 17, Application US/09063667C  
Patent No. 6225291  
GENERAL INFORMATION:  
APPLICANT: LEWIN, ALFRED S.  
APPLICANT: HAUSWIRTH, WILLIAM W.  
APPLICANT: DRENER, KIMBERLY  
TITLE OF INVENTION: MATERIALS AND METHODS FOR RIBOZYME TREATMENT OF  
FILE REFERENCE: 4300.011500  
CURRENT APPLICATION NUMBER: US/09/063,667C  
CURRENT FILING DATE: 1998-04-21  
EARLIER APPLICATION NUMBER: 60/046,147  
EARLIER FILING DATE: 1997-05-09  
EARLIER APPLICATION NUMBER: 60/044,492  
EARLIER FILING DATE: 1997-04-21  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 14  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
US-09-063-667-17

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388  
|||||  
Db 14 CGAAGTACTCCGA 1

RESULT 228  
US-09-205-337-2  
Sequence 2, Application US/09205337  
Patent No. 6325998  
GENERAL INFORMATION:  
APPLICANT: PODSAKOFF, GREGORY M.  
APPLICANT: KURTZMAN, GARY J.  
TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING  
RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESS: ADDRESS:  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,337  
FILING DATE: 04-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/785,750  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415) 325-7823  
FORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
205-337-2

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCGAGCTGCTTACA 328  
|||||  
1 GGCGAGCTGCTTACA 14

229  
406-362-1  
ence 1, Application US/09406362  
nt No. 6335011  
NERAL INFORMATION:  
APPLICANT: PODSAKOFF, GREGORY M.  
KESSLER, PAUL D.  
BYRNE, BARRY J.  
KURTZMAN, GARY J.  
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,362  
FILING DATE: 28-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/784,757  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415) 325-7823  
FORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
406-362-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCGAGCTGCTTACA 328  
|||||  
1 GGCGAGCTGCTTACA 14

RESULT 230  
US-09-755-734-1  
; Sequence 1, Application US/09755734  
; Patent No. 6391858  
; GENERAL INFORMATION:  
; APPLICANT: PODSAKOFF, GREGORY M.  
; KESSLER, PAUL D.  
; BYRNE, BARRY J.  
; KURTZMAN, GARY J.  
; TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
; CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/755,734  
; FILING DATE: 04-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/588,355  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCracken, THOMAS P.  
; REGISTRATION NUMBER: 38,548  
; REFERENCE/DOCKET NUMBER: 0800-0009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 325-7812  
; TELEFAX: (650) 325-7823  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
; US-09-755-734-1

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCGAGCTGCTTACA 328  
|||||  
DB 1 GGCGAGCTGCTTACA 14

RESULT 231  
US-09-406-363-1  
; Sequence 1, Application US/09406363  
; Patent No. 6482633  
; GENERAL INFORMATION:  
; APPLICANT: COLOSI, PETER C.  
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN  
; RECOMBINANT AAV VIRION PRODUCTION  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED & ROBINS LLP  
; STREET: 285 HAMILTON AVENUE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA

ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,363  
FILING DATE: 28-Sep-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/745,357  
FILING DATE: 11-Jul-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 327-3400  
TELEFAX: (415)327-3231  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
-406-363-1  
Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
Indels 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
315 GGCAGCTGCTTACA 328  
|||||||  
1 GGCAGCTGCTTACA 14  
222  
-649-890-1  
ence 1, Application US/09649890  
nt No. 6531456  
GENERAL INFORMATION:  
APPLICANT: KURTZMAN, GARY J.  
COLOSI, PETER C.  
YOSHIDA, JUN  
MIZUNO, MASAAKI  
OKADA, HIDEO  
TITLE OF INVENTION: GENE THERAPY FOR THE TREATMENT OF SOLID  
TUMORS USING RECOMBINANT ADENO-ASSOCIATED VIRUS VECTORS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/649,890  
FILING DATE: 28-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,102  
FILING DATE: 05-MAR-1997  
APPLICATION NUMBER: US 60/013,209  
FILING DATE: 06-MAR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415) 325-7823  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-649-890-1  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 315 GGCAGCTGCTTACA 328  
|||||||  
Db 1 GGCAGCTGCTTACA 14  
RESULT 233  
US-09-969-204A-1  
Sequence 1, Application US/09969204A  
Patent No. 6610290  
GENERAL INFORMATION:  
APPLICANT: PODSAKOFF, GREGORY M.  
KESSLER, PAUL D.  
BYRNE, BARRY J.  
KURTZMAN, GARY J.  
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS  
VIRIONS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/969,204A  
FILING DATE: 01-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,362  
FILING DATE: 28-Sep-1999  
APPLICATION NUMBER: 08/784,757  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0009,20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 325-7812  
TELEFAX: (415)325-7823  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
969-204A-1

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

315 GGCACTGCTTACA 328  
|||||  
1 GGCACTGCTTACA 14

234  
874-601-6  
ence 6, Application US/09874601  
nt No. 6632057  
RAL INFORMATION:  
LICANT: LEMIN, ALFRED S.  
LICANT: SHAM, LYNN C.  
LICANT: GRANT, MARIA B.  
LE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
E REFERENCE: 4300.014100  
RENT FILING DATE: 2001-05-01  
OR APPLICATION NUMBER: 09/063,667  
OR FILING DATE: 1998-04-21  
OR APPLICATION NUMBER: 60/046,147  
OR FILING DATE: 1997-05-09  
OR APPLICATION NUMBER: 60/044,492  
OR FILING DATE: 1997-04-21  
BER OF SEQ ID NOS: 182  
TMARE: Patentin version 3.0  
ID NO 6  
NGTH: 14  
PE: RNA  
GANISM: Artificial Sequence  
ATURE:  
ME/KEY: misc feature  
CATION: (1..7)  
HER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
874-601-6

Y Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 64.3%; Pred. No. 1.5e+02;  
hes 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

689 TGCTGGCTTCCC 702  
|||||  
1 UGUGGUCUCCCC 14

235  
177-871-1  
ence 1, Application US/10177871  
nt No. 6897063  
NERAL INFORMATION:  
APPLICANT: COLOSI, PETER C.  
TITLE OF INVENTION: RECOMBINANT AAV VIRION PRODUCTION

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED & ROBINS LLP  
STREET: 285 HAMILTON AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/177,871  
FILING DATE: 19-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/745,957  
FILING DATE: 07-NOV-1996  
APPLICATION NUMBER: US 60/006,402  
FILING DATE: 09-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCracken, THOMAS P.  
REGISTRATION NUMBER: 38,548  
REFERENCE/DOCKET NUMBER: 0800-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 327-3400  
TELEFAX: (415)327-3231  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-177-871-1

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 315 GGCACTGCTTACA 328  
|||||  
Db 1 GGCACTGCTTACA 14

RESULT 236  
US-09-341-700A-1573  
; Sequence 1573, Application US/09341700A  
; Patent No. 6972171  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Briesch, Wolfgang  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
; FILE REFERENCE: 10496/P63763USO  
; CURRENT APPLICATION NUMBER: US/09/341,700A  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: PCT/EP98/00497  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1573  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antisense oligonucleotide  
US-09-341-700A-1573

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1145 TCCGCTGGGCTTC 1158  
|||||  
Db 1 TCCCTTGGGCTTC 14

RESULT 237  
US-09-543-679A-1511

ence 1511, Application US/09543679A  
ent No. 7034007  
GENERAL INFORMATION:  
APPLICANT: NICE, Jonathan W.  
TITLE OF INVENTION: LOW ADENOSINE AMT1-SENSE OLIGONUCLEOTIDE,  
COMPOSITIONS, KIT & METHOD FOR TREATMENT  
OF AIRWAY DISORDERS ASSOCIATED WITH  
BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
NUMBER OF SEQUENCES: 3111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: NJ  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-R  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: N/A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/543,679A  
FILING DATE: 13-Apr-2000  
CLASSIFICATION: UNKNOWN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/127,958  
FILING DATE: 1998-08-03  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-0067191b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
FORMATION FOR SEQ ID NO: 1511:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1511:  
-543-679A-1511  
Match 0.7%; Score 12.4; DB 1; Length 14;  
Local Similarity 92.9%; Pred. No. 1.5e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
344 CCTCTGTGTGGGC 357  
1 CCTCTGTGTGGGC 14  
238  
-363-240A-619/C  
ence 619, Application US/08363240A  
nt No. 5705388  
GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwigen, James  
APPLICANT: Biesaler, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: PREVENTION, INHIBITION OF  
TITLE OF INVENTION: PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
FORMATION FOR SEQ ID NO: 619:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-619  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1253 TGTACAAAGTCAGC 1266  
DB 14 TGGACAAAGTCAGC 1  
RESULT 239  
US-08-585-684B-797/C  
Sequence 797, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELE: 67-3510  
 ORAMATION FOR SEQ ID NO: 797:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 585-684B-797

y Match 0.7%; Score 12.4; DB 1; Length 15;  
 Local Similarity 92.9%; Pred. No. 1.7e+02;  
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

296 CCTGCAATTGTC 309  
 |||||  
 15 CCTGCAATTGTC 2

240  
 585-684B-798/C  
 ence 798, Application US/08585684B  
 ne No. 5877021  
 ERAL INFORMATION:  
 PPLICANT: Stinchcomb, Daniel T.  
 PPLICANT: Jarvis, Thale  
 PPLICANT: McSwiggen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 UMBER OF SEQUENCES: 2751  
 ORRESPONDENCE ADDRESS:  
 ADDRESSER: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 URRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/585,684B  
 FILING DATE: January 16, 1996  
 RIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,951  
 FILING DATE: July 7, 1995  
 TTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELE: 67-3510  
 ORAMATION FOR SEQ ID NO: 798:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 585-684B-798  
 y Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 296 CCTGCAATTGTC 309  
 |||||  
 Db 14 CCTGCAATTGTC 1

RESULT 241  
 US-08-585-684B-2099  
 ; Sequence 2099, Application US/08585684B  
 ; Patent No. 5877021  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stinchcomb, Daniel T.  
 ; APPLICANT: Jarvis, Thale  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 ; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 ; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 ; NUMBER OF SEQUENCES: 2751  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/585,684B  
 ; FILING DATE: January 16, 1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/000,951  
 ; FILING DATE: July 7, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 218/078  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELE: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 2099:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-585-684B-2099  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;



TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/585,684B  
 FILING DATE: January 16, 1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,951  
 FILING DATE: July 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2295:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -585-684B-2295  
 Match 0.7%; Score 12.4; DB 1; Length 15;  
 Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Mismatches 5; Indels 0; Gaps 0;  
 1409 GCTTCTCTCCCAAT 1422  
 ||::||:||||:  
 2 GCUCUCUCUCAU 15  
 243  
 -585-684B-2296  
 hence 2296, Application US/08585684B  
 int No. 5877021  
 GENERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 APPLICANT: McSwigen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/585,684B  
 FILING DATE: January 16, 1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,951  
 FILING DATE: July 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2296:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -585-684B-2296  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 1409 GCTTCTCTCCCAAT 1422  
 ||::||:||||:  
 DB 1 GCUCUCUCUCAU 14  
 RESULT 244  
 US-08-550-120-13/C  
 Sequence 13, Application US/08550120  
 Patent No. 5985554  
 GENERAL INFORMATION:  
 APPLICANT: Hiroshi TANIMURA et al.  
 TITLE OF INVENTION: METHOD FOR PROBING THE FUNCTION OF A PROTEIN  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/550,120  
 FILING DATE: October 30, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-269417  
 FILING DATE: No. 598554ember 2, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 NUCLEIC TYPE: other nucleic acid, synthetic DNA  
 550-120-13

Y Match 0.7%; Score 12.4; DB 1; Length 15;  
 Local Similarity 92.9%; Pred. No. 1.7e+02;  
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

910 GACCGCTACACGCA 923  
 |||||  
 14 GACCGGTACACGCA 1

245  
 269-519A-2/C  
 ence 2, Application US/09269519A  
 nt No. 6180347

AL INFORMATION:  
 LICANT: Iida, Yukari  
 LICANT: Koshimoto, Hiroyuki  
 LICANT: Kondo, Satoshi  
 LICANT: Tsuji, Akihiko  
 LE OF INVENTION: Method for Monitoring Transcriptional Synthesis of RNA  
 E REFERENCE: 200783  
 RENT APPLICATION NUMBER: US/09/269,519A  
 RENT FILING DATE: 1999-04-02  
 OR APPLICATION NUMBER: PCT/JP98/00444  
 OR FILING DATE: 1998-02-03  
 OR APPLICATION NUMBER: JP 020632/1997  
 OR FILING DATE: 1997-02-03  
 BER OF SEQ ID NOS: 11  
 TWARE: PatentIn Ver. 2.1  
 ID NO 2

NGTH: 15  
 PE: DNA  
 GANISM: Artificial Sequence  
 ATURE:  
 HER INFORMATION: Description of Artificial Sequence: XELF-IF  
 HER INFORMATION: acceptor probe  
 269-519A-2

Y Match 0.7%; Score 12.4; DB 1; Length 15;  
 Local Similarity 92.9%; Pred. No. 1.7e+02;  
 hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1155 CTTCAAGCATGGCT 1168  
 |||||  
 14 CTTCAAGTATGGCT 1

246  
 038-073-797/C  
 ence 797, Application US/09038073  
 nt No. 6194150

ERAL INFORMATION:  
 PPICANT: Stinchcomb, Daniel T.  
 PPICANT: Jarvis, Thale  
 PPICANT: McSwigen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 UMBER OF SEQUENCES: 2751  
 ORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 OMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEO Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/038,073  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585,684  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wardburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 797:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-038-073-797

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CTTGCAATTTGC 309  
 |||||  
 Db 15 CTTGGAATTTGC 2

RESULT 247  
 US-09-038-073-798/C  
 Sequence 798, Application US/09038073  
 Patent No. 6194150  
 GENERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 APPLICANT: McSwigen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEO Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/038,073  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585,684  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wardburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 798:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -038-073-798

Local Similarity 92.9%; Score 12.4; DB 1; Length 15;  
 Mismatches 0; Indels 0; Gaps 0;  
 Conservative 1;

296 CCTGCAATTGTC 309  
 |||||  
 14 CCTGGGAATTGTC 1

248  
 -038-073-2099  
 ence 2099, Application US/09038073  
 ent No. 6194150  
 ERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/038,073  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585,684

FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440

TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2099:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -038-073-2099

Local Similarity 0.7%; Score 12.4; DB 1; Length 15;  
 Mismatches 0; Indels 0; Gaps 0;  
 Conservative 5;

1409 GCTTCTCCTCCAT 1422  
 ||::||:|:|||||:

Db 2 GCUUCUCCCAU 15

RESULT 249  
 US-09-038-073-2295  
 Sequence 2295, Application US/09038073  
 Patent No. 6194150  
 GENERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/038,073  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/585,684

FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440

TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2295:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-038-073-2295

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 GCTTCTCCTCCAT 1422  
 ||::||:|:|||||:

Db 2 GCUUCUCCCAU 15

RESULT 250  
 US-09-038-073-2296  
 Sequence 2296, Application US/09038073  
 Patent No. 6194150  
 GENERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,073  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,684  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078

ELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
ORAMATION FOR SEQ ID NO: 2296:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

038-073-2296

Y Match 0.7%; Score 12.4; DB 1; Length 15;  
Local Similarity 57.1%; Pred. No. 1.7e+02;  
hes 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

1409 GCTTCCTCCCAAT 1422  
||:|:|:|:|:  
1 GCUCUCUCUCAU 14

251  
081-646-167/c  
ence 167, Application US/09081646  
nt No. 6333152

RAL INFORMATION:  
LICANT: Kinzler, Kenneth  
LICANT: Vogelstein, Bert  
LICANT: Zhang, Lin  
LICANT: Zhou, Wei  
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

E REFERENCE: 01107.74664  
RENT APPLICATION NUMBER: US/09/081,646  
RENT FILING DATE: 1998-05-20  
LIER APPLICATION NUMBER: 60/047,352  
LIER FILING DATE: 1997-05-21

BER OF SEQ ID NOS: 871  
TWARE: FastSeq for Windows Version 3.0  
ID NO 167  
NGTH: 15

PE: DNA  
GANISM: Homo sapiens  
081-646-167

Y Match 0.7%; Score 12.4; DB 1; Length 15;  
Local Similarity 92.9%; Pred. No. 1.7e+02;  
hes 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

367 GTGATGTGATCAT 380

Db 15 GCGATGTGATCAT 2

RESULT 252  
US-09-856-662-4  
; Sequence 4, Application US/09856662  
; Patent No. 6790616

; GENERAL INFORMATION:  
; APPLICANT: MORIBE, Toyoki et al.  
; TITLE OF INVENTION: Method for typing HLA class 1 genes  
; FILE REFERENCE: 0032-0261P

; CURRENT APPLICATION NUMBER: US/09/856,662  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: JP P1998-335151  
; PRIOR FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 4

; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:DNA probe A239A  
US-09-856-662-4

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGAG 1320  
|||||||  
Db 2 AGGAGAGCCGAG 15

RESULT 253  
US-09-341-700A-196/c  
; Sequence 196, Application US/09341700A  
; Patent No. 6972171

; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
; FILE REFERENCE: 10496/P63763USO

; CURRENT APPLICATION NUMBER: US/09/341,700A  
; CURRENT FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: PCT/EP98/00497  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31

; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 196

; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antisense oligonucleotide  
US-09-341-700A-196

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 CAAGCGCAAGTGG 949  
|||||||  
Db 14 CAAGCGCAAGTGG 1

RESULT 254  
US-10-156-306B-7875  
; Sequence 7875, Application US/10156306B

```

nt No. 7022828
RAL INFORMATION:
LICANT: Ribozyme Pharmaceuticals, Inc.
LE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
LE OF INVENTION: Levels of IKK-Gamma and PKR
REFERENCE: MBH01-664-A (400/050)
RENT APPLICATION NUMBER: US/10/156,306B
RENT FILING DATE: 2002-05-28
BER OF SEQ ID NOS: 8014
TWARE: PatentIn version 3.0
ID NO 7875
NGTH: 15
PE: RNA
GANISM: Homo sapiens
-156-306B-7875

y March 0.7%; Score 12.4; DB 1; Length 15;
Local Similarity 57.1%; Pred. No. 1.7e+02;
hes 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

105 CCCTCTGTCTGCT 118
|||:|:|:|:|:|
1 CCCUUCUGUCUCU 14

t 255
93-12600-15/c
ence 15, Application PC/TUS9312600
ERAL INFORMATION:
PLICANT: Denner, Larry A.
PLICANT: Rege, Ajay A.
ITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
ITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
UMBER OF SEQUENCES: 29
ORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Shore &
ADDRESSEE: Milnamow, Ltd.
REET: 180 North Steetson, Suite 4700
ITY: Chicago
STATE: Illinois
OUNTRY: USA
ZIP: 60601
OMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
TTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
ORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
OLECULE TYPE: DNA (genomic)
93-12600-15

y Match 0.7%; Score 12.4; DB 1; Length 15;
y Local Similarity 92.9%; Pred. No. 1.7e+02;

```

```

Matches      13:  Conservative      0:  Mismatches      1:  Indels      0:  Gaps      0:
QY      1202  ATGAGGGGCTGGAA 1215
      ||| |||||
      15  ATGTGGGGCTGGAA 2

RESULT 256
US-08-513-974B-61
; Sequence 61, Application US/08513974B
; Patent No. 6114139
;
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235

```

REFERENCE/DOCKET NUMBER: 45753  
ELECTRONIC INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
ORAMTION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OLECUE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA  
FEATURE:  
OTHER INFORMATION: N = inosine  
513-974B-61

Y Match 0.7%; Score 12.4; DB 1; Length 29;  
Local Similarity 65.0%; Pred.No.3.le+02;  
hes 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1046 TGAAGAGTTTATCCGACG 1065  
::|::||| |  
2 KGWAGWAGGGCACGCCAGCG 21

257  
776-971-32  
ence 32, Application US/08776971B  
nt No. 6228984  
NERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
Habata, Yugo  
Kawamata, Yuji  
Hosoya, Masaki  
Fuji, Ryo  
Fukusumi, Shoji  
Kitada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
City: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSO for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,971B  
FILING DATE: 06-Feb-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/03821  
FILING DATE: 28-Dec-1996  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-Dec-1995  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-Mar-1996  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-Aug-1996  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-Sep-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Conlin, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 47176  
ELECTRONIC INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440

```

1      INFORMATION FOR SEQ ID NO: 32:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 29 base pairs
4          TYPE: nucleic acid
5          STRANDEDNESS: single
6          TOPOLOGY: linear
7      MOLECULE TYPE: other nucleic acid
8      DESCRIPTION: /desc = "synthetic DNA"
9      SEQUENCE DESCRIPTION: SEQ ID NO: 32:
10     US-08-776-971-32
11
12     Query Match      0.7%; Score 12.4; DB 1; Length 29;
13     Best Local Similarity 65.0%; Pre. Min. 5.1e+02;
14     Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0.
15
16     Oy      1046 TGAAGAAGTTATCCAGCAG 1065
17     Db      2 KGMAGMAGCGACGCCAGCAG 21
18
19     RESULT 258
20     US-09-461-436B-61
21     Sequence 61, Application US/09461436B
22     Patent No. 6538107
23     GENERAL INFORMATION:
24     APPLICANT: Shuji Hinuma
25     Yasuaki Ito
26     Ryo Fujii
27     TITLE OF INVENTION: G Protein Coupled Receptor Protein,
28     Production, And Use Thereof
29
30     NUMBER OF SEQUENCES: 61
31     CORRESPONDENCE ADDRESS:
32     ADDRESSEE: Edwards & Angell, LLP
33     STREET: 101 Federal Street
34     CITY: BOSTON
35     STATE: MA
36     COUNTRY: USA
37     ZIP: 02209
38
39     COMPUTER READABLE FORM:
40     MEDIUM TYPE: Floppy disk
41     COMPUTER: IBM PC compatible
42     OPERATING SYSTEM: PC-DOS/MS-DOS
43     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
44     CURRENT APPLICATION DATA:
45     APPLICATION NUMBER: US/09/461,436B
46     FILING DATE: 14-Dec-1999
47     CLASSIFICATION: <Unknown>
48
49     PRIOR APPLICATION DATA:
50     APPLICATION NUMBER: 08/513,974
51     FILING DATE: 14-SEP-1995
52     APPLICATION NUMBER: PCT/JP95/01599
53     FILING DATE: 10-AUG-1995
54     APPLICATION NUMBER: 7-093989
55     FILING DATE: 19-APR-1995
56     APPLICATION NUMBER: 7-057186
57     FILING DATE: 16-MAR-1995
58     APPLICATION NUMBER: 7-007177
59     FILING DATE: 20-JAN-1995
60     APPLICATION NUMBER: 6-326611
61     FILING DATE: 28-DEC-1994
62     APPLICATION NUMBER: 6-270017
63     FILING DATE: 02-NOV-1994
64     APPLICATION NUMBER: 6-236357
65     FILING DATE: 30-SEP-1994
66     APPLICATION NUMBER: 6-236356
67     FILING DATE: 30-SEP-1994
68     APPLICATION NUMBER: 6-189274
69     FILING DATE: 11-AUG-1994
70     APPLICATION NUMBER: 6-189273
71     FILING DATE: 11-AUG-1994
72     APPLICATION NUMBER: 6-189272
73     FILING DATE: 11-AUG-1994
74
75     ATTORNEY/AGENT INFORMATION:

```

```

FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-576-290-32

Query Match 0.7%; Score 12.4; DB 1; Length 29;
Best Local Similarity 65.0%; Pred. No. 3.1e+02;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0

CY 1046 TGAAGAGTTTATCCAGCAG 1065
      |||:|||||
Db 2 KGMAGWAGGCGAGCCAGCAG 21

RESULT 260
US-09-716-147-32
Sequence 32, Application US/09716147
Patent No. 6881545
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
          Habata, Yugo
          Kawamata, Yuji
          Hosoya, Masaki
          Fujii, Ryo
          Fukusumi, Shoji
          Kitada, Chieko
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/716.147
FILING DATE: 17-NOV-6881545-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026

```





## ATTORNEY/AGENT INFORMATION:

NAME: Fugit, Donna R.  
 REGISTRATION NUMBER: 32,135  
 REFERENCE/DOCKET NUMBER: P-5550  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -608-584-8

Y Match 0.7%; Score 12; DB 1; Length 14;  
 Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

935 CCAAGCGCAAGG 946  
 |||||  
 14 CCAAGCGCAAGG 3

264  
 -720-435A-38/c  
 ence 38, Application US/09720435A  
 nt No. 6803187  
 ERAL INFORMATION:  
 PLICANT: Stuyver, Lieven  
 LE OF INVENTION: Method for detection of drug-selected mutations in the protease  
 E REFERENCE: 11362.0030.PCUS00 INNS.030  
 REENT APPLICATION NUMBER: US/09/720,435A  
 REENT FILING DATE: 2001-06-25  
 OR APPLICATION NUMBER: PCT/EP99/04317  
 OR FILING DATE: 1999-06-22  
 OR APPLICATION NUMBER: 98870143.9  
 OR FILING DATE: 1998-06-24  
 BER OF SEQ ID NOS: 529  
 TMWARE: Patentin version 3.2  
 ID NO 38  
 NGTH: 14  
 PE: DNA  
 GANISM: Aids-associated retrovirus  
 -720-435A-38

Y Match 0.7%; Score 12; DB 1; Length 14;  
 Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

663 CTGTGTCATCTG 674  
 |||||  
 13 CTGTGTCATCTG 2

265  
 -588-595-1  
 ence 1, Application US/08588595  
 nt No. 5958769  
 ERAL INFORMATION:  
 PLICANT: Roberts, James M.  
 PLICANT: Coats, Steven R.  
 PLICANT: Fero, Matthew L.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MEDIATING  
 TLE OF INVENTION: CELL CYCLE PROGRESSION  
 UMBER OF SEQUENCES: 13  
 ORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew  
 STREET: One Market Plaza, Stuart Street Tower  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105-1492  
 OMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/588,595  
 FILING DATE: 18-JAN-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parmelee, Steven W.  
 REGISTRATION NUMBER: 31,990  
 REFERENCE/DOCKET NUMBER: 14538A-19  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-467-9600  
 TELEFAX: 415-543-5043  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleotide  
 US-08-588-595-1

Query Match 0.7%; Score 12; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGCTCTCCTGC 691  
 :|||:|:|:|:|:  
 Db 1 UGCGUCUCCUGC 12

RESULT 266  
 US-09-180-437-143/c  
 Sequence 143, Application US/09180437  
 Patent No. 6251873  
 GENERAL INFORMATION:  
 APPLICANT: FUKUSAKO, Shioji  
 APPLICANT: MORISAWA, Yoshihumi  
 APPLICANT: KUSUYAMA, Takehi  
 TITLE OF INVENTION: Antisense Compounds to CD14  
 FILE REFERENCE: 1110-209P  
 CURRENT APPLICATION NUMBER: US/09/180,437  
 CURRENT FILING DATE: 1998-11-06  
 EARLIER APPLICATION NUMBER: PCT/JP98/00953  
 EARLIER FILING DATE: 1998-03-09  
 EARLIER APPLICATION NUMBER: 09-053518 JAPAN  
 EARLIER FILING DATE: 1997-03-07  
 NUMBER OF SEQ ID NOS: 289  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 143  
 LENGTH: 15  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: other nucleic  
 OTHER INFORMATION: acid  
 US-09-180-437-143

Query Match 0.7%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCCACAGACT 157  
 |||||  
 Db 12 AGCCACAGACT 1

RESULT 267  
 US-09-275-850-31/c  
 Sequence 31, Application US/09275850A  
 Patent No. 6261774  
 GENERAL INFORMATION:

LICANT: Pagratis, Nikos  
LICANT: Gold, Larry  
LICANT: Sheatland, Timur  
LICANT: Javornik, Brenda  
LE OF INVENTION: Truncation SELEX Method  
E REFERENCE: NEX 79  
RENT APPLICATION NUMBER: US/09/275, 850A  
RENT FILING DATE: 1999-03-24  
BER OF SEQ ID NOS: 351  
TWARE: Patentin Ver. 2.0  
ID NO 31  
NGTH: 15  
PE: RNA  
GANISM: E. coli  
275-850-31

Y Match 0.7%; Score 12; DB 1; Length 15;  
Local Similarity 100.0%; Pred. No. 1.9e+02;  
hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

832 CCCCTGCTGTG 843  
|||||  
14 CCCCTGCTGTG 3

268  
081-646-49/c  
ence 49, Application US/09081646  
nt No. 6333152  
RAL INFORMATION:  
LICANT: Kinzler, Kenneth  
LICANT: Vogelstein, Bert  
LICANT: Zhang, Lin  
LICANT: Zhou, Wei  
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and  
LE OF INVENTION: Cancer Cells  
E REFERENCE: 01107.74664  
RENT APPLICATION NUMBER: US/09/081, 646  
RENT FILING DATE: 1998-05-20  
LIER APPLICATION NUMBER: 60/047,352  
LIER FILING DATE: 1997-05-21  
BER OF SEQ ID NOS: 871  
TWARE: PastSeq for Windows Version 3.0  
ID NO 49  
NGTH: 15  
PE: DNA  
GANISM: Homo sapiens  
081-646-49

Y Match 0.7%; Score 12; DB 1; Length 15;  
Local Similarity 100.0%; Pred. No. 1.9e+02;  
hes 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1522 GAAACACCCCTCA 1533  
|||||  
14 GAAACACCCCTCA 3

269  
081-646-560/c  
ence 560, Application US/09081646  
nt No. 6333152  
RAL INFORMATION:  
LICANT: Kinzler, Kenneth  
LICANT: Vogelstein, Bert  
LICANT: Zhang, Lin  
LICANT: Zhou, Wei  
LE OF INVENTION: Gene Expression Profiles in No. 6333152mal and  
LE OF INVENTION: Cancer Cells  
E REFERENCE: 01107.74664  
RENT APPLICATION NUMBER: US/09/081, 646  
RENT FILING DATE: 1998-05-20  
LIER APPLICATION NUMBER: 60/047,352

EARLIER FILING DATE: 1997-05-21  
NUMBER OF SEQ ID NOS: 871  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 560  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-081-646-560

Query Match 0.7%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 CCTCCCTTCATG 1491  
|||||  
Db 12 CCTCCCTTCATG 1

RESULT 270  
US-09-015-188-6/c  
Sequence 6, Application US/09015188C  
Patent No. 6399358  
GENERAL INFORMATION:  
APPLICANT: Williams, Kevin J  
APPLICANT: Tabas, Ira  
TITLE OF INVENTION: A Human Gene Encoding Human Chondroitin  
FILE REFERENCE: JEPF-0231  
CURRENT APPLICATION NUMBER: US/09/015,188C  
CURRENT FILING DATE: 1998-01-29  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-015-188-6

Query Match 0.7%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 641 CCACAGCCACCA 652  
|||||  
Db 12 CCACAGCCACCA 1

RESULT 271  
US-09-720-435A-39/c  
Sequence 39, Application US/09720435A  
Patent No. 6803187  
GENERAL INFORMATION:  
APPLICANT: Stuyver, Lieven  
TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease  
FILE REFERENCE: 11362.0030.PCUS00 INNS:030  
CURRENT APPLICATION NUMBER: US/09/720,435A  
CURRENT FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: PCT/EP99/04317  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 98870143.9  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 529  
SOFTWARE: Patentin Version 3.2  
SEQ ID NO 39  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Aids-associated retrovirus  
US-09-720-435A-39

Query Match 0.7%; Score 12; DB 1; Length 15;

: Local Similarity 100.0%; Pred. No. 1.9e+02;  
: Res 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

663 CTGTGTCATCTG 674

|||||  
12 CTGTGTCATCTG 1

: 272

: 907-111-31/C  
: Invention 31, Application US/09907111

: Patent No. 6855496

: SERIAL INFORMATION:

: APPLICANT: Pagratia, Nikos

: APPLICANT: Gold, Larry

: APPLICANT: Sheatland, Timur

: APPLICANT: Javornik, Brenda

: TITLE OF INVENTION: Truncation SELEX Method

: PREFERENCE: NEX 79

: CURRENT APPLICATION NUMBER: US/09/907,111

: PRIOR FILING DATE: 2001-07-17

: PRIOR APPLICATION NUMBER: 09/275,850

: PRIOR FILING DATE: 1999-03-24

: NUMBER OF SEQ ID NOS: 351

: TWARE: PatentIn Ver. 2.0

: ID NO 31

: LENGTH: 15

: ORGANISM: E. coli

: 907-111-31

: Match 0.7%; Score 12; DB 1; Length 15;

: Local Similarity 100.0%; Pred. No. 1.9e+02;  
: Res 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

832 CCCCTGCTGTG 843

|||||  
14 CCCCTGCTGTG 3

: completed: June 12, 2006, 07:38:01  
: time : 6 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:21:45 ; Search time 30 Seconds  
(without alignments)  
3.467 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766

Sequence: 1 aatcagagccaccgcgcggc.....cgagtctcatctcagatg 1766

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1462 seqs, 29446 residues

Total number of hits satisfying chosen parameters: 2924

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Database : us-09-930-503a-6.sl.rnpbms4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	1.6	28	1	US-10-310-914A-386265
2	28	1.6	28	1	US-10-310-914A-386265
3	27	1.5	27	1	US-10-005-956-1216
4	26	1.5	26	1	US-10-310-914A-386278
5	26	1.5	27	1	US-10-005-956-1305
6	25	1.4	25	1	US-09-747-429-12
7	25	1.4	25	1	US-09-747-429-13
8	25	1.4	25	1	US-10-005-956-1125
9	25	1.4	25	1	US-10-005-956-1300
10	25	1.4	25	1	US-10-005-956-1300
11	25	1.4	25	1	US-10-628-066-12
12	25	1.4	25	1	US-10-628-066-13
13	25	1.4	25	1	US-10-719-900-67259
14	25	1.4	25	1	US-10-719-900-67259
15	25	1.4	25	1	US-10-719-900-67259
16	25	1.4	25	1	US-10-809-189-67915
17	25	1.4	25	1	US-10-809-189-67915
18	25	1.4	25	1	US-10-809-189-67915
19	25	1.4	25	1	US-11-060-756-34834
20	25	1.4	25	1	US-11-060-756-34834
21	25	1.4	25	1	US-11-060-756-34834
22	25	1.4	25	1	US-11-060-756-34834
23	25	1.4	25	1	US-11-060-756-34834
24	25	1.4	25	1	US-11-060-756-34834
25	25	1.4	25	1	US-11-060-756-34834
26	25	1.4	25	1	US-11-060-756-34834
27	25	1.4	25	1	US-11-060-756-34834
28	25	1.4	25	1	US-11-060-756-34834
29	25	1.4	25	1	US-11-060-756-34834
30	25	1.4	25	1	US-11-060-756-34834
31	25	1.4	25	1	US-11-060-756-34834
32	25	1.4	25	1	US-11-060-756-34834
33	25	1.4	25	1	US-11-060-756-34834

107	25	1.4	25	1	US-11-060-756-196323	Sequence 196323,
108	25	1.4	25	1	US-11-060-756-197870	Sequence 197870,
109	25	1.4	25	1	US-11-060-756-198758	Sequence 198758,
110	25	1.4	25	1	US-11-060-756-202952	Sequence 202952,
111	25	1.4	25	1	US-11-060-756-204546	Sequence 204546,
112	25	1.4	25	1	US-11-060-756-205830	Sequence 205830,
113	25	1.4	25	1	US-11-060-756-206207	Sequence 206207,
114	25	1.4	25	1	US-11-060-756-207277	Sequence 207277,
115	25	1.4	25	1	US-11-060-756-207312	Sequence 207312,
116	25	1.4	25	1	US-11-060-756-213399	Sequence 213399,
117	25	1.4	25	1	US-11-060-756-220646	Sequence 220646,
118	25	1.4	25	1	US-11-060-756-227033	Sequence 227033,
119	25	1.4	25	1	US-11-060-756-238277	Sequence 238277,
120	25	1.4	25	1	US-11-060-756-242329	Sequence 242329,
121	25	1.4	25	1	US-11-060-756-246182	Sequence 246182,
122	25	1.4	25	1	US-11-060-756-247883	Sequence 247883,
123	25	1.4	25	1	US-11-060-756-251001	Sequence 251001,
124	25	1.4	25	1	US-11-060-756-256929	Sequence 256929,
125	25	1.4	25	1	US-11-060-756-264993	Sequence 264993,
126	25	1.4	25	1	US-11-060-756-266512	Sequence 266512,
127	25	1.4	25	1	US-11-060-756-267837	Sequence 267837,
128	25	1.4	25	1	US-11-060-756-271421	Sequence 271421,
129	25	1.4	25	1	US-11-060-756-271732	Sequence 271732,
130	25	1.4	25	1	US-11-060-756-273114	Sequence 273114,
131	25	1.4	25	1	US-11-060-756-273130	Sequence 273130,
132	25	1.4	25	1	US-11-060-756-274710	Sequence 274710,
133	25	1.4	25	1	US-11-060-756-274779	Sequence 274779,
134	25	1.4	25	1	US-11-060-756-275674	Sequence 275674,
135	25	1.4	25	1	US-11-060-756-276554	Sequence 276554,
136	25	1.4	25	1	US-11-060-756-281504	Sequence 281504,
137	25	1.4	25	1	US-11-060-756-283191	Sequence 283191,
138	25	1.4	25	1	US-11-060-756-285749	Sequence 285749,
139	25	1.4	25	1	US-11-060-756-285791	Sequence 285791,
140	25	1.4	25	1	US-11-060-756-290567	Sequence 290567,
141	25	1.4	25	1	US-11-060-756-300784	Sequence 300784,
142	25	1.4	25	1	US-11-060-756-301167	Sequence 301167,
143	25	1.4	25	1	US-11-121-849-111033	Sequence 111033,
144	25	1.4	25	1	US-11-121-849-111034	Sequence 111033,
145	25	1.4	25	1	US-11-121-849-111035	Sequence 111033,
146	25	1.4	25	1	US-11-121-849-111036	Sequence 111033,
147	25	1.4	25	1	US-11-121-849-111037	Sequence 111037,
148	25	1.4	25	1	US-11-121-849-111038	Sequence 111038,
149	25	1.4	25	1	US-11-121-849-111039	Sequence 111039,
150	25	1.4	25	1	US-11-121-849-111040	Sequence 111040,
151	25	1.4	25	1	US-11-121-849-111041	Sequence 111041,
152	25	1.4	25	1	US-11-121-849-111042	Sequence 111042,
153	25	1.4	25	1	US-11-121-849-111043	Sequence 111043,
154	25	1.4	25	1	US-11-121-849-192687	Sequence 192687,
155	25	1.4	25	1	US-11-121-849-192688	Sequence 192688,
156	25	1.4	25	1	US-11-121-849-192689	Sequence 192689,
157	25	1.4	25	1	US-11-121-849-192690	Sequence 192690,
158	25	1.4	25	1	US-11-121-849-192691	Sequence 192691,
159	25	1.4	25	1	US-11-121-849-192692	Sequence 192692,
160	25	1.4	25	1	US-11-121-849-192693	Sequence 192693,
161	25	1.4	25	1	US-11-121-849-192694	Sequence 192694,
162	25	1.4	25	1	US-11-121-849-192695	Sequence 192695,
163	25	1.4	25	1	US-11-121-849-192696	Sequence 192696,
164	25	1.4	25	1	US-11-121-849-192697	Sequence 192697,
165	25	1.4	25	1	US-11-121-849-192698	Sequence 192698,
166	25	1.4	25	1	US-11-036-317-481475	Sequence 1306, Ap
167	25	1.4	25	1	US-10-005-956-1304	Sequence 481475,
168	25	1.4	25	1	US-10-044-597-23	Sequence 1304, Ap
169	25	1.4	25	1	US-10-278-087A-61	Sequence 23, Appl
170	25	1.4	25	1	US-11-054-211-32	Sequence 61, Appl
171	25	1.4	25	1	US-10-005-956-1215	Sequence 32, Appl
172	25	1.4	25	1	US-10-005-956-1215	Sequence 1215, Ap
173	25	1.4	25	1	US-10-719-900-67260	Sequence 67260, A
174	25	1.4	25	1	US-10-719-900-237659	Sequence 237659,
175	25	1.4	25	1	US-10-719-900-247410	Sequence 247410,
176	25	1.4	25	1	US-10-719-900-253859	Sequence 253859,
177	25	1.4	25	1	US-10-719-900-890393	Sequence 890393,
178	25	1.4	25	1	US-10-809-189-67914	Sequence 67914, A
179	25	1.4	25	1	US-10-809-189-67926	Sequence 67926, A
	23.4	1.3	25	1	US-11-036-317-400602	Sequence 400602,

180	23.4	1.3	25	1	US-11-036-317-444773	Sequence 444773,
181	23.4	1.3	25	1	US-11-036-317-466837	Sequence 466837,
182	23.4	1.3	25	1	US-11-060-756-169932	Sequence 169932,
183	23.4	1.3	25	1	US-09-893-512-4	Sequence 4, Appl1
184	23.4	1.3	29	1	US-10-799-736-4	Sequence 4, Appl1
185	23.4	1.3	29	1	US-10-005-956-1128	Sequence 1128, Ap
186	23	1.3	23	1	US-10-310-914A-386270	Sequence 386270,
187	23	1.3	23	1	US-10-310-914A-386274	Sequence 386274,
188	23	1.3	23	1	US-10-310-914A-386275	Sequence 386275,
189	23	1.3	23	1	US-10-310-914A-386284	Sequence 386284,
190	23	1.3	23	1	US-10-310-914A-386298	Sequence 386298,
191	23	1.3	24	1	US-09-930-503-34	Sequence 34, Appl
192	23	1.3	24	1	US-11-036-317-490648	Sequence 490648,
193	22.4	1.3	25	1	US-11-060-756-34830	Sequence 14830, A
194	22	1.2	22	1	US-10-005-956-11301	Sequence 11301, Ap
195	22	1.2	22	1	US-10-310-914A-386285	Sequence 386285,
196	22	1.2	22	1	US-10-310-914A-386297	Sequence 386297,
197	22	1.2	22	1	US-10-310-914A-386305	Sequence 386305,
198	22	1.2	22	1	US-10-809-189-67908	Sequence 67908, A
199	22	1.2	25	1	US-10-719-900-237660	Sequence 237660,
200	21.8	1.2	25	1	US-10-719-900-455081	Sequence 455081,
201	21.8	1.2	25	1	US-10-719-900-479312	Sequence 479312, A
202	21.8	1.2	25	1	US-10-809-189-679313	Sequence 679313, A
203	21.8	1.2	25	1	US-11-060-756-34801	Sequence 34801, A
204	21.8	1.2	25	1	US-11-060-756-34809	Sequence 34809, A
205	21.8	1.2	25	1	US-11-060-756-34810	Sequence 34810, A
206	21.8	1.2	25	1	US-11-060-756-34811	Sequence 34811, A
207	21.8	1.2	25	1	US-11-060-756-34831	Sequence 34831, A
208	21.8	1.2	25	1	US-11-060-756-36931	Sequence 36931, A
209	21.8	1.2	25	1	US-11-060-756-36932	Sequence 36932, A
210	21.8	1.2	25	1	US-11-060-756-232071	Sequence 232071,
211	21.8	1.2	25	1	US-11-060-756-260556	Sequence 260556,
212	21.8	1.2	25	1	US-11-060-756-270235	Sequence 270235,
213	21.8	1.2	27	1	US-08-796-570A-8	Sequence 8, Appl1
214	21.8	1.2	27	1	US-09-929-752-6	Sequence 6, Appl1
215	21.8	1.2	27	1	US-10-064-497-21	Sequence 21, Appl1
216	21.8	1.2	27	1	US-10-067-477-8	Sequence 8, Appl1
217	21.8	1.2	27	1	US-10-090-569-8	Sequence 8, Appl1
218	21.8	1.2	27	1	US-10-184-722-6	Sequence 6, Appl1
219	21.8	1.2	27	1	US-10-184-722-6	Sequence 6, Appl1
220	21.8	1.2	27	1	US-10-278-087A-2	Sequence 2, Appl1
221	21.8	1.2	27	1	US-11-054-211-301	Sequence 301, Appl
222	21.8	1.2	25	1	US-11-060-756-34818	Sequence 34818, A
223	21.8	1.2	25	1	US-09-930-503-23	Sequence 23, Appl
224	21.4	1.2	21	1	US-09-930-503-24	Sequence 24, Appl
225	21	1.2	21	1	US-09-930-503-26	Sequence 26, Appl
226	21	1.2	21	1	US-09-930-503-28	Sequence 28, Appl
227	21	1.2	21	1	US-09-930-503-31	Sequence 31, Appl
228	21	1.2	21	1	US-09-930-503-33	Sequence 33, Appl
229	21	1.2	21	1	US-09-930-503-38	Sequence 38, Appl
230	21	1.2	21	1	US-09-930-503-40	Sequence 40, Appl
231	21	1.2	21	1	US-09-930-503-42	Sequence 42, Appl
232	21	1.2	21	1	US-09-930-503-43	Sequence 43, Appl
233	21	1.2	21	1	US-09-930-503-45	Sequence 45, Appl
234	21	1.2	21	1	US-09-930-503-47	Sequence 47, Appl
235	21	1.2	21	1	US-09-930-503-50	Sequence 50, Appl
236	21	1.2	21	1	US-09-930-503-52	Sequence 52, Appl
237	21	1.2	21	1	US-09-930-503-53	Sequence 53, Appl
238	21	1.2	21	1	US-09-930-503-57	Sequence 57, Appl
239	21	1.2	21	1	US-09-930-503-59	Sequence 59, Appl
240	21	1.2	21	1	US-10-005-956-404	Sequence 404, App
241	21	1.2	21	1	US-10-005-956-407	Sequence 407, App
242	21	1.2	21	1	US-10-005-956-408	Sequence 408, App
243	21	1.2	21	1	US-10-005-956-409	Sequence 409, App
244	21	1.2	21	1	US-10-005-956-467	Sequence 467, App
245	21	1.2	21	1	US-10-005-956-473	Sequence 473, App
246	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
247	21	1.2	21	1	US-10-005-956-535	Sequence 535, App
248	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
249	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
250	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
251	21	1.2	21	1	US-10-005-956-534	Sequence 534, App
252	21	1.2	21	1	US-10-005-956-1212	Sequence 1212, Ap

253	21	1.2	21	1	US-10-005-956-1217	Sequence 1217, App	326	21	1.2	21	1	US-11-127-877-501	Sequence 501, App	
C 254	21	1.2	21	1	US-10-310-914A-386280	Sequence 386280, App	327	21	1.2	21	1	US-11-127-877-502	Sequence 502, App	
C 255	21	1.2	21	1	US-10-310-914A-386281	Sequence 386281, App	328	21	1.2	21	1	US-11-127-877-503	Sequence 503, App	
C 256	21	1.2	21	1	US-10-310-914A-386282	Sequence 386282, App	329	21	1.2	21	1	US-11-127-877-504	Sequence 504, App	
C 257	21	1.2	21	1	US-10-310-914A-386299	Sequence 386299, App	330	21	1.2	21	1	US-11-127-877-505	Sequence 505, App	
258	21	1.2	21	1	US-11-127-877-430	Sequence 430, App	331	21	1.2	21	1	US-11-127-877-506	Sequence 506, App	
259	21	1.2	21	1	US-11-127-877-431	Sequence 431, App	332	21	1.2	21	1	US-11-127-877-507	Sequence 507, App	
260	21	1.2	21	1	US-11-127-877-432	Sequence 432, App	333	21	1.2	21	1	US-11-127-877-508	Sequence 508, App	
261	21	1.2	21	1	US-11-127-877-433	Sequence 433, App	334	21	1.2	21	1	US-11-127-877-509	Sequence 509, App	
262	21	1.2	21	1	US-11-127-877-434	Sequence 434, App	335	21	1.2	21	1	US-11-127-877-510	Sequence 510, App	
263	21	1.2	21	1	US-11-127-877-435	Sequence 435, App	336	21	1.2	21	1	US-11-127-877-511	Sequence 511, App	
264	21	1.2	21	1	US-11-127-877-436	Sequence 436, App	337	21	1.2	21	1	US-11-127-877-512	Sequence 512, App	
265	21	1.2	21	1	US-11-127-877-437	Sequence 437, App	338	21	1.2	21	1	US-11-127-877-513	Sequence 513, App	
266	21	1.2	21	1	US-11-127-877-438	Sequence 438, App	339	21	1.2	21	1	US-11-127-877-514	Sequence 514, App	
267	21	1.2	21	1	US-11-127-877-439	Sequence 439, App	340	21	1.2	21	1	US-11-127-877-515	Sequence 515, App	
268	21	1.2	21	1	US-11-127-877-440	Sequence 440, App	341	21	1.2	21	1	US-11-127-877-516	Sequence 516, App	
269	21	1.2	21	1	US-11-127-877-441	Sequence 441, App	342	21	1.2	21	1	US-11-127-877-517	Sequence 517, App	
270	21	1.2	21	1	US-11-127-877-442	Sequence 442, App	343	21	1.2	21	1	US-11-127-877-518	Sequence 518, App	
271	21	1.2	21	1	US-11-127-877-443	Sequence 443, App	344	21	1.2	21	1	US-11-127-877-519	Sequence 519, App	
272	21	1.2	21	1	US-11-127-877-444	Sequence 444, App	345	21	1.2	21	1	US-11-127-877-520	Sequence 520, App	
273	21	1.2	21	1	US-11-127-877-445	Sequence 445, App	346	21	1.2	21	1	US-11-127-877-521	Sequence 521, App	
274	21	1.2	21	1	US-11-127-877-446	Sequence 446, App	347	21	1.2	21	1	US-11-127-877-522	Sequence 522, App	
275	21	1.2	21	1	US-11-127-877-447	Sequence 447, App	348	21	1.2	21	1	US-11-127-877-523	Sequence 523, App	
276	21	1.2	21	1	US-11-127-877-448	Sequence 448, App	349	21	1.2	21	1	US-11-127-877-524	Sequence 524, App	
277	21	1.2	21	1	US-11-127-877-449	Sequence 449, App	350	21	1.2	21	1	US-11-127-877-525	Sequence 525, App	
278	21	1.2	21	1	US-11-127-877-450	Sequence 450, App	351	21	1.2	21	1	US-11-127-877-526	Sequence 526, App	
279	21	1.2	21	1	US-11-127-877-451	Sequence 451, App	352	21	1.2	21	1	US-11-127-877-527	Sequence 527, App	
280	21	1.2	21	1	US-11-127-877-452	Sequence 452, App	353	21	1.2	21	1	US-11-127-877-528	Sequence 528, App	
281	21	1.2	21	1	US-11-127-877-453	Sequence 453, App	354	21	1.2	21	1	US-11-127-877-529	Sequence 529, App	
282	21	1.2	21	1	US-11-127-877-454	Sequence 454, App	355	21	1.2	21	1	US-11-127-877-530	Sequence 530, App	
283	21	1.2	21	1	US-11-127-877-455	Sequence 455, App	356	21	1.2	21	1	US-11-127-877-531	Sequence 531, App	
284	21	1.2	21	1	US-11-127-877-456	Sequence 456, App	357	21	1.2	21	1	US-11-127-877-532	Sequence 532, App	
285	21	1.2	21	1	US-11-127-877-457	Sequence 457, App	358	21	1.2	21	1	US-11-127-877-533	Sequence 533, App	
286	21	1.2	21	1	US-11-127-877-458	Sequence 458, App	359	21	1.2	21	1	US-11-127-877-534	Sequence 534, App	
287	21	1.2	21	1	US-11-127-877-459	Sequence 459, App	360	21	1.2	21	1	US-11-127-877-535	Sequence 535, App	
288	21	1.2	21	1	US-11-127-877-460	Sequence 460, App	C 361		21	1.2	22	1	US-10-310-914A-386286	Sequence 386286, App
289	21	1.2	21	1	US-11-127-877-461	Sequence 461, App	362	20.8	1.2	25	1	US-10-809-189-67919	Sequence 67919, A	
290	21	1.2	21	1	US-11-127-877-462	Sequence 462, App	363	20.8	1.2	25	1	US-11-036-317-443229	Sequence 443229, A	
291	21	1.2	21	1	US-11-127-877-463	Sequence 463, App	364	20.8	1.2	25	1	US-11-060-756-34802	Sequence 34802, A	
292	21	1.2	21	1	US-11-127-877-464	Sequence 464, App	365	20.8	1.2	25	1	US-11-060-756-36930	Sequence 36930, A	
293	21	1.2	21	1	US-11-127-877-465	Sequence 465, App	366	20.8	1.2	25	1	US-11-060-756-36933	Sequence 36933, A	
294	21	1.2	21	1	US-11-127-877-466	Sequence 466, App	367	20.8	1.2	25	1	US-11-060-756-36934	Sequence 36934, A	
295	21	1.2	21	1	US-11-127-877-467	Sequence 467, App	368	20.8	1.2	25	1	US-11-060-756-36935	Sequence 36935, A	
296	21	1.2	21	1	US-11-127-877-468	Sequence 468, App	369	20.8	1.2	25	1	US-11-060-756-233624	Sequence 233624, A	
297	21	1.2	21	1	US-11-127-877-469	Sequence 469, App	370	20.8	1.2	25	1	US-11-060-756-233625	Sequence 233625, A	
298	21	1.2	21	1	US-11-127-877-470	Sequence 470, App	371	20.6	1.2	24	1	US-10-005-956-1129	Sequence 1129, App	
299	21	1.2	21	1	US-11-127-877-471	Sequence 471, App	C 372		20.6	1.2	24	1	US-10-278-087A-15	Sequence 15, App1
300	21	1.2	21	1	US-11-127-877-472	Sequence 472, App	373	20.4	1.2	25	1	US-11-060-756-34807	Sequence 34807, A	
301	21	1.2	21	1	US-11-127-877-473	Sequence 473, App	374	20.2	1.1	25	1	US-10-719-956-382728	Sequence 382728, A	
302	21	1.2	21	1	US-11-127-877-475	Sequence 475, App	375	20.2	1.1	25	1	US-10-719-900-331659	Sequence 331659, A	
303	21	1.2	21	1	US-11-127-877-476	Sequence 476, App	376	20.2	1.1	25	1	US-10-719-900-146776	Sequence 146776, A	
304	21	1.2	21	1	US-11-127-877-477	Sequence 477, App	377	20.2	1.1	25	1	US-10-719-900-152541	Sequence 152541, A	
305	21	1.2	21	1	US-11-127-877-478	Sequence 478, App	378	20.2	1.1	25	1	US-10-719-900-455080	Sequence 455080, A	
306	21	1.2	21	1	US-11-127-877-479	Sequence 479, App	379	20.2	1.1	25	1	US-10-809-189-67918	Sequence 67918, A	
307	21	1.2	21	1	US-11-127-877-480	Sequence 480, App	380	20.2	1.1	25	1	US-10-809-189-67917	Sequence 67917, A	
308	21	1.2	21	1	US-11-127-877-481	Sequence 481, App	381	20.2	1.1	25	1	US-10-809-189-67930	Sequence 67930, A	
309	21	1.2	21	1	US-11-127-877-484	Sequence 484, App	382	20.2	1.1	25	1	US-10-809-189-67931	Sequence 67931, A	
310	21	1.2	21	1	US-11-127-877-485	Sequence 485, App	383	20.2	1.1	25	1	US-10-956-157-170659	Sequence 170659, A	
311	21	1.2	21	1	US-11-127-877-486	Sequence 486, App	384	20.2	1.1	25	1	US-11-036-317-411229	Sequence 411229, A	
312	21	1.2	21	1	US-11-127-877-487	Sequence 487, App	385	20.2	1.1	25	1	US-11-036-317-413994	Sequence 413994, A	
313	21	1.2	21	1	US-11-127-877-488	Sequence 488, App	386	20.2	1.1	25	1	US-11-060-756-272657	Sequence 272657, A	
314	21	1.2	21	1	US-11-127-877-489	Sequence 489, App	387	20.2	1.1	25	1	US-11-060-756-34785	Sequence 34785, A	
315	21	1.2	21	1	US-11-127-877-490	Sequence 490, App	388	20.2	1.1	25	1	US-11-060-756-34795	Sequence 34795, A	
316	21	1.2	21	1	US-11-127-877-491	Sequence 491, App	389	20.2	1.1	25	1	US-11-060-756-34800	Sequence 34800, A	
317	21	1.2	21	1	US-11-127-877-492	Sequence 492, App	390	20.2	1.1	25	1	US-11-060-756-34804	Sequence 34804, A	
318	21	1.2	21	1	US-11-127-877-493	Sequence 493, App	391	20.2	1.1	25	1	US-11-060-756-36619	Sequence 36619, A	
319	21	1.2	21	1	US-11-127-877-494	Sequence 494, App	392	20.2	1.1	25	1	US-11-060-756-36624	Sequence 36624, A	
320	21	1.2	21	1	US-11-127-877-495	Sequence 495, App	393	20.2	1.1	25	1	US-11-060-756-36940	Sequence 36940, A	
321	21	1.2	21	1	US-11-127-877-496	Sequence 496, App	394	20.2	1.1	25	1	US-11-060-756-56876	Sequence 56876, A	
322	21	1.2	21	1	US-11-127-877-497	Sequence 497, App	395	20.2	1.1	25	1	US-11-060-756-56877	Sequence 56877, A	
323	21	1.2	21	1	US-11-127-877-498	Sequence 498, App	396	20.2	1.1	25	1	US-11-060-756-56878	Sequence 56878, A	
324	21	1.2	21	1	US-11-127-877-499	Sequence 499, App	397	20.2	1.1	25	1	US-11-060-756-122999	Sequence 122999, A	
325	21	1.2	21	1	US-11-127-877-500	Sequence 500, App	398	20.2	1.1	25	1	US-11-060-756-123000	Sequence 123000, A	





545	19	1.1	19	1	US-11-083-784-491234	Sequence	491234,	618	19	1.1	19	1	US-11-101-244-491156	Sequence	491156
546	19	1.1	19	1	US-11-083-784-491236	Sequence	491236,	619	19	1.1	19	1	US-11-101-244-491157	Sequence	491157
547	19	1.1	19	1	US-11-083-784-491237	Sequence	491237,	620	19	1.1	19	1	US-11-101-244-491158	Sequence	491158
548	19	1.1	19	1	US-11-083-784-491238	Sequence	491238	621	19	1.1	19	1	US-11-101-244-491159	Sequence	491159
549	19	1.1	19	1	US-11-083-784-491241	Sequence	491241,	622	19	1.1	19	1	US-11-101-244-491160	Sequence	491160
550	19	1.1	19	1	US-11-083-784-491244	Sequence	491244,	623	19	1.1	19	1	US-11-101-244-491161	Sequence	491161
551	19	1.1	19	1	US-11-083-784-491245	Sequence	491245,	624	19	1.1	19	1	US-11-101-244-491162	Sequence	491162
552	19	1.1	19	1	US-11-083-784-491248	Sequence	491248,	625	19	1.1	19	1	US-11-101-244-491163	Sequence	491163
553	19	1.1	19	1	US-11-083-784-491251	Sequence	491251,	626	19	1.1	19	1	US-11-101-244-491164	Sequence	491164
554	19	1.1	19	1	US-11-083-784-491252	Sequence	491252	627	19	1.1	19	1	US-11-101-244-491165	Sequence	491165
555	19	1.1	19	1	US-11-083-784-491256	Sequence	491256	628	19	1.1	19	1	US-11-101-244-491166	Sequence	491166
556	19	1.1	19	1	US-11-083-784-491262	Sequence	491262,	629	19	1.1	19	1	US-11-101-244-491167	Sequence	491167
557	19	1.1	19	1	US-11-083-784-491263	Sequence	491263,	630	19	1.1	19	1	US-11-101-244-491168	Sequence	491168
558	19	1.1	19	1	US-11-083-784-491264	Sequence	491264,	631	19	1.1	19	1	US-11-101-244-491169	Sequence	491169
559	19	1.1	19	1	US-11-083-784-491265	Sequence	491265,	632	19	1.1	19	1	US-11-101-244-491170	Sequence	491170
560	19	1.1	19	1	US-11-083-784-491268	Sequence	491268	633	19	1.1	19	1	US-11-101-244-491171	Sequence	491171
561	19	1.1	19	1	US-11-083-784-491269	Sequence	491269	634	19	1.1	19	1	US-11-101-244-491172	Sequence	491172
562	19	1.1	19	1	US-11-083-784-491270	Sequence	491270,	635	19	1.1	19	1	US-11-101-244-491173	Sequence	491173
563	19	1.1	19	1	US-11-083-784-491271	Sequence	491271,	636	19	1.1	19	1	US-11-101-244-491174	Sequence	491174
564	19	1.1	19	1	US-11-083-784-491272	Sequence	491272,	637	19	1.1	19	1	US-11-101-244-491175	Sequence	491175
565	19	1.1	19	1	US-11-083-784-491273	Sequence	491273,	638	19	1.1	19	1	US-11-101-244-491176	Sequence	491176
566	19	1.1	19	1	US-11-083-784-491274	Sequence	491274,	639	19	1.1	19	1	US-11-101-244-491177	Sequence	491177
567	19	1.1	19	1	US-11-083-784-491275	Sequence	491275,	640	19	1.1	19	1	US-11-101-244-491178	Sequence	491178
568	19	1.1	19	1	US-11-083-784-491276	Sequence	491276,	641	19	1.1	19	1	US-11-101-244-491179	Sequence	491179
569	19	1.1	19	1	US-11-083-784-491278	Sequence	491278,	642	19	1.1	19	1	US-11-101-244-491180	Sequence	491180
570	19	1.1	19	1	US-11-083-784-491279	Sequence	491279,	643	19	1.1	19	1	US-11-101-244-491181	Sequence	

691	19	1.1	19	1	US-11-101-244-491233	Sequence 491233,	C 764	17.8	1.0	22	1	US-10-310-914A-467164	Sequence 467164,
692	19	1.1	19	1	US-11-101-244-491234	Sequence 491234,	C 765	17.8	1.0	22	1	US-10-310-914A-965080	Sequence 965080,
693	19	1.1	19	1	US-11-101-244-491236	Sequence 491236,	C 766	17.8	1.0	22	1	US-10-310-914A-184635	Sequence 184635,
694	19	1.1	19	1	US-11-101-244-491237	Sequence 491237,	C 767	17.4	1.0	19	1	US-10-005-956-82	Sequence 82, Appl
695	19	1.1	19	1	US-11-101-244-491238	Sequence 491238,	C 768	17.4	1.0	19	1	US-10-005-956-86	Sequence 86, Appl
696	19	1.1	19	1	US-11-101-244-491241	Sequence 491241,	C 769	17.4	1.0	19	1	US-10-005-956-144	Sequence 144, Appl
697	19	1.1	19	1	US-11-101-244-491244	Sequence 491244,	C 770	17.4	1.0	19	1	US-10-005-956-150	Sequence 150, Appl
698	19	1.1	19	1	US-11-101-244-491245	Sequence 491245,	C 771	17.4	1.0	19	1	US-10-310-914A-88048	Sequence 88048, A
699	19	1.1	19	1	US-11-101-244-491248	Sequence 491248,	C 772	17.4	1.0	19	1	US-10-310-914A-1153363	Sequence 1153363,
700	19	1.1	19	1	US-11-101-244-491251	Sequence 491251,	C 773	17.4	1.0	19	1	US-11-083-784-49660	Sequence 49660, A
701	19	1.1	19	1	US-11-101-244-491252	Sequence 491252,	C 774	17.4	1.0	19	1	US-11-083-784-103957	Sequence 103957,
702	19	1.1	19	1	US-11-101-244-491256	Sequence 491256,	C 775	17.4	1.0	19	1	US-11-083-784-490758	Sequence 490758,
703	19	1.1	19	1	US-11-101-244-491262	Sequence 491262,	C 776	17.4	1.0	19	1	US-11-083-784-490759	Sequence 490759,
704	19	1.1	19	1	US-11-101-244-491263	Sequence 491263,	C 777	17.4	1.0	19	1	US-11-083-784-490763	Sequence 490763,
705	19	1.1	19	1	US-11-101-244-491264	Sequence 491264,	C 778	17.4	1.0	19	1	US-11-083-784-491328	Sequence 491328,
706	19	1.1	19	1	US-11-101-244-491265	Sequence 491265,	C 779	17.4	1.0	19	1	US-11-083-784-491368	Sequence 491368,
707	19	1.1	19	1	US-11-101-244-491269	Sequence 491269,	C 780	17.4	1.0	19	1	US-11-083-784-491376	Sequence 491376,
708	19	1.1	19	1	US-11-101-244-491269	Sequence 491269,	C 781	17.4	1.0	19	1	US-11-083-784-491384	Sequence 491384,
709	19	1.1	19	1	US-11-101-244-491270	Sequence 491270,	C 782	17.4	1.0	19	1	US-11-083-784-491392	Sequence 491392,
710	19	1.1	19	1	US-11-101-244-491271	Sequence 491271,	C 783	17.4	1.0	19	1	US-11-083-784-854916	Sequence 854916,
711	19	1.1	19	1	US-11-101-244-491272	Sequence 491272,	C 784	17.4	1.0	19	1	US-11-083-784-877764	Sequence 877764,
712	19	1.1	19	1	US-11-101-244-491273	Sequence 491273,	C 785	17.4	1.0	19	1	US-11-083-784-946470	Sequence 946470,
713	19	1.1	19	1	US-11-101-244-491274	Sequence 491274,	C 786	17.4	1.0	19	1	US-11-083-784-946470	Sequence 946470,
714	19	1.1	19	1	US-11-101-244-491275	Sequence 491275,	C 787	17.4	1.0	19	1	US-11-083-784-141173	Sequence 141173,
715	19	1.1	19	1	US-11-101-244-491276	Sequence 491276,	C 788	17.4	1.0	19	1	US-11-083-784-141173	Sequence 141173,
716	19	1.1	19	1	US-11-101-244-491278	Sequence 491278,	C 789	17.4	1.0	19	1	US-11-101-244-96667	Sequence 96667, A
717	19	1.1	19	1	US-11-101-244-491279	Sequence 491279,	C 790	17.4	1.0	19	1	US-11-101-244-103957	Sequence 103957,
718	19	1.1	19	1	US-11-101-244-491280	Sequence 491280,	C 791	17.4	1.0	19	1	US-11-101-244-490758	Sequence 490758,
719	19	1.1	19	1	US-11-101-244-491281	Sequence 491281,	C 792	17.4	1.0	19	1	US-11-101-244-490759	Sequence 490759,
720	19	1.1	19	1	US-11-101-244-491282	Sequence 491282,	C 793	17.4	1.0	19	1	US-11-101-244-490763	Sequence 490763,
721	19	1.1	19	1	US-11-101-244-491283	Sequence 491283,	C 794	17.4	1.0	19	1	US-11-101-244-491328	Sequence 491328,
722	19	1.1	19	1	US-11-101-244-491284	Sequence 491284,	C 795	17.4	1.0	19	1	US-11-101-244-491368	Sequence 491368,
723	19	1.1	19	1	US-11-101-244-491285	Sequence 491285,	C 796	17.4	1.0	19	1	US-11-101-244-491376	Sequence 491376,
724	19	1.1	19	1	US-11-101-244-491286	Sequence 491286,	C 797	17.4	1.0	19	1	US-11-101-244-491384	Sequence 491384,
725	19	1.1	19	1	US-11-101-244-491287	Sequence 491287,	C 798	17.4	1.0	19	1	US-11-101-244-491392	Sequence 491392,
726	19	1.1	19	1	US-11-101-244-491288	Sequence 491288,	C 799	17.4	1.0	19	1	US-11-101-244-854916	Sequence 854916,
727	19	1.1	19	1	US-11-101-244-491291	Sequence 491291,	C 800	17.4	1.0	19	1	US-11-101-244-877764	Sequence 877764,
728	19	1.1	19	1	US-11-101-244-491292	Sequence 491292,	C 801	17.4	1.0	19	1	US-11-101-244-946470	Sequence 946470,
729	19	1.1	19	1	US-11-101-244-491294	Sequence 491294,	C 802	17.4	1.0	19	1	US-11-101-244-1141173	Sequence 1141173,
730	19	1.1	19	1	US-11-101-244-491294	Sequence 491294,	C 803	17.4	1.0	19	1	US-11-101-244-124667	Sequence 124667,
731	19	1.1	19	1	US-11-101-244-491296	Sequence 491296,	C 804	17.4	1.0	19	1	US-10-310-914A-515099	Sequence 515099,
732	19	1.1	19	1	US-11-101-244-491297	Sequence 491297,	C 805	17.4	1.0	21	1	US-10-310-914A-138766	Sequence 138766,
733	19	1.1	19	1	US-11-101-244-491298	Sequence 491298,	C 806	17.4	1.0	21	1	US-10-310-914A-1265096	Sequence 1265096,
734	19	1.1	19	1	US-11-127-877-153	Sequence 153, App	C 807	17.4	1.0	21	1	US-10-310-914A-160462	Sequence 160462,
735	19	1.1	19	1	US-11-127-877-154	Sequence 154, App	C 808	17	1.0	20	1	US-10-023-066A-25	Sequence 25, Appl
736	19	1.1	19	1	US-11-127-877-155	Sequence 155, App	C 809	17	1.0	21	1	US-10-023-066A-41	Sequence 41, Appl
737	19	1.1	19	1	US-11-127-877-156	Sequence 156, App	C 810	17	1.0	21	1	US-10-023-066A-43	Sequence 43, Appl
738	19	1.1	19	1	US-11-127-877-474	Sequence 474, App	C 811	17	1.0	21	1	US-10-804-678-45	Sequence 45, Appl
739	18.8	1.1	22	1	US-10-310-914A-51927	Sequence 51927, A	C 812	17	1.0	21	1	US-10-804-678-41	Sequence 41, Appl
740	18.8	1.1	22	1	US-10-310-914A-746504	Sequence 746504, A	C 813	17	1.0	19	1	US-11-101-244-128453	Sequence 128453,
741	18.4	1.0	23	1	US-10-770-726-10445	Sequence 10445, A	C 814	17	1.0	19	1	US-11-101-244-128453	Sequence 128453,
742	18.4	1.0	23	1	US-10-310-914A-1313224	Sequence 1313224,	C 815	17	1.0	19	1	US-11-101-244-128543	Sequence 128543,
743	18.4	1.0	23	1	US-10-310-914A-1313247	Sequence 1313247,	C 816	17	1.0	19	1	US-11-101-244-1265096	Sequence 1265096,
744	18	1.0	18	1	US-09-930-503-39	Sequence 39, Appl	C 817	17	1.0	20	1	US-10-310-914A-160462	Sequence 160462,
745	18	1.0	18	1	US-09-930-503-58	Sequence 58, Appl	C 818	17	1.0	21	1	US-10-023-066A-25	Sequence 25, Appl
746	18	1.0	18	1	US-10-146-354A-32	Sequence 32, Appl	C 819	17	1.0	21	1	US-10-023-066A-41	Sequence 41, Appl
747	18	1.0	18	1	US-10-005-956-1124	Sequence 1124, Ap	C 820	17	1.0	21	1	US-10-023-066A-43	Sequence 43, Appl
748	18	1.0	18	1	US-10-005-956-1218	Sequence 1218, Ap	C 821	17	1.0	21	1	US-10-804-678-45	Sequence 45, Appl
749	18	1.0	18	1	US-10-310-914A-386268	Sequence 386268,	C 822	16.8	1.0	21	1	US-10-804-678-41	Sequence 41, Appl
750	18	1.0	18	1	US-10-310-914A-386291	Sequence 386291,	C 823	16.8	1.0	20	1	US-10-310-914A-279471	Sequence 279471,
751	18	1.0	18	1	US-10-310-914A-386293	Sequence 386293,	C 824	16.8	1.0	20	1	US-10-310-914A-440474	Sequence 440474,
752	18	1.0	18	1	US-10-310-914A-1157285	Sequence 1157285,	C 825	16.8	1.0	20	1	US-10-310-914A-800870	Sequence 800870,
753	18	1.0	18	1	US-10-310-914A-386292	Sequence 386292,	C 826	16.8	1.0	20	1	US-10-310-914A-843549	Sequence 843549,
754	18	1.0	19	1	US-11-083-784-491261	Sequence 491261,	C 827	16.8	1.0	21	1	US-10-310-914A-151367	Sequence 151367,
755	18	1.0	19	1	US-11-101-244-491261	Sequence 491261,	C 828	16.8	1.0	21	1	US-10-310-914A-412673	Sequence 412673,
756	18	1.0	19	1	US-11-101-244-491269	Sequence 491269,	C 829	16.8	1.0	21	1	US-10-310-914A-444744	Sequence 444744,
757	18	1.0	22	1	US-10-005-956-1303	Sequence 1303, Ap	C 830	16.8	1.0	21	1	US-10-310-914A-800870	Sequence 800870,
758	17.8	1.0	22	1	US-10-201-187-44	Sequence 1403, Ap	C 831	16.8	1.0	21	1	US-10-310-914A-843549	Sequence 843549,
759	17.8	1.0	21	1	US-10-603-566-38	Sequence 38, Appl	C 832	16.8	1.0	21	1	US-10-310-914A-843549	Sequence 843549,
760	17.8	1.0	21	1	US-10-893-485-38	Sequence 38, Appl	C 833	16.8	1.0	21	1	US-10-310-914A-843549	Sequence 843549,
761	17.8	1.0	21	1	US-10-310-914A-322519	Sequence 38, Appl	C 834	16.8	1.0	21	1	US-10-310-914A-843549	Sequence 843549,
762	17.8	1.0											

C 837	16.4	0.9	18	1	US-10-951-303-2971	Sequence 2971, App	C 910	16	0.9	20	1	US-10-370-860A-10	Sequence 10, App1
C 838	16.4	0.9	18	1	US-10-310-914A-336642	Sequence 336642, App	C 911	16	0.9	20	1	US-10-370-860A-12	Sequence 12, App1
839	16.4	0.9	18	1	US-10-310-914A-999588	Sequence 999588, App	912	16	0.9	20	1	US-10-310-914A-157270	Sequence 157270, App
840	16.4	0.9	18	1	US-10-310-914A-1071407	Sequence 1071407, App	913	16	0.9	20	1	US-10-310-914A-454995	Sequence 454995, App
841	16.4	0.9	18	1	US-10-310-914A-1378476	Sequence 1378476, App	C 914	15.8	0.9	19	1	US-10-206-693-14	Sequence 14, App1
842	16.4	0.9	19	1	US-10-310-914A-687663	Sequence 687663, App	915	15.8	0.9	19	1	US-10-206-693-240	Sequence 240, App
843	16.4	0.9	19	1	US-10-310-914A-1378477	Sequence 1378477, App	916	15.8	0.9	19	1	US-10-310-914A-151357	Sequence 151357, App
C 844	16.4	0.9	19	1	US-10-310-914A-1384285	Sequence 1384285, App	C 917	15.8	0.9	19	1	US-10-310-914A-223218	Sequence 223218, App
C 845	16.4	0.9	19	1	US-11-083-784-49684	Sequence 49684, A	918	15.8	0.9	19	1	US-10-310-914A-360899	Sequence 360899, App
C 846	16.4	0.9	19	1	US-11-083-784-209546	Sequence 209546, App	919	15.8	0.9	19	1	US-10-310-914A-432064	Sequence 432064, App
C 847	16.4	0.9	19	1	US-11-083-784-405179	Sequence 405179, App	920	15.8	0.9	19	1	US-10-310-914A-542218	Sequence 542218, App
848	16.4	0.9	19	1	US-11-083-784-427206	Sequence 427206, App	C 921	15.8	0.9	19	1	US-10-310-914A-854052	Sequence 854052, App
849	16.4	0.9	19	1	US-11-083-784-491396	Sequence 491396, App	922	15.8	0.9	19	1	US-10-310-914A-855297	Sequence 855297, App
850	16.4	0.9	19	1	US-11-083-784-521114	Sequence 521114, App	C 923	15.8	0.9	19	1	US-10-310-914A-1016265	Sequence 1016265, App
851	16.4	0.9	19	1	US-11-083-784-531574	Sequence 531574, App	924	15.8	0.9	19	1	US-10-310-914A-1023203	Sequence 1023203, App
852	16.4	0.9	19	1	US-11-083-784-531575	Sequence 531575, App	925	15.8	0.9	19	1	US-10-310-914A-1026538	Sequence 1026538, App
853	16.4	0.9	19	1	US-11-083-784-531674	Sequence 531674, App	C 926	15.8	0.9	19	1	US-10-310-914A-1078351	Sequence 1078351, App
854	16.4	0.9	19	1	US-11-083-784-531675	Sequence 531675, App	C 927	15.8	0.9	19	1	US-10-310-914A-1105562	Sequence 1105562, App
855	16.4	0.9	19	1	US-11-083-784-531774	Sequence 531774, App	C 928	15.8	0.9	19	1	US-10-310-914A-1138736	Sequence 1138736, App
856	16.4	0.9	19	1	US-11-083-784-531775	Sequence 531775, App	929	15.8	0.9	19	1	US-10-310-914A-1153367	Sequence 1153367, App
857	16.4	0.9	19	1	US-11-083-784-531872	Sequence 531872, App	C 930	15.8	0.9	19	1	US-11-014-373-335	Sequence 235, App
858	16.4	0.9	19	1	US-11-083-784-531873	Sequence 531873, App	931	15.8	0.9	19	1	US-11-014-373-512	Sequence 512, App
859	16.4	0.9	19	1	US-11-083-784-531972	Sequence 531972, App	932	15.8	0.9	19	1	US-11-083-784-2836	Sequence 2836, App
860	16.4	0.9	19	1	US-11-083-784-531973	Sequence 531973, App	933	15.8	0.9	19	1	US-11-083-784-496532	Sequence 496532, A
861	16.4	0.9	19	1	US-11-083-784-532071	Sequence 532071, App	934	15.8	0.9	19	1	US-11-083-784-49652	Sequence 49652, A
862	16.4	0.9	19	1	US-11-083-784-532072	Sequence 532072, App	935	15.8	0.9	19	1	US-11-083-784-96612	Sequence 96612, A
C 863	16.4	0.9	19	1	US-11-083-784-578805	Sequence 578805, App	C 936	15.8	0.9	19	1	US-11-083-784-1042334	Sequence 104233, App
864	16.4	0.9	19	1	US-11-083-784-723652	Sequence 723652, App	937	15.8	0.9	19	1	US-11-083-784-1169311	Sequence 116931, App
865	16.4	0.9	19	1	US-11-083-784-723752	Sequence 723752, App	938	15.8	0.9	19	1	US-11-083-784-1169884	Sequence 116988, App
866	16.4	0.9	19	1	US-11-083-784-911949	Sequence 911949, App	939	15.8	0.9	19	1	US-11-083-784-117020	Sequence 117020, App
C 867	16.4	0.9	19	1	US-11-083-784-928479	Sequence 928479, App	940	15.8	0.9	19	1	US-11-083-784-117049	Sequence 117049, App
868	16.4	0.9	19	1	US-11-083-784-1141172	Sequence 1141172, App	941	15.8	0.9	19	1	US-11-083-784-117107	Sequence 117107, App
C 869	16.4	0.9	19	1	US-11-083-784-1259943	Sequence 1259943, App	942	15.8	0.9	19	1	US-11-083-784-117181	Sequence 117181, App
C 870	16.4	0.9	19	1	US-11-083-784-1473036	Sequence 1473036, App	943	15.8	0.9	19	1	US-11-083-784-117250	Sequence 117250, App
871	16.4	0.9	19	1	US-11-083-784-1484938	Sequence 1484938, App	944	15.8	0.9	19	1	US-11-083-784-117250	Sequence 117250, App
872	16.4	0.9	19	1	US-11-101-244-49684	Sequence 49684, A	945	15.8	0.9	19	1	US-11-083-784-155785	Sequence 155785, App
C 873	16.4	0.9	19	1	US-11-101-244-209546	Sequence 209546, App	946	15.8	0.9	19	1	US-11-083-784-190805	Sequence 190805, App
C 874	16.4	0.9	19	1	US-11-101-244-405179	Sequence 405179, App	947	15.8	0.9	19	1	US-11-083-784-190884	Sequence 190884, App
875	16.4	0.9	19	1	US-11-101-244-427206	Sequence 427206, App	948	15.8	0.9	19	1	US-11-083-784-198455	Sequence 198455, App
876	16.4	0.9	19	1	US-11-101-244-491396	Sequence 491396, App	949	15.8	0.9	19	1	US-11-083-784-198486	Sequence 198486, App
877	16.4	0.9	19	1	US-11-101-244-521114	Sequence 521114, App	950	15.8	0.9	19	1	US-11-083-784-198511	Sequence 198511, App
878	16.4	0.9	19	1	US-11-101-244-531574	Sequence 531574, App	951	15.8	0.9	19	1	US-11-083-784-198533	Sequence 198533, App
879	16.4	0.9	19	1	US-11-101-244-531575	Sequence 531575, App	952	15.8	0.9	19	1	US-11-083-784-198551	Sequence 198551, App
880	16.4	0.9	19	1	US-11-101-244-531674	Sequence 531674, App	953	15.8	0.9	19	1	US-11-083-784-198589	Sequence 198589, App
881	16.4	0.9	19	1	US-11-101-244-531675	Sequence 531675, App	954	15.8	0.9	19	1	US-11-083-784-198623	Sequence 198623, App
882	16.4	0.9	19	1	US-11-101-244-531774	Sequence 531774, App	955	15.8	0.9	19	1	US-11-083-784-198673	Sequence 198673, App
883	16.4	0.9	19	1	US-11-101-244-531775	Sequence 531775, App	956	15.8	0.9	19	1	US-11-083-784-198715	Sequence 198715, App
884	16.4	0.9	19	1	US-11-101-244-531872	Sequence 531872, App	957	15.8	0.9	19	1	US-11-083-784-207465	Sequence 207465, App
885	16.4	0.9	19	1	US-11-101-244-531873	Sequence 531873, App	958	15.8	0.9	19	1	US-11-083-784-222312	Sequence 222312, App
886	16.4	0.9	19	1	US-11-101-244-531972	Sequence 531972, App	959	15.8	0.9	19	1	US-11-083-784-225150	Sequence 225150, App
887	16.4	0.9	19	1	US-11-101-244-531973	Sequence 531973, App	C 960	15.8	0.9	19	1	US-11-083-784-256569	Sequence 256569, App
888	16.4	0.9	19	1	US-11-101-244-532071	Sequence 532071, App	C 961	15.8	0.9	19	1	US-11-083-784-256617	Sequence 256617, App
889	16.4	0.9	19	1	US-11-101-244-532072	Sequence 532072, App	C 962	15.8	0.9	19	1	US-11-083-784-259212	Sequence 259212, App
C 890	16.4	0.9	19	1	US-11-101-244-578805	Sequence 578805, App	C 963	15.8	0.9	19	1	US-11-083-784-275438	Sequence 275438, App
891	16.4	0.9	19	1	US-11-101-244-723652	Sequence 723652, App	964	15.8	0.9	19	1	US-11-083-784-396635	Sequence 396635, App
892	16.4	0.9	19	1	US-11-101-244-723752	Sequence 723752, App	C 965	15.8	0.9	19	1	US-11-083-784-411303	Sequence 411303, App
893	16.4	0.9	19	1	US-11-101-244-911949	Sequence 911949, App	C 966	15.8	0.9	19	1	US-11-083-784-425415	Sequence 425415, App
C 894	16.4	0.9	19	1	US-11-101-244-928479	Sequence 928479, App	967	15.8	0.9	19	1	US-11-083-784-482386	Sequence 482386, App
C 895	16.4	0.9	19	1	US-11-101-244-9141172	Sequence 9141172, App	968	15.8	0.9	19	1	US-11-083-784-482438	Sequence 482438, App
C 896	16.4	0.9	19	1	US-11-101-244-1259943	Sequence 1259943, App	969	15.8	0.9	19	1	US-11-083-784-490736	Sequence 490736, App
C 897	16.4	0.9	19	1	US-11-101-244-1473036	Sequence 1473036, App	970	15.8	0.9	19	1	US-11-083-784-490744	Sequence 490744, App
898	16.4	0.9	19	1	US-11-101-244-1484938	Sequence 1484938, App	971	15.8	0.9	19	1	US-11-083-784-490754	Sequence 490754, App
C 899	16.4	0.9	20	1	US-09-967-669-87	Sequence 87, App1	972	15.8	0.9	19	1	US-11-083-784-491346	Sequence 491346, App
900	16.4	0.9	20	1	US-10-996-951-3	Sequence 3, App1	973	15.8	0.9	19	1	US-11-083-784-491367	Sequence 491367, App
901	16.4	0.9	20	1	US-10-310-914A-157159	Sequence 157159, App	974	15.8	0.9	19	1	US-11-083-784-491377	Sequence 491377, App
902	16.4	0.9	20	1	US-10-310-914A-428826	Sequence 428826, App	975	15.8	0.9	19	1	US-11-083-784-491377	Sequence 491377, App
903	16.4	0.9	20	1	US-10-310-914A-677516	Sequence 677516, App	976	15.8	0.9	19	1	US-11-083-784-504820	Sequence 504820, App
C 904	16.4	0.9	20	1	US-10-310-914A-1236794	Sequence 1236794, App	C 977	15.8	0.9	19	1	US-11-083-784-520347	Sequence 520347, App
905	16	0.9	17	1	US-09-780-164-770	Sequence 770, App	978	15.8	0.9	19	1	US-11-083-784-521051	Sequence 521051, App
C 906	16	0.9	19	1	US-11-083-784-523603	Sequence 523603, App	C 979	15.8	0.9	19	1	US-11-083-784-537233	Sequence 537233, App
C 907	16	0.9	19	1	US-11-083-784-1146200	Sequence 1146200, App	980	15.8	0.9	19	1	US-11-083-784-548577	Sequence 548577, App
C 908	16	0.9	19	1	US-11-101-244-523603	Sequence 523603, App	981	15.8	0.9	19	1	US-11-083-784-647566	Sequence 647566, App
C 909	16	0.9	19	1	US-11-101-244-1146200	Sequence 1146200, App	982	15.8	0.9	19	1	US-11-083-784-647654	Sequence 647654, App

c 983	15.8	0.9	19	1	US-11-083-784-651197	Sequence 651197,
c 984	15.8	0.9	19	1	US-11-083-784-692671	Sequence 692671,
c 985	15.8	0.9	19	1	US-11-083-784-809922	Sequence 809922,
c 986	15.8	0.9	19	1	US-11-083-784-835805	Sequence 835805,
c 987	15.8	0.9	19	1	US-11-083-784-895312	Sequence 895312,
c 988	15.8	0.9	19	1	US-11-083-784-946407	Sequence 946407,
c 989	15.8	0.9	19	1	US-11-083-784-951796	Sequence 951796,
c 990	15.8	0.9	19	1	US-11-083-784-973051	Sequence 973051,
c 991	15.8	0.9	19	1	US-11-083-784-978358	Sequence 978358,
c 992	15.8	0.9	19	1	US-11-083-784-1073668	Sequence 1073668,
c 993	15.8	0.9	19	1	US-11-083-784-1077487	Sequence 1077487,
c 994	15.8	0.9	19	1	US-11-083-784-1112807	Sequence 1112807,
c 995	15.8	0.9	19	1	US-11-083-784-1112871	Sequence 1112871,
c 996	15.8	0.9	19	1	US-11-083-784-1115683	Sequence 1115683,
c 997	15.8	0.9	19	1	US-11-083-784-1115733	Sequence 1115733,
c 998	15.8	0.9	19	1	US-11-083-784-1115733	Sequence 1115733,
c 999	15.8	0.9	19	1	US-11-083-784-1145497	Sequence 1145497,
c1000	15.8	0.9	19	1	US-11-083-784-1159730	Sequence 1159730,
c1001	15.8	0.9	19	1	US-11-083-784-1257590	Sequence 1257590,
c1002	15.8	0.9	19	1	US-11-083-784-1323231	Sequence 1323231,
c1003	15.8	0.9	19	1	US-11-083-784-1350821	Sequence 1350821,
c1004	15.8	0.9	19	1	US-11-083-784-1351424	Sequence 1351424,
c1005	15.8	0.9	19	1	US-11-083-784-1370891	Sequence 1370891,
c1006	15.8	0.9	19	1	US-11-083-784-1388942	Sequence 1388942,
c1007	15.8	0.9	19	1	US-11-083-784-1513262	Sequence 1513262,
c1008	15.8	0.9	19	1	US-11-083-784-1513262	Sequence 1513262,
c1009	15.8	0.9	19	1	US-11-083-784-1564341	Sequence 1564341,
c1010	15.8	0.9	19	1	US-11-083-784-1564341	Sequence 1564341,
c1011	15.8	0.9	19	1	US-11-101-244-2836	Sequence 2836, Ap
c1012	15.8	0.9	19	1	US-11-101-244-49632	Sequence 49632, A
c1013	15.8	0.9	19	1	US-11-101-244-49652	Sequence 49652, A
c1014	15.8	0.9	19	1	US-11-101-244-49652	Sequence 49652, A
c1015	15.8	0.9	19	1	US-11-101-244-104234	Sequence 104234,
c1016	15.8	0.9	19	1	US-11-101-244-116911	Sequence 116911,
c1017	15.8	0.9	19	1	US-11-101-244-116984	Sequence 116984,
c1018	15.8	0.9	19	1	US-11-101-244-117020	Sequence 117020,
c1019	15.8	0.9	19	1	US-11-101-244-117049	Sequence 117049,
c1020	15.8	0.9	19	1	US-11-101-244-117107	Sequence 117107,
c1021	15.8	0.9	19	1	US-11-101-244-117181	Sequence 117181,
c1022	15.8	0.9	19	1	US-11-101-244-117219	Sequence 117219,
c1023	15.8	0.9	19	1	US-11-101-244-117250	Sequence 117250,
c1024	15.8	0.9	19	1	US-11-101-244-155785	Sequence 155785,
c1025	15.8	0.9	19	1	US-11-101-244-190805	Sequence 190805,
c1026	15.8	0.9	19	1	US-11-101-244-190884	Sequence 190884,
c1027	15.8	0.9	19	1	US-11-101-244-198455	Sequence 198455,
c1028	15.8	0.9	19	1	US-11-101-244-198486	Sequence 198486,
c1029	15.8	0.9	19	1	US-11-101-244-198511	Sequence 198511,
c1030	15.8	0.9	19	1	US-11-101-244-198553	Sequence 198553,
c1031	15.8	0.9	19	1	US-11-101-244-198553	Sequence 198553,
c1032	15.8	0.9	19	1	US-11-101-244-198589	Sequence 198589,
c1033	15.8	0.9	19	1	US-11-101-244-198623	Sequence 198623,
c1034	15.8	0.9	19	1	US-11-101-244-198673	Sequence 198673,
c1035	15.8	0.9	19	1	US-11-101-244-198715	Sequence 198715,
c1036	15.8	0.9	19	1	US-11-101-244-207465	Sequence 207465,
c1037	15.8	0.9	19	1	US-11-101-244-223212	Sequence 223212,
c1038	15.8	0.9	19	1	US-11-101-244-225150	Sequence 225150,
c1039	15.8	0.9	19	1	US-11-101-244-225659	Sequence 225659,
c1040	15.8	0.9	19	1	US-11-101-244-256217	Sequence 256217,
c1041	15.8	0.9	19	1	US-11-101-244-259212	Sequence 259212,
c1042	15.8	0.9	19	1	US-11-101-244-275438	Sequence 275438,
c1043	15.8	0.9	19	1	US-11-101-244-398635	Sequence 398635,
c1044	15.8	0.9	19	1	US-11-101-244-411203	Sequence 411203,
c1045	15.8	0.9	19	1	US-11-101-244-425415	Sequence 425415,
c1046	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,
c1047	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,
c1048	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,
c1049	15.8	0.9	19	1	US-11-101-244-482386	Sequence 482386,
c1050	15.8	0.9	19	1	US-11-101-244-490744	Sequence 490744,
c1051	15.8	0.9	19	1	US-11-101-244-490754	Sequence 490754,
c1052	15.8	0.9	19	1	US-11-101-244-491301	Sequence 491301,
c1053	15.8	0.9	19	1	US-11-101-244-491346	Sequence 491346,
c1054	15.8	0.9	19	1	US-11-101-244-491367	Sequence 491367,
c1055	15.8	0.9	19	1	US-11-101-244-491377	Sequence 491377,
c1056	15.8	0.9	19	1	US-11-101-244-504820	Sequence 504820,
c1057	15.8	0.9	19	1	US-11-101-244-520347	Sequence 520347,
c1058	15.8	0.9	19	1	US-11-101-244-521051	Sequence 521051,
c1059	15.8	0.9	19	1	US-11-101-244-531233	Sequence 531233,
c1060	15.8	0.9	19	1	US-11-101-244-548572	Sequence 548572,
c1061	15.8	0.9	19	1	US-11-101-244-647656	Sequence 647656,
c1062	15.8	0.9	19	1	US-11-101-244-647656	Sequence 647656,
c1063	15.8	0.9	19	1	US-11-101-244-651197	Sequence 651197,
c1064	15.8	0.9	19	1	US-11-101-244-659671	Sequence 659671,
c1065	15.8	0.9	19	1	US-11-101-244-809922	Sequence 809922,
c1066	15.8	0.9	19	1	US-11-101-244-835805	Sequence 835805,
c1067	15.8	0.9	19	1	US-11-101-244-835805	Sequence 835805,
c1068	15.8	0.9	19	1	US-11-101-244-946407	Sequence 946407,
c1069	15.8	0.9	19	1	US-11-101-244-951796	Sequence 951796,
c1070	15.8	0.9	19	1	US-11-101-244-973051	Sequence 973051,
c1071	15.8	0.9	19	1	US-11-101-244-978358	Sequence 978358,
c1072	15.8	0.9	19	1	US-11-101-244-1073668	Sequence 1073668,
c1073	15.8	0.9	19	1	US-11-101-244-1077487	Sequence 1077487,
c1074	15.8	0.9	19	1	US-11-101-244-1112807	Sequence 1112807,
c1075	15.8	0.9	19	1	US-11-101-244-1115683	Sequence 1115683,
c1076	15.8	0.9	19	1	US-11-101-244-1115733	Sequence 1115733,
c1077	15.8	0.9	19	1	US-11-101-244-1145497	Sequence 1145497,
c1078	15.8	0.9	19	1	US-11-101-244-1159730	Sequence 1159730,
c1079	15.8	0.9	19	1	US-11-101-244-1257590	Sequence 1257590,
c1080	15.8	0.9	19	1	US-11-101-244-1323231	Sequence 1323231,
c1081	15.8	0.9	19	1	US-11-101-244-1350821	Sequence 1350821,
c1082	15.8	0.9	19	1	US-11-101-244-1351424	Sequence 1351424,
c1083	15.8	0.9	19	1	US-11-101-244-1370891	Sequence 1370891,
c1084	15.8	0.9	19	1	US-11-101-244-1388942	Sequence 1388942,
c1085	15.8	0.9	19	1	US-11-101-244-1513262	Sequence 1513262,
c1086	15.8	0.9	19	1	US-11-101-244-1513262	Sequence 1513262,
c1087	15.8	0.9	19	1	US-11-101-244-1564341	Sequence 1564341,
c1088	15.8	0.9	19	1	US-11-101-244-1564341	Sequence 1564341,
c1089	15.8	0.9	19	1	US-11-101-244-1582659	Sequence 1582659,
c1090	15.8	0.9	19	1	US-11-069-611-235	Sequence 235, App
c1091	15.4	0.9	17	1	US-09-780-533A-1841	Sequence 1841, Ap
c1092	15.4	0.9	17	1	US-09-848-754A-3109	Sequence 3109, Ap
c1093	15.4	0.9	17	1	US-10-138-674-2435	Sequence 2435, Ap
c1094	15.4	0.9	17	1	US-10-287-949A-2435	Sequence 2435, Ap
c1095	15.4	0.9	17	1	US-10-712-672-1375	Sequence 1375, Ap
c1096	15.4	0.9	17	1	US-10-951-303-2435	Sequence 2435, Ap
c1097	15.4	0.9	18	1	US-09-850-948-19	Sequence 19, App1
c1098	15.4	0.9	18	1	US-10-273-575-19	Sequence 19, App1
c1099	15.4	0.9	18	1	US-10-680-402-70	Sequence 70, App1
c1100	15.4	0.9	18	1	US-10-310-914A-230274	Sequence 230274,
c1101	15.4	0.9	18	1	US-10-310-914A-677466	Sequence 677466,
c1102	15.4	0.9	18	1	US-10-310-914A-677474	Sequence 677474,
c1103	15.4	0.9	18	1	US-10-310-914A-800869	Sequence 800869,
c1104	15.4	0.9	18	1	US-10-310-914A-888641	Sequence 888641,
c1105	15.4	0.9	18	1	US-10-310-914A-892826	Sequence 892826,
c1106	15.4	0.9	18	1	US-10-310-914A-1042518	Sequence 1042518,
c1107	15.4	0.9	18	1	US-10-310-914A-1145229	Sequence 1145229,
c1108	15.4	0.9	18	1	US-10-310-914A-1350814	Sequence 1350814,
c1109	15.4	0.9	19	1	US-10-665-951-1515	Sequence 1515, Ap
c1110	15.4	0.9	19	1	US-10-665-951-1762	Sequence 1762, Ap
c1111	15.4	0.9	19	1	US-10-758-155-1515	Sequence 1515, Ap
c1112	15.4	0.9	19	1	US-10-758-155-1762	Sequence 1762, Ap
c1113	15.4	0.9	19	1	US-10-831-620-1515	Sequence 1515, Ap
c1114	15.4	0.9	19	1	US-10-831-620-1762	Sequence 1762, Ap
c1115	15.4	0.9	19	1	US-10-923-330-2166	Sequence 216, App
c1116	15.4	0.9	19	1	US-10-923-330-339	Sequence 339, App
c1117	15.4	0.9	19	1	US-10-844-076-1515	Sequence 1515, Ap
c1118	15.4	0.9	19	1	US-10-844-076-1762	Sequence 1762, Ap
c1119	15.4	0.9	19	1	US-10-923-182-62	Sequence 62, App1
c1120	15.4	0.9	19	1	US-10-923-182-149	Sequence 149, App
c1121	15.4	0.9	19	1	US-10-962-888-1515	Sequence 1515, Ap
c1122	15.4	0.9	19	1	US-10-962-888-1762	Sequence 1762, Ap
c1123	15.4	0.9	19	1	US-10-944-611-1515	Sequence 1515, Ap
c1124	15.4	0.9	19	1	US-10-944-611-1762	Sequence 1762, Ap
c1125	15.4	0.9	19	1	US-10-206-693-35	Sequence 35, App1
c1126	15.4	0.9	19	1	US-10-206-693-61	Sequence 61, App
c1127	15.4	0.9	19	1	US-10-310-914A-288078	Sequence 288078,
c1128	15.4	0.9	19	1	US-10-310-914A-394088	Sequence 394088,

c1129	15.4	0.9	19	1	US-10-310-914A-410563	Sequence 410563,
1130	15.4	0.9	19	1	US-10-310-914A-477720	Sequence 477720,
1131	15.4	0.9	19	1	US-10-310-914A-522254	Sequence 522254,
1132	15.4	0.9	19	1	US-10-310-914A-522262	Sequence 522262,
c1133	15.4	0.9	19	1	US-10-310-914A-629950	Sequence 629950,
1134	15.4	0.9	19	1	US-10-310-914A-742052	Sequence 742052,
c1135	15.4	0.9	19	1	US-10-310-914A-860138	Sequence 860138,
1136	15.4	0.9	19	1	US-10-310-914A-181389	Sequence 181389,
c1137	15.4	0.9	19	1	US-10-310-914A-1280868	Sequence 1280868,
1138	15.4	0.9	19	1	US-10-310-914A-1309499	Sequence 1309499,
1139	15.4	0.9	19	1	US-10-310-914A-1319661	Sequence 1319661,
c1140	15.4	0.9	19	1	US-10-310-914A-1375299	Sequence 1375299,
1141	15.4	0.9	19	1	US-11-083-784-2195	Sequence 2195, Ap
c1142	15.4	0.9	19	1	US-11-083-784-19634	Sequence 19634, A
1143	15.4	0.9	19	1	US-11-083-784-51038	Sequence 51038, A
c1144	15.4	0.9	19	1	US-11-083-784-61485	Sequence 61485, A
c1145	15.4	0.9	19	1	US-11-083-784-66269	Sequence 66269, A
c1146	15.4	0.9	19	1	US-11-083-784-66270	Sequence 66270, A
c1147	15.4	0.9	19	1	US-11-083-784-133295	Sequence 133295,
c1148	15.4	0.9	19	1	US-11-083-784-143402	Sequence 143402,
c1149	15.4	0.9	19	1	US-11-083-784-202084	Sequence 202084,
1150	15.4	0.9	19	1	US-11-083-784-202197	Sequence 202197,
1151	15.4	0.9	19	1	US-11-083-784-202174	Sequence 202174,
1152	15.4	0.9	19	1	US-11-083-784-202116	Sequence 202116,
c1153	15.4	0.9	19	1	US-11-083-784-202197	Sequence 202197,
c1154	15.4	0.9	19	1	US-11-083-784-232135	Sequence 232135,
c1155	15.4	0.9	19	1	US-11-083-784-232235	Sequence 232235,
c1156	15.4	0.9	19	1	US-11-083-784-237477	Sequence 237477,
1157	15.4	0.9	19	1	US-11-083-784-262644	Sequence 262644,
1158	15.4	0.9	19	1	US-11-083-784-304519	Sequence 304519,
1159	15.4	0.9	19	1	US-11-083-784-360639	Sequence 360639,
c1160	15.4	0.9	19	1	US-11-083-784-368528	Sequence 368528,
c1161	15.4	0.9	19	1	US-11-083-784-371445	Sequence 371445,
c1162	15.4	0.9	19	1	US-11-083-784-421451	Sequence 421451,
1163	15.4	0.9	19	1	US-11-083-784-425085	Sequence 425085,
c1164	15.4	0.9	19	1	US-11-083-784-460346	Sequence 460346,
c1165	15.4	0.9	19	1	US-11-083-784-460400	Sequence 460400,
1166	15.4	0.9	19	1	US-11-083-784-501423	Sequence 501423,
c1167	15.4	0.9	19	1	US-11-083-784-578794	Sequence 578794,
c1168	15.4	0.9	19	1	US-11-083-784-671090	Sequence 671090,
1169	15.4	0.9	19	1	US-11-083-784-674587	Sequence 674587,
c1170	15.4	0.9	19	1	US-11-083-784-688433	Sequence 688433,
1171	15.4	0.9	19	1	US-11-083-784-704511	Sequence 704511,
c1172	15.4	0.9	19	1	US-11-083-784-704520	Sequence 704520,
c1173	15.4	0.9	19	1	US-11-083-784-751946	Sequence 751946,
c1174	15.4	0.9	19	1	US-11-083-784-820807	Sequence 820807,
c1175	15.4	0.9	19	1	US-11-083-784-896406	Sequence 896406,
1176	15.4	0.9	19	1	US-11-083-784-911965	Sequence 911965,
c1177	15.4	0.9	19	1	US-11-083-784-917716	Sequence 917716,
c1178	15.4	0.9	19	1	US-11-083-784-926899	Sequence 926899,
c1179	15.4	0.9	19	1	US-11-083-784-976398	Sequence 976398,
c1180	15.4	0.9	19	1	US-11-083-784-1028300	Sequence 1028300,
1181	15.4	0.9	19	1	US-11-083-784-1077507	Sequence 1077507,
c1182	15.4	0.9	19	1	US-11-083-784-1098844	Sequence 1098844,
c1183	15.4	0.9	19	1	US-11-083-784-1245691	Sequence 1245691,
c1184	15.4	0.9	19	1	US-11-083-784-1277052	Sequence 1277052,
c1185	15.4	0.9	19	1	US-11-083-784-1277082	Sequence 1277082,
1186	15.4	0.9	19	1	US-11-083-784-1299074	Sequence 1299074,
1187	15.4	0.9	19	1	US-11-083-784-1302380	Sequence 1302380,
c1188	15.4	0.9	19	1	US-11-083-784-1332687	Sequence 1332687,
1189	15.4	0.9	19	1	US-11-083-784-1352689	Sequence 1352689,
c1190	15.4	0.9	19	1	US-11-083-784-1374698	Sequence 1374698,
c1191	15.4	0.9	19	1	US-11-083-784-1410088	Sequence 1410088,
1192	15.4	0.9	19	1	US-11-083-784-1450085	Sequence 1450085,
c1193	15.4	0.9	19	1	US-11-083-784-1464506	Sequence 1464506,
c1194	15.4	0.9	19	1	US-11-083-784-1474304	Sequence 1474304,
c1195	15.4	0.9	19	1	US-11-083-784-1485805	Sequence 1485805,
1196	15.4	0.9	19	1	US-11-083-784-1498825	Sequence 1498825,
c1197	15.4	0.9	19	1	US-11-083-784-1498858	Sequence 1498858,
c1198	15.4	0.9	19	1	US-11-083-784-1515526	Sequence 1515526,
c1199	15.4	0.9	19	1	US-11-083-784-1515845	Sequence 1515845,
c1200	15.4	0.9	19	1	US-11-101-244-19634	Sequence 19634, A
c1201	15.4	0.9	19	1	US-11-101-244-51038	Sequence 51038, A
c1202	15.4	0.9	19	1	US-11-101-244-61485	Sequence 61485, A
c1203	15.4	0.9	19	1	US-11-101-244-66269	Sequence 66269, A
c1204	15.4	0.9	19	1	US-11-101-244-66270	Sequence 66270, A
c1205	15.4	0.9	19	1	US-11-101-244-119668	Sequence 119668,
c1206	15.4	0.9	19	1	US-11-101-244-132395	Sequence 132395,
c1207	15.4	0.9	19	1	US-11-101-244-143402	Sequence 143402,
c1208	15.4	0.9	19	1	US-11-101-244-202084	Sequence 202084,
1209	15.4	0.9	19	1	US-11-101-244-202116	Sequence 202116,
1210	15.4	0.9	19	1	US-11-101-244-202174	Sequence 202174,
1211	15.4	0.9	19	1	US-11-101-244-202197	Sequence 202197,
1212	15.4	0.9	19	1	US-11-101-244-232135	Sequence 232135,
c1213	15.4	0.9	19	1	US-11-101-244-232235	Sequence 232235,
c1214	15.4	0.9	19	1	US-11-101-244-262644	Sequence 262644,
c1215	15.4	0.9	19	1	US-11-101-244-304519	Sequence 304519,
1216	15.4	0.9	19	1	US-11-101-244-368528	Sequence 368528,
1217	15.4	0.9	19	1	US-11-101-244-425085	Sequence 425085,
1218	15.4	0.9	19	1	US-11-101-244-460346	Sequence 460346,
1219	15.4	0.9	19	1	US-11-101-244-460400	Sequence 460400,
c1220	15.4	0.9	19	1	US-11-101-244-501423	Sequence 501423,
c1221	15.4	0.9	19	1	US-11-101-244-578794	Sequence 578794,
1222	15.4	0.9	19	1	US-11-101-244-671090	Sequence 671090,
c1223	15.4	0.9	19	1	US-11-101-244-674587	Sequence 674587,
c1224	15.4	0.9	19	1	US-11-101-244-688433	Sequence 688433,
c1225	15.4	0.9	19	1	US-11-101-244-704511	Sequence 704511,
c1226	15.4	0.9	19	1	US-11-101-244-704520	Sequence 704520,
1227	15.4	0.9	19	1	US-11-101-244-751946	Sequence 751946,
c1228	15.4	0.9	19	1	US-11-101-244-820807	Sequence 820807,
c1229	15.4	0.9	19	1	US-11-101-244-896406	Sequence 896406,
1230	15.4	0.9	19	1	US-11-101-244-911965	Sequence 911965,
1231	15.4	0.9	19	1	US-11-101-244-917716	Sequence 917716,
c1232	15.4	0.9	19	1	US-11-101-244-926899	Sequence 926899,
c1233	15.4	0.9	19	1	US-11-101-244-976398	Sequence 976398,
c1234	15.4	0.9	19	1	US-11-101-244-1028300	Sequence 1028300,
1235	15.4	0.9	19	1	US-11-101-244-1077507	Sequence 1077507,
c1236	15.4	0.9	19	1	US-11-101-244-1098844	Sequence 1098844,
c1237	15.4	0.9	19	1	US-11-101-244-1245691	Sequence 1245691,
c1238	15.4	0.9	19	1	US-11-101-244-1277052	Sequence 1277052,
c1239	15.4	0.9	19	1	US-11-101-244-1277082	Sequence 1277082,
c1240	15.4	0.9	19	1	US-11-101-244-1299074	Sequence 1299074,
1241	15.4	0.9	19	1	US-11-101-244-1302380	Sequence 1302380,
c1242	15.4	0.9	19	1	US-11-101-244-1352687	Sequence 1352687,
c1243	15.4	0.9	19	1	US-11-101-244-1374698	Sequence 1374698,
c1244	15.4	0.9	19	1	US-11-101-244-1410088	Sequence 1410088,
1245	15.4	0.9	19	1	US-11-101-244-1450085	Sequence 1450085,
1246	15.4	0.9	19	1	US-11-101-244-1464506	Sequence 1464506,
c1247	15.4	0.9	19	1	US-11-101-244-1474304	Sequence 1474304,
c1248	15.4	0.9	19	1	US-11-101-244-1485805	Sequence 1485805,
c1249	15.4	0.9	19	1	US-11-101-244-1498825	Sequence 1498825,
c1250	15.4	0.9	19	1	US-11-101-244-1498858	Sequence 1498858,
1251	15.4	0.9	19	1	US-11-101-244-1515526	Sequence 1515526,
c1252	15.4	0.9	19	1	US-11-101-244-1515845	Sequence 1515845,
c1253	15.4	0.9	19	1	US-11-101-244-155845	Sequence 155845,
c1254	15.4	0.9	19	1	US-11-101-244-19634	Sequence 19634, A
c1255	15.4	0.9	19	1	US-11-101-244-51038	Sequence 51038, A
c1256	15.4	0.9	19	1	US-11-101-244-61485	Sequence 61485, A
c1257	15.4	0.9	19	1	US-11-101-244-66269	Sequence 66269, A
c1258	15.4	0.9	19	1	US-11-101-244-66270	Sequence 66270, A
1259	15.4	0.9	19	1	US-11-101-244-119668	Sequence 119668,
c1260	15.4	0.9	19	1	US-11-101-244-132395	Sequence 132395,
1261	15.4	0.9	19	1	US-11-101-244-143402	Sequence 143402,
1262	15.4	0.9	19	1	US-11-101-244-202084	Sequence 202084,
1263	15.4	0.9	19	1	US-11-101-244-202116	Sequence 202116,
1264	15.4	0.9	19	1	US-11-101-244-202174	Sequence 202174,
1265	15.4	0.9	19	1	US-11-101-244-232135	Sequence 232135,
1266	15.4	0.9	19	1	US-11-101-244-262644	Sequence 262644,
1267	15.4	0.9	19	1	US-11-101-244-304519	Sequence 304519,
1268	15.4	0.9	19	1	US-11-101-244-368528	Sequence 368528,
1269	15.4	0.9	19	1	US-11-101-244-425085	Sequence 425085,
c1270	15.4	0.9	19	1	US-11-101-244-460346	Sequence 460346,
c1271	15.4	0.9	19	1	US-11-101-244-460400	Sequence 460400,
c1272	15.4	0.9	19	1	US-11-101-244-501423	Sequence 501423,
c1273	15.4	0.9	19	1	US-11-101-244-578794	Sequence 578794,
c1274	15.4	0.9	19	1	US-11-101-244-671090	Sequence 671090,
1275	15.4	0.9	19	1	US-11-101-244-674587	Sequence 674587,
1276	15.4	0.9	19	1	US-11-101-244-688433	Sequence 688433,
1277	15.4	0.9	19	1	US-11-101-244-704511	Sequence 704511,
1278	15.4	0.9	19</			

c1275	15	0.8	18	1	US-11-044-498-3	Sequence 3, Appl1	1348	14.4	0.8	18	1	US-10-138-674-3013	Sequence 10970, A
c1276	14.8	0.8	18	1	US-09-067-638B-50	Sequence 50, Appl	c1349	14.4	0.8	18	1	US-10-138-674-3013	Sequence 3013, Ap
c1277	14.8	0.8	18	1	US-10-116-325-50	Sequence 50, Appl	c1350	14.4	0.8	18	1	US-10-287-949A-3013	Sequence 3013, Ap
c1278	14.8	0.8	18	1	US-10-388-263-50	Sequence 50, Appl	1351	14.4	0.8	18	1	US-10-702-817-9	Sequence 9, Appl1
c1279	14.8	0.8	18	1	US-10-016-248-66	Sequence 66, Appl	c1352	14.4	0.8	18	1	US-10-509-009-22	Sequence 22, Appl
c1280	14.8	0.8	18	1	US-10-698-689-50	Sequence 50, Appl	c1353	14.4	0.8	18	1	US-10-951-303-3013	Sequence 3013, Ap
c1281	14.8	0.8	18	1	US-10-698-689-214	Sequence 214, App	1354	14.4	0.8	18	1	US-10-750-185-14622	Sequence 14622, A
c1282	14.8	0.8	18	1	US-10-830-475-50	Sequence 50, Appl	1355	14.4	0.8	18	1	US-10-750-623-14622	Sequence 14622, A
c1283	14.8	0.8	18	1	US-10-649-467-50	Sequence 89, Appl	1356	14.4	0.8	18	1	US-10-310-914A-72534	Sequence 72534, A
c1284	14.8	0.8	18	1	US-10-934-798-89	Sequence 208, App	c1357	14.4	0.8	18	1	US-10-310-914A-183276	Sequence 183276, A
c1285	14.8	0.8	18	1	US-10-934-798-89	Sequence 77047, A	c1358	14.4	0.8	18	1	US-10-310-914A-199415	Sequence 199415, A
1286	14.8	0.8	18	1	US-10-310-914A-77047	Sequence 83639, A	c1359	14.4	0.8	18	1	US-10-310-914A-249340	Sequence 249340, A
1287	14.8	0.8	18	1	US-10-310-914A-83639	Sequence 101443,3	1360	14.4	0.8	18	1	US-10-310-914A-4241734	Sequence 4241734, A
1288	14.8	0.8	18	1	US-10-310-914A-101443	Sequence 213729,	c1361	14.4	0.8	18	1	US-10-310-914A-4241734	Sequence 4241734, A
1289	14.8	0.8	18	1	US-10-310-914A-213729	Sequence 309009,	c1362	14.4	0.8	18	1	US-10-310-914A-4362306	Sequence 4362306, A
c1290	14.8	0.8	18	1	US-10-310-914A-309009	Sequence 336351,	c1363	14.4	0.8	18	1	US-10-310-914A-4362306	Sequence 4362306, A
c1291	14.8	0.8	18	1	US-10-310-914A-336351	Sequence 427752,	c1364	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1292	14.8	0.8	18	1	US-10-310-914A-427752	Sequence 465296,	1365	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1293	14.8	0.8	18	1	US-10-310-914A-465296	Sequence 519019,	c1366	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1294	14.8	0.8	18	1	US-10-310-914A-472856	Sequence 519948,	1367	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1295	14.8	0.8	18	1	US-10-310-914A-519019	Sequence 519948,	1368	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1296	14.8	0.8	18	1	US-10-310-914A-519948	Sequence 519969,	1369	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1297	14.8	0.8	18	1	US-10-310-914A-519969	Sequence 585840,	c1370	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1298	14.8	0.8	18	1	US-10-310-914A-585840	Sequence 601989,	c1371	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1299	14.8	0.8	18	1	US-10-310-914A-601989	Sequence 645930,	1372	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1300	14.8	0.8	18	1	US-10-310-914A-645930	Sequence 666092,	c1373	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1301	14.8	0.8	18	1	US-10-310-914A-696092	Sequence 707873,	c1374	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1302	14.8	0.8	18	1	US-10-310-914A-707873	Sequence 768979,	c1375	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1303	14.8	0.8	18	1	US-10-310-914A-768979	Sequence 795204,	c1376	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1304	14.8	0.8	18	1	US-10-310-914A-795204	Sequence 809520,	c1377	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1305	14.8	0.8	18	1	US-10-310-914A-809520	Sequence 847106,	1378	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1306	14.8	0.8	18	1	US-10-310-914A-847106	Sequence 874025,	c1379	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1307	14.8	0.8	18	1	US-10-310-914A-874025	Sequence 885132,	c1380	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1308	14.8	0.8	18	1	US-10-310-914A-885132	Sequence 923895,	1381	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1309	14.8	0.8	18	1	US-10-310-914A-923895	Sequence 937032,	c1382	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1310	14.8	0.8	18	1	US-10-310-914A-937032	Sequence 965107,	c1383	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1311	14.8	0.8	18	1	US-10-310-914A-946378	Sequence 971333,	1384	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1312	14.8	0.8	18	1	US-10-310-914A-965107	Sequence 981336,	c1385	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1313	14.8	0.8	18	1	US-10-310-914A-971333	Sequence 984119,	c1386	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1314	14.8	0.8	18	1	US-10-310-914A-981336	Sequence 990023,	1387	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1315	14.8	0.8	18	1	US-10-310-914A-984119	Sequence 990023,	1388	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1316	14.8	0.8	18	1	US-10-310-914A-990023	Sequence 999624,	1389	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1317	14.8	0.8	18	1	US-10-310-914A-999624	Sequence 1004988,	1390	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1318	14.8	0.8	18	1	US-10-310-914A-1004988	Sequence 1093902,	c1391	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1319	14.8	0.8	18	1	US-10-310-914A-1093902	Sequence 1169386,	1392	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1320	14.8	0.8	18	1	US-10-310-914A-1169386	Sequence 1219917,	1393	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
1321	14.8	0.8	18	1	US-10-310-914A-1219917	Sequence 1234776,	1394	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1322	14.8	0.8	18	1	US-10-310-914A-1234776	Sequence 1249080,	c1395	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1323	14.8	0.8	18	1	US-10-310-914A-1249080	Sequence 1255023,	1396	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1324	14.8	0.8	18	1	US-10-310-914A-1255023	Sequence 1329744,	1397	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1325	14.8	0.8	18	1	US-10-310-914A-1329744	Sequence 1337516,	c1398	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1326	14.8	0.8	18	1	US-10-310-914A-1337516	Sequence 1366802,	1399	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1327	14.8	0.8	18	1	US-10-310-914A-1366802	Sequence 1366802,	c1400	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1328	14.8	0.8	18	1	US-10-310-914A-1366802	Sequence 3801, Ap	1401	14.4	0.8	18	1	US-10-310-914A-441528	Sequence 448431, A
c1329	14.8	0.8	18	1	US-11-069-908-3801	Sequence 3801, Ap	1402	14.4	0.8	18	1	US-10-712-672-343	Sequence 344, App
c1330	14.8	0.8	18	1	US-11-069-908-3801	Sequence 467163,	1403	14.4	0.8	18	1	US-10-712-672-343	Sequence 344, App
1331	14.6	0.8	22	1	US-10-310-914A-467163	Sequence 467164,	1404	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, Ap
1332	14.6	0.8	22	1	US-10-310-914A-467164	Sequence 467164,	1405	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, Ap
c1333	14.4	0.8	16	1	US-09-930-503-14	Sequence 14164,	1406	14.4	0.8	18	1	US-10-723-361-6965	Sequence 6965, Ap
1334	14.4	0.8	16	1	US-10-712-672-1732	Sequence 1732, Ap	1407	14.4	0.8	18	1	US-10-712-672-343	Sequence 22, Appl
c1335	14.4	0.8	17	1	US-09-864-785-1566	Sequence 1566, Ap	1408	14.4	0.8	18	1	US-11-069-377-22	Sequence 22, Appl
1336	14.4	0.8	17	1	US-09-864-785-1566	Sequence 1566, Ap	1409	14.4	0.8	18	1	US-11-090-399-22	Sequence 22, Appl
c1337	14.4	0.8	17	1	US-09-930-503-13	Sequence 920, App	1410	14.4	0.8	18	1	US-11-090-399-22	Sequence 22, Appl
c1338	14.4	0.8	17	1	US-09-780-533A-920	Sequence 3108, Ap	1411	13.8	0.8	17	1	US-09-866-108-7574	Sequence 7674, Ap
c1339	14.4	0.8	17	1	US-09-848-754A-3108	Sequence 1361, Ap	1412	13.8	0.8	17	1	US-09-866-108-7574	Sequence 7674, Ap
c1340	14.4	0.8	17	1	US-09-930-423-1361	Sequence 769, App	1413	13.8	0.8	17	1	US-09-864-785-336	Sequence 336, App
1341	14.4	0.8	17	1	US-09-780-164-769	Sequence 1361, Ap	1414	13.8	0.8	17	1		

US-10-310-914A-386265/c  
; Sequence 386265, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200,CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386265  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386265

## ALIGNMENTS

Sequence 891, App  
Sequence 990, App  
Sequence 1483, App  
Sequence 1525, App  
Sequence 250, App  
Sequence 839, App  
Sequence 381, App  
Sequence 966, App  
Sequence 966, App  
Sequence 4268, App  
Sequence 6951, App  
Sequence 1453, App  
Sequence 381, App  
Sequence 1039, App  
Sequence 2345, App  
Sequence 2346, App  
Sequence 1714, App  
Sequence 1886, App  
Sequence 6345, App  
Sequence 1714, App  
Sequence 1886, App  
Sequence 6345, App  
Sequence 345, App  
Sequence 506, App  
Sequence 763, App  
Sequence 764, App  
Sequence 765, App  
Sequence 766, App  
Sequence 2148, App  
Sequence 3557, App  
Sequence 2756, App  
Sequence 7674, App  
Sequence 376, App  
Sequence 1855, App  
Sequence 2044, App  
Sequence 4268, App  
Sequence 1714, App  
Sequence 1886, App  
Sequence 397, App  
Sequence 397, App  
Sequence 1002, App  
Sequence 9, App11

US-10-310-914A-386265/c  
; Sequence 386265, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200,CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386265  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386265

Query Match 1.6%; Score 28; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-310-914A-386265/c  
; Sequence 386265, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200,CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386265  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386265

Query Match 1.5%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-310-914A-386265/c  
; Sequence 386265, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087,0200,CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386265  
; LENGTH: 28  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386265



```
; APPLICANT: Shuler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386278
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386278

Query Match          1.5%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1538 GGGACTTGCAAAAAGGTCAGTATGG 1563  
Db 26 GGGACTTGCAAAAAGGTCAGTATGG 1

RESULT 5  
US-10-005-956-1305/C  
; Sequence 1305, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1305  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.  
US-10-005-956-1305

Query Match 1.5%; Score 26; DB 1; Length 27;  
Best Local Similarity 96.3%; Pred. No. 1.9e+02;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1539 GGACTTGCAAAAAGGTCAGTATGGGT 1565  
Db 27 GGACTTGCAAAAAGGTCAGTATGGGT 1

RESULT 6  
US-09-747-429-12/C  
; Sequence 12, Application US/09747429  
; Patent No. US20020146810A1  
; GENERAL INFORMATION:  
; APPLICANT: Rameshwar, Pranela  
; APPLICANT: Gascon, Pedro  
; TITLE OF INVENTION: A Human Preprothachykinin Gene Promoter  
; FILE REFERENCE: UMDNJ NIMS 97-16  
; CURRENT APPLICATION NUMBER: US/09/747,429  
; CURRENT FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/171,970  
; PRIOR FILING DATE: 1999-12-23

```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-747-429-12

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1041 CTACCTGAGAGAGTTATCCAGCAG 1065  
Db 25 CTACCTGAGAGAGTTATCCAGCAG 1

RESULT 7  
US-09-747-429-13  
; Sequence 13, Application US/09747429  
; Patent No. US20020146810A1  
; GENERAL INFORMATION:  
; APPLICANT: Rameshwar, Pranela  
; APPLICANT: Gascon, Pedro  
; TITLE OF INVENTION: A Human Preprothachykinin Gene Promoter  
; FILE REFERENCE: UMDNJ NIMS 97-16  
; CURRENT APPLICATION NUMBER: US/09/747,429  
; CURRENT FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/171,970  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-09-747-429-13

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 AGGACAGTGAGCACTTTTCTGG 424  
Db 1 AGGACAGTGAGCACTTTTCTGG 25

RESULT 8  
US-10-005-956-1125/C  
; Sequence 1125, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1125  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens



US-10-005-956-1125

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 707 GCTACTACTCAACACAGAGCCAT 731  
DB 25 GCTACTACTCAACACAGAGCCAT 1

RESULT 9

US-10-005-956-1300/c  
; Sequence 1300, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23/273,037  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1300  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-005-956-1300

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 CCCATCGCCGCTGCTTCGCCAGTA 568  
DB 25 CCCATCGCCGCTGCTTCGCCAGTA 1

RESULT 10  
US-10-628-066-12/c  
; Sequence 12, Application US/10628066  
; Publication No. US20040086919A1  
; GENERAL INFORMATION:  
; APPLICANT: Rameshwar, Prianela  
; APPLICANT: Gascon, Pedro  
; TITLE OF INVENTION: A Human Preprotachykinin Gene Promoter  
; FILE REFERENCE: UMDNJ NIMS 97-16  
; CURRENT APPLICATION NUMBER: US/10/628,066  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/747,429  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/171,970  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-628-066-12

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1041 CTACCTGAGAGCTTTATCCAGCAG 1065  
DB 25 CTACCTGAGAGAGTTTATCCAGCAG 1

RESULT 11

US-10-628-066-13  
; Sequence 13, Application US/10628066  
; Publication No. US20040086919A1  
; GENERAL INFORMATION:  
; APPLICANT: Rameshwar, Prianela  
; APPLICANT: Gascon, Pedro  
; TITLE OF INVENTION: A Human Preprotachykinin Gene Promoter  
; FILE REFERENCE: UMDNJ NIMS 97-16  
; CURRENT APPLICATION NUMBER: US/10/628,066  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/747,429  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/171,970  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-628-066-13

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 AGGACAGTGAAGAACTATTTCTCG 424  
DB 1 AGGACAGTGAAGAACTATTTCTCG 25

RESULT 12  
US-10-719-900-67259  
; Sequence 67259, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 67259  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-67259

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 926 AAGTCTCTGCCAAGCGCAGGTGAT 950  
DB 1 AAGTCTCTGCCAAGCGCAGGTGAT 25

RESULT 13  
US-10-719-900-247409  
; Sequence 247409, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:

```

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-247409

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db      1 ATCTACTGCTGCTCAATGACAGGT 25

RESULT 14
US-10-719-900-253860
; Sequence 253860, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 253860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-253860

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1136 ATGACAGTTCGCTCGGGCTTCAA 1160
Db      1 ATGACAGTTCGCTCGGGCTTCAA 25

RESULT 15
US-10-809-189-67915
; Sequence 67915, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67915

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-10-809-189-67915

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1261 GTGAGCGCGCTGGAGACCACTATCT 1285
Db      1 GTGAGCGCGCTGGAGACCACTATCT 25

RESULT 16
US-10-809-189-67925
; Sequence 67925, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-10-809-189-67925

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1123 TACTGCTGCTCAATGACAGTTCC 1147
Db      1 TACTGCTGCTCAATGACAGTTCC 25

RESULT 17
US-11-060-756-34833
; Sequence 34833, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.1.2
; SEQ ID NO 34833
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
; US-11-060-756-34833

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      394 AGAATGAGACAGTGAAGACTATT 418

```

Db 1 AGAATGAGCAGCTGACGACTATT 25

RESULT 18  
US-11-060-756-34834  
; Sequence 34834, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34834  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-34834

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 AAGAATGAGCAGCTGACGACTATT 417  
Db 1 AAGAATGAGCAGCTGACGACTATT 25

RESULT 19  
US-11-060-756-34835  
; Sequence 34835, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34835  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-34835

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 801 CATCTGTGTGACTGTGCTGATCTAC 825  
Db 1 CATCTGTGTGACTGTGCTGATCTAC 25

RESULT 20  
US-11-060-756-34836  
; Sequence 34836, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756

CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34836  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-34836

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 771 TCCGACAGATTATGAGAAAGTG 795  
Db 1 TCCGACAGATTATGAGAAAGTG 25

RESULT 21  
US-11-060-756-34837  
; Sequence 34837, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34837  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-34837

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 802 ATCTGTGACTGTGCTGATCTACT 826  
Db 1 ATCTGTGACTGTGCTGATCTACT 25

RESULT 22  
US-11-060-756-34838  
; Sequence 34838, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34838  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-34838

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 GCATCCGACAGATTATGAGAAA 792

```
Db          1 GCATCCGACACAGATTATGAGAAA 25

RESULT 23
US-11-060-756-34839
; Sequence 34839, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34839

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          767 AGCATCCGACACAGATTATGAGAA 791
Db          1 AGCATCCGACACAGATTATGAGAA 25

RESULT 24
US-11-060-756-34840
; Sequence 34840, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34840

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          765 AGAGCATCCGACACAGATTATGAG 789
Db          1 AGAGCATCCGACACAGATTATGAG 25

RESULT 25
US-11-060-756-34841
; Sequence 34841, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34841

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          766 GAGCATCCGACACAGATTATGAGA 790
Db          1 GAGCATCCGACACAGATTATGAGA 25

RESULT 26
US-11-060-756-34842
; Sequence 34842, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34842

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1047 GAAGAAGTTATCCAGCAGAGTCTAC 1071
Db          1 GAAGAAGTTATCCAGCAGAGTCTAC 25

RESULT 27
US-11-060-756-34843
; Sequence 34843, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34843

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1637 GAGCTGAACCAATCATGTAAGTTT 1661
Db          1 GAGCTGAACCAATCATGTAAGTTT 25
```

```
RESULT 28
US-11-060-756-34844
; Sequence 34844, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34844

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 708 CTACTACTCAACACAGAGACCATG 732
Db 1 CTACTACTCAACACAGAGACCATG 25

RESULT 29
US-11-060-756-34845
; Sequence 34845, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34845

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 CAGGCAATCCGAACAAGATTATGA 788
Db 1 CAGGCAATCCGAACAAGATTATGA 25

RESULT 30
US-11-060-756-34846
; Sequence 34846, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
```

```
SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34846

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1597 ATCTCAATCTCTCCCTATCTTGCC 1621
Db 1 ATCTCAATCTCTCCCTATCTTGCC 25

RESULT 31
US-11-060-756-34847
; Sequence 34847, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34847
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34847

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TGAAGAAGTTATCCAGCAGGTCTA 1070
Db 1 TGAAGAAGTTATCCAGCAGGTCTA 25

RESULT 32
US-11-060-756-34848
; Sequence 34848, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34848

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 770 ATCCGAACAAGATTATGAGAAAGT 794
Db 1 ATCCGAACAAGATTATGAGAAAGT 25
```

```
RESULT 33
US-11-060-756-34849
; Sequence 34849, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34849
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34849

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1596 AATCTCAATTCCTCCATCTTTCG 1620
Db      1 AATCTCAATTCCTCCATCTTTCG 25
|||||

RESULT 34
US-11-060-756-34850
; Sequence 34850, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34850
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34850

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      395 GAATGAGACAGTGAAGCACTATT 419
Db      1 GAATGAGACAGTGAAGCACTATT 25
|||||

RESULT 35
US-11-060-756-34851
; Sequence 34851, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 34851
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34851

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1636 TGACTCAAAACCAATCAGTGAAGT 1660
Db      1 TGACTCAAAACCAATCAGTGAAGT 25
|||||

RESULT 36
US-11-060-756-34852
; Sequence 34852, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34852
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34852

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1037 ATCTCACTGGAAGAGTTATCCA 1061
Db      1 ATCTCACTGGAAGAGTTATCCA 25
|||||

RESULT 37
US-11-060-756-34853
; Sequence 34853, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34853

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      772 CCGAACAAGATTATGAGAAAGTGT 796
Db      1 CCGAACAAGATTATGAGAAAGTGT 25
|||||
```

```
RESULT 38
US-11-060-756-34854
; Sequence 34854, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34854

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 769 CATCGAACAAGATTATGAGAAG 793
Db 1 CATCGAACAAGATTATGAGAAG 25
|||||

RESULT 39
US-11-060-756-34855
; Sequence 34855, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34855

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 804 CTGTGTGACTGTGCTGATCTACTTC 828
Db 1 CTGTGTGACTGTGCTGATCTACTTC 25
|||||

RESULT 40
US-11-060-756-34856
; Sequence 34856, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34856

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 800 ACATCTGTGACTGTGCTGATCTA 824
Db 1 ACATCTGTGACTGTGCTGATCTA 25
|||||

RESULT 41
US-11-060-756-34857
; Sequence 34857, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34857
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34857

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1599 CTCATATCTTCCCTATCTTTGCCAC 1623
Db 1 CTCATATCTTCCCTATCTTTGCCAC 25
|||||

RESULT 42
US-11-060-756-34858
; Sequence 34858, Application US/11060756
; Publication No. US20050221354A1
; ORGANISM: probe
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34858
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34858

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1039 CTCACCTGAAGAAGTTATTCACGC 1063
Db 1 CTCACCTGAAGAAGTTATTCACGC 25
|||||

RESULT 43
```

```
US-11-060-756-34859
; Sequence 34859, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34859

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1038 TCTCTACCTGAAGAAGTTATCCAG 1062
Db      1 TCTCTACCTGAAGAAGTTATCCAG 25

RESULT 44
US-11-060-756-34860
; Sequence 34860, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34860
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34860

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      763 CCAGAGCATCCGACAGATTATG 787
Db      1 CCAGAGCATCCGACAGATTATG 25

RESULT 45
US-11-060-756-34861
; Sequence 34861, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34861
; LENGTH: 25

; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34861

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1598 TCTCAATCTTCCCTATCTTTGCCA 1622
Db      1 TCTCAATCTTCCCTATCTTTGCCA 25

RESULT 46
US-11-060-756-34862
; Sequence 34862, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34862

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1041 CTACCTGAGAGAAGTTATCCAGCAG 1065
Db      1 CTACCTGAGAGAAGTTATCCAGCAG 25

RESULT 47
US-11-060-756-34863
; Sequence 34863, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34863
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34863

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      392 AAAGATGAGACAGCTGACGAACCTA 416
Db      1 AAAGATGAGACAGCTGACGAACCTA 25

RESULT 48
US-11-060-756-34864
```



```
; Sequence 34864, Application US/11060756
; Publication NO. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34864

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1040 TCTACTGAAGAAGTTATCCAGCA 1064
Db      1 TCTACTGAAGAAGTTATCCAGCA 25

RESULT 49
US-11-060-756-34865
; Sequence 34865, Application US/11060756
; Publication NO. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34865
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34865

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      803 TCTGTGACTGTGCTGATCTACTT 827
Db      1 TCTGTGACTGTGCTGATCTACTT 25

RESULT 50
US-11-060-756-34866
; Sequence 34866, Application US/11060756
; Publication NO. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34866
; LENGTH: 25
; TYPE: DNA

; ORGANISM: probe
US-11-060-756-34866

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1048 AAGAAGTTATCCAGCAGCTTACC 1072
Db      1 AAGAAGTTATCCAGCAGCTTACC 25

RESULT 51
US-11-060-756-34867
; Sequence 34867, Application US/11060756
; Publication NO. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34867
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34867

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      783 TTATGAGAAGTGATCCACATCTGT 807
Db      1 TTATGAGAAGTGATCCACATCTGT 25

RESULT 52
US-11-060-756-34868
; Sequence 34868, Application US/11060756
; Publication NO. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34868
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34868

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 GATCTTACTGAAGAAGTTATCC 1060
Db      1 GATCTTACTGAAGAAGTTATCC 25

RESULT 53
US-11-060-756-34869
; Sequence 34869, Application US/11060756
```

```
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34869
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34869

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 707 GCTACTACTCAACGACGAGCCAT 731
Db 1 GCTACTACTCAACGACGAGACCAT 25

RESULT 54
US-11-060-756-34870
; Sequence 34870, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34870

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GAACCTTACCTATGCTGTCACAC 498
Db 1 GAACCTTACCTATGCTGTCACAC 25

RESULT 55
US-11-060-756-34871
; Sequence 34871, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
```

```
US-11-060-756-34871

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 782 TTTATGAGAAAGTGATCACCATCTG 806
Db 1 TTTATGAGAAAGTGATCACCATCTG 25

RESULT 56
US-11-060-756-34872
; Sequence 34872, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34872

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 GCATTCAATACAGTGTGAACCTCA 481
Db 1 GCATTCAATACAGTGTGAACCTCA 25

RESULT 57
US-11-060-756-34873
; Sequence 34873, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34873

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 CTTCTCCCAATGCTGCTCCTAG 1434
Db 1 CTTCTCCCAATGCTGCTCCTAG 25

RESULT 58
US-11-060-756-34874
; Sequence 34874, Application US/11060756
; Publication No. US20050221354A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34874

```

```

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 807 TGTGACTGTGCTGATCTACTCTC 831
Db 1 TGTGACTGTGCTGATCTACTCTC 25

```

```

RESULT 59
US-11-060-756-34875
; Sequence 34875, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34875

```

```

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 554 CTGCTTCGCCAGATCTACTCCAT 578
Db 1 CTGCTTCGCCAGATCTACTCCAT 25

```

```

RESULT 60
US-11-060-756-34876
; Sequence 34876, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34876

```

```

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 776 ACAAGATTTATGAGAAAGTGACCA 800
Db 1 ACAAGATTTATGAGAAAGTGACCA 25

```

```

RESULT 61
US-11-060-756-117862
; Sequence 117862, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-117862

```

```

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1715 ATTCCATTTCTGGAAGTACTTGG 1739
Db 1 ATTCCATTTCTGGAAGTACTTGG 25

```

```

RESULT 62
US-11-060-756-121089
; Sequence 121089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-121089

```

```

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1508 ATCTGAACCATCAGAAACACCTC 1532
Db 1 ATCTGAACCATCAGAAACACCTC 25

```

```

RESULT 63
US-11-060-756-124386
; Sequence 124386, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124386
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-124386

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1628 ATGCTGTGACTCAACCAATCA 1652
1 ATGCTGTGACTCAACCAATCA 25

RESULT 64
US-11-060-756-124823
; Sequence 124823, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124823
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-124823

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1711 ATGCATTCATTCTCGAAGTACT 1735
1 ATGCATTCATTCTCGAAGTACT 25

RESULT 65
US-11-060-756-127403
; Sequence 127403, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-127403

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1493 ATGGAATTCCTTCATCTGAACC 1517
1 ATGGAATTCCTTCATCTGAACC 25

RESULT 66
US-11-060-756-130804
; Sequence 130804, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-130804

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1378 AGTACTCCAGACCATGACAGAGA 1402
1 AGTACTCCAGACCATGACAGAGA 25

RESULT 67
US-11-060-756-138470
; Sequence 138470, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-138470

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1644 ACCAATCATGAACTTGTGAGC 1668
1 ACCAATCATGAACTTGTGAGC 25

RESULT 68
US-11-060-756-139174
; Sequence 139174, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 139174  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-139174

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1279 ACCATCTCCACAGTGTGGGGCCC 1303  
Db 1 ACCATCTCCACAGTGTGGGGCCC 25

RESULT 69  
US-11-060-756-140183  
Sequence 140183, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 140183  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-140183

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1240 ACCCAGGCGAGTGTGTACAAAGTCA 1264  
Db 1 ACCCAGGCGAGTGTGTACAAAGTCA 25

RESULT 70  
US-11-060-756-147282  
Sequence 147282, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 147282  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-147282

Query Match 1.4%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1214 AAATGAATCCACCCGGTATCTCCA 1238  
Db 1 AAATGAATCCACCCGGTATCTCCA 25

RESULT 71  
US-11-060-756-149065  
Sequence 149065, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 149065  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-149065

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1572 AACATTCATCTCTGAGTCAAAA 1596  
Db 1 AACATTCATCTCTGAGTCAAAA 25

RESULT 72  
US-11-060-756-149921  
Sequence 149921, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 149921  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-149921

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1592 AAAAATCTCAATCTTCCCTATCT 1616  
Db 1 AAAAATCTCAATCTTCCCTATCT 25

RESULT 73  
US-11-060-756-149974  
Sequence 149974, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin

```
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149974
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-149974

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1593 AAAAATCTCAATTTCTTCCCTATCTT 1617
Db      1 AAAAATCTCAATTTCTTCCCTATCTT 25

RESULT 74
US-11-060-756-151784
; Sequence 151784, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-151784

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1363 AACTGCTCTTCACGAGTACTCCA 1387
Db      1 AACTGCTCTTCACGAGTACTCCA 25

RESULT 75
US-11-060-756-152840
; Sequence 152840, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-152840

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1643 AACCAATCATCTGAACTTGTCTGAG 1667
Db      1 AACCAATCATCTGAACTTGTCTGAG 25

RESULT 76
US-11-060-756-154707
; Sequence 154707, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 154707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-154707

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1702 AAGAGCCCAATGATTCATTCTCG 1726
Db      1 AAGAGCCCAATGATTCATTCTCG 25

RESULT 77
US-11-060-756-160866
; Sequence 160866, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-160866

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1701 CAAGAGCCCAATGATTCATTCT 1725
Db      1 CAAGAGCCCAATGATTCATTCT 25

RESULT 78
US-11-060-756-162417
; Sequence 162417, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
```

;; TITLE OF INVENTION: Target Genes  
;; FILE REFERENCE: AM101083 (031896-042000)  
;; CURRENT APPLICATION NUMBER: US/11/060,756  
;; CURRENT FILING DATE: 2005-02-18  
;; NUMBER OF SEQ ID NOS: 303284  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 162417  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: probe  
US-11-060-756-162417

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1646 CAAATCACTGAACCTTGCTGAGCCT 1670  
Db 1 CAAATCACTGAACCTTGCTGAGCCT 25

RESULT 79  
US-11-060-756-163702  
; Sequence 163702, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 163702  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-163702

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1651 CACTGAACCTTGCTGAGCCTGTAA 1675  
Db 1 CACTGAACCTTGCTGAGCCTGTAA 25

RESULT 80  
US-11-060-756-164016  
; Sequence 164016, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 164016  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-164016

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1373 CACGAAGTACTCCAGACCATGAC 1397  
Db 1 CACGAAGTACTCCAGACCATGAC 25

RESULT 81  
US-11-060-756-167974  
; Sequence 167974, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 167974  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-167974

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1248 CAGTGTACAAAGTCAGCGCCTG 1272  
Db 1 CAGTGTACAAAGTCAGCGCCTG 25

RESULT 82  
US-11-060-756-169980  
; Sequence 169980, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 169980  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-169980

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 CATCAGCCCGCGCATATGAGGG 1209  
Db 1 CATCAGCCCGCGCATATGAGGG 25

RESULT 83  
US-11-060-756-170236  
; Sequence 170236, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

```
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170236
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-170236

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

1627 CATGCTGTGACTCACCAACCAATC 1651
|||||
1 CATGCTGTGACTCACCAACCAATC 25

Db

RESULT 84
US-11-060-756-170323
Sequence 170323, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170323
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-170323

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

1488 CATGCATGGAATTCCTTCATCTG 1512
|||||
1 CATGCATGGAATTCCTTCATCTG 25

Db

RESULT 85
US-11-060-756-170981
Sequence 170981, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170981
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-170981

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
```

```
QY 1575 CATTCATCTTGTGACCAAAAATC 1599
|||||
Db 1 CATTCATCTTGTGACCAAAAATC 25

RESULT 86
US-11-060-756-171771
Sequence 171771, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 171771
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-171771

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
```

```
QY 1714 CATTCATTTCTGGAAGTGACTTG 1738
|||||
Db 1 CATTCATTTCTGGAAGTGACTTG 25
```

```
RESULT 87
US-11-060-756-171898
Sequence 171898, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 171898
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-171898

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 25;
Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;
```

```
QY 1719 CATTCGGAAGTGACTTGGCTGC 1743
|||||
Db 1 CATTCGGAAGTGACTTGGCTGC 25
```

```
RESULT 88
US-11-060-756-173421
Sequence 173421, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
```



CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 173421  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-173421

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1370 CTCACGAGTCAAGCCAT 1394  
Db 1 CTCACGAGTCAAGCCAT 25

RESULT 89  
US-11-060-756-174120  
Sequence 174120, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 174120  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-174120

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 CTTTCTCAAGCCCATGATTT 1717  
Db 1 CTTTCTCAAGCCCATGATTT 25

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 90  
US-11-060-756-176669  
Sequence 176669, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 176669  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-176669

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1699 CTCAGAGCCCATGATTCATTT 1723

Db 1 CTCAGAGCCCATGATTCATTT 25

RESULT 91  
US-11-060-756-177313  
Sequence 177313, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 177313  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-177313

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1625 CTCATGCTGTGTGACTCAACCAAA 1649  
Db 1 CTCATGCTGTGTGACTCAACCAAA 25

RESULT 92  
US-11-060-756-177851  
Sequence 177851, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 177851  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-177851

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 CTCCTTCATGATGGAATTCCTT 1505  
Db 1 CTCCTTCATGATGGAATTCCTT 25

RESULT 93  
US-11-060-756-178612  
Sequence 178612, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756

;; CURRENT FILING DATE: 2005-02-18  
;; NUMBER OF SEQ ID NOS: 303284  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 178612  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: probe  
US-11-060-756-178612

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1359 CTCCACGCTGCTTCACGAAGTGAC 1383  
DB 1 CTCCACTGCTCTTCACGAAGTGAC 25

## RESULT 94

US-11-060-756-178926  
; Sequence 178926, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 178926  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-178926

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1284 CTCACAGTGTGGGGCCCCACAG 1308  
DB 1 CTCACAGTGTGGGGCCCCACAG 25

## RESULT 95

US-11-060-756-179517  
; Sequence 179517, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 179517  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-179517

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1740 CTGCATGCGAGTGTCTATTTCAGGA 1764  
|||||

DB 1 CTGCATGCGAGTGTCTATTTCAGGA 25

## RESULT 96

US-11-060-756-179873  
; Sequence 179873, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 179873  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-179873

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1365 CTGCTCTTCACGAAGTGATCCGAAG 1389  
DB 1 CTGCTCTTCACGAAGTGATCCGAAG 25

## RESULT 97

US-11-060-756-182148  
; Sequence 182148, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 182148  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-182148

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 CTGTGTGACTCAACCAATCAGTG 1655  
DB 1 CTGTGTGACTCAACCAATCAGTG 25

## RESULT 98

US-11-060-756-182797  
; Sequence 182797, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT FILING DATE: 2005-02-18

NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 182797  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-182797

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1510 CTGAACCATCGAAGAACCTCTC 1534  
Db 1 CTGAACCATCGAAGAACCTCTC 25

RESULT 99  
US-11-060-756-185584  
Sequence 185584, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 185584  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-185584

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1375 CGAAGTGACTCCAGACCATGACG 1399  
Db 1 CGAAGTGACTCCAGACCATGACG 25

RESULT 100  
US-11-060-756-187465  
Sequence 187465, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 187465  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-187465

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1483 CCTTCATGATGAGAAATTCCTTC 1507  
Db 1 CCTTCATGATGAGAAATTCCTTC 25

RESULT 101  
US-11-060-756-192020  
Sequence 192020, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 192020  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-192020

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1131 CCTCATGACAGGTTCCGCTGAGC 1155  
Db 1 CCTCATGACAGGTTCCGCTGAGC 25

RESULT 102  
US-11-060-756-192401  
Sequence 192401, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 192401  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-192401

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1624 CCTCATGCTGTGTGATCAACCA 1648  
Db 1 CCTCATGCTGTGTGATCAACCA 25

RESULT 103  
US-11-060-756-193467  
Sequence 193467, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-193467

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1280 CCATCTCCACAGTGTGTGGGGCCCA 1304
DB      1 CCATCTCCACAGTGTGTGGGGCCCA 25

RESULT 104
US-11-060-756-193692
; Sequence 193692, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-193692

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1718 CCATTCTGGAAGTGACTTTGGCTG 1742
DB      1 CCATTCTGGAAGTGACTTTGGCTG 25

RESULT 105
US-11-060-756-195758
; Sequence 195758, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195758
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-195758

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 106
US-11-060-756-195777
; Sequence 195777, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195777
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-195777

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1286 CCACAGTGTGTGGGGCCACAGAGA 1310
DB      1 CCACAGTGTGTGGGGCCACAGAGA 25

RESULT 107
US-11-060-756-196323
; Sequence 196323, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-196323

Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1645 CCAATCACTGAAGCTTGTGAGCC 1669
DB      1 CCAATCACTGAAGCTTGTGAGCC 25

RESULT 108
US-11-060-756-197870
; Sequence 197870, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
```

SEQ ID NO 197870  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-197870

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 GCCTCCCTTCATGCATGGAATTC 1503  
Db 1 GCCTCCCTTCATGCATGGAATTC 25

RESULT 109  
US-11-060-756-198758  
; Sequence 198758, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 198758  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-198758

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1130 GCCTCAATGACAGGTCGCTGGG 1154  
Db 1 GCCTCAATGACAGGTCGCTGGG 25

RESULT 110  
US-11-060-756-202952  
; Sequence 202952, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 202952  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-202952

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1630 GCTGTGACTCAACCAATCACT 1654  
Db 1 GCTGTGACTCAACCAATCACT 25

RESULT 111  
US-11-060-756-204546  
; Sequence 204546, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 204546  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-204546

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 GCCTTCACGAGTCAAGCTCCAGAC 1391  
Db 1 GCCTTCACGAGTCAAGCTCCAGAC 25

RESULT 112  
US-11-060-756-205830  
; Sequence 205830, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 205830  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-205830

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1692 GCTTTCTCAAGGCCCAATGCAT 1716  
Db 1 GCTTTCTCAAGGCCCAATGCAT 25

RESULT 113  
US-11-060-756-206207  
; Sequence 206207, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 206207

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-206207

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1713 GCATTCATTCTCGAAGTACCTT 1737
Db 1 GCATTCATTCTCGAAGTACCTT 25

RESULT 114
US-11-060-756-207277
; Sequence 207277, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-207277

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1247 GCAGTGTGTACAAAGTCAGCCGCT 1271
Db 1 GCAGTGTGTACAAAGTCAGCCGCT 25

RESULT 115
US-11-060-756-207312
; Sequence 207312, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-207312

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1742 GCATGCGAGTGTCTCATTTGAGATG 1766
Db 1 GCATGCGAGTGTCTCATTTGAGATG 25

RESULT 116
US-11-060-756-213399
; Sequence 213399, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-213399

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1376 GAAGTACTCCAGACCATGACAGA 1400
Db 1 GAAGTACTCCAGACCATGACAGA 25

RESULT 117
US-11-060-756-220646
; Sequence 220646, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 220646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-220646

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 GACTCCAAGACCATGACAGAGCT 1405
Db 1 GACTCCAAGACCATGACAGAGCT 25

RESULT 118
US-11-060-756-227033
; Sequence 227033, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227033
; LENGTH: 25
```

;; TYPE: DNA  
;; ORGANISM: probe  
US-11-060-756-227033

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1204 GAGGGCTGGAATGAATCCACC 1228  
DB 1 GAGGGCTGGAATGAATCCACC 25

RESULT 119  
US-11-060-756-238277  
; Sequence 238277, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 238277  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-238277

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1589 GTCAAAAATCTCAATTTCTCCCTA 1613  
DB 1 GTCAAAAATCTCAATTTCTCCCTA 25

RESULT 120  
US-11-060-756-242329  
; Sequence 242329, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 242329  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-242329

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1670 TGTAAATATAAGTCGACCCAGCT 1694  
DB 1 TGTAAATATAAGTCGACCCAGCT 25

RESULT 121  
US-11-060-756-246182

; Sequence 246182, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 246182  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-246182

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1207 GAGCTGGAATGAATCCACCCGCT 1231  
DB 1 GAGCTGGAATGAATCCACCCGCT 25

RESULT 122  
US-11-060-756-247883  
; Sequence 247883, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 247883  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-247883

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1538 GGAAGTTGCAAAAAGGTCAGTATG 1562  
DB 1 GGAAGTTGCAAAAAGGTCAGTATG 25

RESULT 123  
US-11-060-756-251001  
; Sequence 251001, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 251001  
; LENGTH: 25  
; TYPE: DNA

```

; ORGANISM: probe
US-11-060-756-251001

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 GGTCAATGAGTGGTGAAGAAACAT 1577
Db 1 GGTCAATGAGTGGTGAAGAAACAT 25

RESULT 124
US-11-060-756-256929
; Sequence 256929, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-256929

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1212 GGAATGAAATCCACCGGTATCTC 1236
Db 1 GGAATGAAATCCACCGGTATCTC 25

RESULT 125
US-11-060-756-264993
; Sequence 264993, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-264993

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1561 TGGGTAGGAAACATTCATCCT 1585
Db 1 TGGGTAGGAAACATTCATCCT 25

RESULT 126
US-11-060-756-266512
; Sequence 266512, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 266512
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-266512

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1632 TGTGTACTCAACCAATCCTGA 1656
Db 1 TGTGTACTCAACCAATCCTGA 25

RESULT 127
US-11-060-756-267837
; Sequence 267837, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 267837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-267837

Query Match
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1253 TGTACAAAGTCAGCGCCTGGAGAC 1277
Db 1 TGTACAAAGTCAGCGCCTGGAGAC 25

RESULT 128
US-11-060-756-271421
; Sequence 271421, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 271421
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-271421
```



US-11-060-756-271421

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1394 TGACAGAGAGCTTCGACCTTCCTC 1418  
Db 1 TGACAGAGAGCTTCGACCTTCCTC 25

RESULT 129

US-11-060-756-271732  
; Sequence 271732, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 271732  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-271732

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1712 TGATTCATTTCTGGAAGTACTT 1736  
Db 1 TGATTCATTTCTGGAAGTACTT 25

RESULT 130

US-11-060-756-273114  
; Sequence 273114, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 273114  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-273114

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TGCATGCGAGTCTCATTTGAGAT 1765  
Db 1 TGCATGCGAGTCTCATTTGAGAT 25

RESULT 131  
US-11-060-756-273130  
; Sequence 273130, Application US/11060756  
; Publication No. US20050221354A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 273130  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-273130

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1490 TGCATGGAATTCCTTCATCTGGA 1514  
Db 1 TGCATGGAATTCCTTCATCTGGA 25

RESULT 132

US-11-060-756-274140  
; Sequence 274140, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 274140  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-274140

Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1629 TGCTGTGACTCAACCAATCAGC 1653  
Db 1 TGCTGTGACTCAACCAATCAGC 25

RESULT 133

US-11-060-756-274779  
; Sequence 274779, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; TITLE OF INVENTION: Target Genes  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 274779  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-274779

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 TGCTCCCTTCATGATGAAATTC 1502
DB 1 TGCTCCCTTCATGATGAAATTC 25

RESULT 134
US-11-060-756-275674
; Sequence 275674, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-275674

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 TCATTTCTGGAAGTGACTTTGGCT 1741
DB 1 TCATTTCTGGAAGTGACTTTGGCT 25

RESULT 135
US-11-060-756-276554
; Sequence 276554, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 276554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-276554

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1697 TCCTCAAGAGCCCATGCAATTCAT 1721
DB 1 TCCTCAAGAGCCCATGCAATTCAT 25

RESULT 136
US-11-060-756-281504
; Sequence 281504, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 281504
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-281504

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1650 TCACTGAACCTTGTGCTGAGCCTGTA 1674
DB 1 TCACTGAACCTTGTGCTGAGCCTGTA 25

RESULT 137
US-11-060-756-283191
; Sequence 283191, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 283191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-283191

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1626 TCATGCTGTGTGACTCAACCAAT 1650
DB 1 TCATGCTGTGTGACTCAACCAAT 25

RESULT 138
US-11-060-756-285749
; Sequence 285749, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-285749
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1700 TCAAGAGCCCAATGCATTCATTTTC 1724
      |||
Db 1 TCAAGAGCCCAATGCATTCATTTTC 25

RESULT 139
US-11-060-756-285791
; Sequence 285791, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-285791

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1133 TCAATGACAGGTTCCGTCGGGCTT 1157
      |||
Db 1 TCAATGACAGGTTCCGTCGGGCTT 25

RESULT 140
US-11-060-756-295627
; Sequence 295627, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 295627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-295627

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1694 TTTCCTCAAGAGCCCAATGCATTC 1718
      |||
Db 1 TTTCCTCAAGAGCCCAATGCATTC 25

RESULT 141
US-11-060-756-300784
; Sequence 300784, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 300784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-300784

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1696 TTCTCAAGAGCCCAATGCATTTCA 1720
      |||
Db 1 TTCTCAAGAGCCCAATGCATTTCA 25

RESULT 142
US-11-060-756-301167
; Sequence 301167, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-301167

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1716 TTCCATTTCTGGAAGTGAATTTGGC 1740
      |||
Db 1 TTCCATTTCTGGAAGTGAATTTGGC 25

RESULT 143
US-11-121-849-111033
; Sequence 111033, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111033
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111033
```

```
Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1363 AACTGCTCTTCACGAGAGTACTCCA 1387
DB 1 AACTGCTCTTCACGAGAGTACTCCA 25

RESULT 144
US-11-121-849-111034
; Sequence 111034, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111034

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 GAAGTACTCCACAGCATGACAGA 1400
DB 1 GAAGTACTCCACAGCATGACAGA 25

RESULT 145
US-11-121-849-111035
; Sequence 111035, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111035
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111035

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1382 ACTCCAAAGCATGACAGAGCTT 1406
DB 1 ACTCCAAAGCATGACAGAGCTT 25

RESULT 146
US-11-121-849-111036
; Sequence 111036, Application US/11121849
; Publication No. US20050272080A1
```

```
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111036

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 AATGTGCTCTCTAGGCCACAGGCC 1444
DB 1 AATGTGCTCTCTAGGCCACAGGCC 25

RESULT 147
US-11-121-849-111037
; Sequence 111037, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111037

Query Match 1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 TGCCCTCTTCATGATGGAATTC 1502
DB 1 TGCCCTCTTCATGATGGAATTC 25

RESULT 148
US-11-121-849-111038
; Sequence 111038, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111038
; LENGTH: 25
```

TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-111038

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1495 GGAATTCCTTCATCTGGAACCAT 1519  
DB 1 GGAATTCCTTCATCTGGAACCAT 25

RESULT 149  
US-11-121-849-111039  
Sequence 111039, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 111039  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-111039

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 ATTCCCTTCATCTGGAACCATGAGA 1523  
DB 1 ATTCCCTTCATCTGGAACCATGAGA 25

RESULT 150  
US-11-121-849-111040  
Sequence 111040, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 111040  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-111040

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 TGGAACTTCAGAAACACCTTCACA 1535  
DB 1 TGGAACTTCAGAAACACCTTCACA 25

RESULT 151  
US-11-121-849-111041  
Sequence 111041, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 111041  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-111041

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1537 TGGGACTTCGAAAGGCTCAGTAT 1561  
DB 1 TGGGACTTCGAAAGGCTCAGTAT 25

RESULT 152  
US-11-121-849-111042  
Sequence 111042, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03  
NUMBER OF SEQ ID NOS: 673904  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 111042  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-11-121-849-111042

Query Match  
Best Local Similarity 1.4%; Score 25; DB 1; Length 25;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 TGGGTTAGGAAACATTCATCCT 1585  
DB 1 TGGGTTAGGAAACATTCATCCT 25

RESULT 153  
US-11-121-849-111043  
Sequence 111043, Application US/11121849  
Publication No. US20050272080A1  
GENERAL INFORMATION:  
APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
FILE REFERENCE: 3684.1  
CURRENT APPLICATION NUMBER: US/11/121,849  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: 60/567,949  
PRIOR FILING DATE: 2004-05-03

```
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-111043
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1570 GAAAAATTCATCTTGAGTCAAA 1594
Db      1 GAAAAATTCATCTTGAGTCAAA 25
```

```
RESULT 154
US-11-121-849-192687
; Sequence 192687, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192687
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1117 ATCATCTGCTGCTGCTCAATGACA 1141
Db      1 ATCATCTGCTGCTGCTCAATGACA 25
```

```
RESULT 155
US-11-121-849-192688
; Sequence 192688, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192688
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192688
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1118 TCATCTACTGCTGCTCAATGACAG 1142
```

```
Db      1 TCATCTACTGCTGCTCAATGACAG 25
```

```
RESULT 156
US-11-121-849-192689
; Sequence 192689, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192689
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db      1 ATCTACTGCTGCTCAATGACAGGT 25
```

```
RESULT 157
US-11-121-849-192690
; Sequence 192690, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192690
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192690
```

```
Query Match          1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1027 ATCAACCCAGATCTCTACTGTAAGA 1051
Db      1 ATCAACCCAGATCTCTACTGTAAGA 25
```

```
RESULT 158
US-11-121-849-192691
; Sequence 192691, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
```

```

; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192691
```

```

Query Match          1.4%: Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1028 TCAACCCAGATCTCTACTGGAAGAA 1052
Db      1 TCAACCCAGATCTCTACTGGAAGAA 25
```

```

RESULT 159
US-11-121-849-192692
; Sequence 192692, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192692
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192692
```

```

Query Match          1.4%: Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1033 CCAGATCTCTACTGGAAGATTTA 1057
Db      1 CCAGATCTCTACTGGAAGATTTA 25
```

```

RESULT 160
US-11-121-849-192693
; Sequence 192693, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192693
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192693
```

```

Query Match          1.4%: Score 25; DB 1; Length 25;
```

```

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1034 CAGATCTCTACTGGAAGATTAT 1058
Db      1 CAGATCTCTACTGGAAGATTAT 25
```

```

RESULT 161
US-11-121-849-192694
; Sequence 192694, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192694
```

```

Query Match          1.4%: Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1036 GATCTCTACTGGAAGATTATCC 1060
Db      1 GATCTCTACTGGAAGATTATCC 25
```

```

RESULT 162
US-11-121-849-192695
; Sequence 192695, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 192695
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-192695
```

```

Query Match          1.4%: Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1039 CTCTACTGGAAGATTATCCAGC 1063
Db      1 CTCTACTGGAAGATTATCCAGC 25
```

```

RESULT 163
US-11-121-849-192696
; Sequence 192696, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ PRIOR FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 192696
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-11-121-849-192696

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1065 GGTCTACTGCGCATCATGTGCTG 1089
Db      1 GGTCTACTGCGCATCATGTGCTG 25

RESULT 164
US-11-121-849-192697
/ Sequence 192697, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ TITLE OF INVENTION: Microarrays
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ PRIOR FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 192697
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-11-121-849-192697

Query Match      1.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1066 GTTACTCTGGCCATCATGTGCTG 1090
Db      1 GTTACTCTGGCCATCATGTGCTG 25

RESULT 165
US-10-005-956-1306/c
/ Sequence 1306, Application US/10005956
/ Publication No. US20030113726A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
/ FILE REFERENCE: D0053NP
/ CURRENT APPLICATION NUMBER: US/10/005,956
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/251,015
/ PRIOR FILING DATE: 2000-12-04
/ PRIOR APPLICATION NUMBER: 60/263,678
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/273,037
/ PRIOR FILING DATE: 2001-03-02
/ NUMBER OF SEQ ID NOS: 1579
/ SOFTWARE: PatentIn version 3.0
```

```
/ SEQ ID NO 1306
/ LENGTH: 27
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
/ NAME/KEY: misc feature
/ LOCATION: (21)..(21)
/ OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
/ US-10-005-956-1306

Query Match      1.4%; Score 25; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 2.3e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1345 TCCCTGAGCCTGACCTCCAACTGCTCT 1371
Db      27 TCCCTGAGCCTGACCTCCAACTGCTCT 1

RESULT 166
US-11-036-317-481475
/ Sequence 481475, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ PRIOR FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 481475
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-11-036-317-481475

Query Match      1.4%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      922 GAGCAAGTCTCTGCCAAGCGCAG 945
Db      2 GAGCAAGTCTCTGCCAAGCGCAG 25

RESULT 167
US-10-005-956-1304
/ Sequence 1304, Application US/10005956
/ Publication No. US20030113726A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
/ FILE REFERENCE: D0053NP
/ CURRENT APPLICATION NUMBER: US/10/005,956
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/251,015
/ PRIOR FILING DATE: 2000-12-04
/ PRIOR APPLICATION NUMBER: 60/263,678
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/273,037
/ PRIOR FILING DATE: 2001-03-02
/ NUMBER OF SEQ ID NOS: 1579
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1304
/ LENGTH: 27
/ TYPE: DNA
```



```

? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (14)..(14)
? OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker
? NAME/KEY: misc feature
? LOCATION: (17)..(17)
? OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker
? NAME/KEY: misc feature
? LOCATION: (20)..(20)
? OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker
? IS-10-005-956-1304
```

Query Match	1.4%	Score 24	DB 1	Length 27
Best Local Similarity	88.9%	Pred. No.	2.8e+02	
Matches 24	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

```
QY      1608 TCCCTATCTTGCACCCCATGCTGT 1634
          |||||
Db       1 TCCCTATCTTGCACCNCTNATGCTGT 27
```

```

RESULT 168
US-10-044-592-23/c
; Sequence 23, Application US/10044592
; Publication No. US2002014152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukushima, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; PRIORITY FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 23
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(29)
; OTHER INFORMATION: mixed synthetic primer described on pg. 98
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: A, G, C or T
; US-10-044-592-23

```

Query Match	1.4%	Score 24	DB 1	Length 29
Best Local Similarity	72.4%	Pred. No. 3	le-02	
Matches	21	Conservative	6	Mismatches 2
				Indels 0
				Gaps 0
OY	979	TTCGCATCTGCTGCTGCTTCCCAT	1007	
		:	: :	
Db	29	TTTCRYSNCTCTGCTGCTTCCCTTWCMT	1	

RESULT 169  
 US-10-278-087A-61/C  
 ; Sequence 61, Application US/10278087A  
 ; Publication No. US20030138817A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shuji Hinuma  
 ; Yasuaki Ito  
 ; Ryo Fujii  
 ; TITLE OF INVENTION: G Protein Coupled Receptor Protein  
 ; Production, And Use Thereof  
 ;

NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edwards & Angel, LLP  
STREET: 101 Federal Street  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02209

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (IPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/278,087A  
FILING DATE: 31-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIORITY INFORMATION DATA: <Unknown>

```

P R I O R  A P P L I C A T I O N  D A T A :
A P P L I C A T I O N  N U M B E R : 09/461,436
F I L I N G  D A T E : 14-DEC-1999
A P P L I C A T I O N  N U M B E R : 09/038,572
F I L I N G  D A T E : 11-MAR-1998
A P P L I C A T I O N  N U M B E R : 08/513,974
F I L I N G  D A T E : 14-SEP-1995
A P P L I C A T I O N  N U M B E R : PCT/JP95/01599
F I L I N G  D A T E : 10-AUG-1995
A P P L I C A T I O N  N U M B E R : 7-093989
F I L I N G  D A T E : 19-APR-1995
A P P L I C A T I O N  N U M B E R : 7-057186
F I L I N G  D A T E : 16-MAR-1995
A P P L I C A T I O N  N U M B E R : 7-007177
F I L I N G  D A T E : 20-JAN-1995
A P P L I C A T I O N  N U M B E R : 6-326611
F I L I N G  D A T E : 28-DEC-1994
A P P L I C A T I O N  N U M B E R : 6-270017
F I L I N G  D A T E : 02-NOV-1994
A P P L I C A T I O N  N U M B E R : 6-236357
F I L I N G  D A T E : 30-SEP-1994
A P P L I C A T I O N  N U M B E R : 6-236356
F I L I N G  D A T E : 30-SEP-1994
A P P L I C A T I O N  N U M B E R : 6-189274
F I L I N G  D A T E : 11-AUG-1994
A P P L I C A T I O N  N U M B E R : 6-189273
F I L I N G  D A T E : 11-AUG-1994
A P P L I C A T I O N  N U M B E R : 6-189272
F I L I N G  D A T E : 11-AUG-1994
A T T O R N E Y / A G E N T  I N F O R M A T I O N :
N A M E : C O N L I N , D A V I D  G .
R E G I S T R A T I O N  N U M B E R : <Unknown>
R E F E R E N C E / D O C K E T  N U M B E R : 45753  D I V 3
T E L E C O M M U N I C A T I O N  I N F O R M A T I O N :
T E L E P H O N E : 617-439-4444
T E L E F A X : 617-439-4170
I N F O R M A T I O N  F O R  S E Q  I D  N O : 61:
S E Q U E N C E  C H A R A C T E R I S T I C S :
L E N G T H : 29  b a s e  p a i r s
T Y P E : n u c l e i c  a c i d
S T R A N D E D N E S S : s i n g l e
T O P O L O G Y : l i n e a r
M O L E C U L E  T Y P E : O t h e r  n u c l e i c  a c i d
D E S C R I P T I O N : / d e s c  =  " s y n t h e t i c  D N A
F E A T U R E :
O T H E R  I N F O R M A T I O N : / n o t e =  N  i s  i n s i n e ,  S  i s  G  o r  C ,  W  i s  A  o r  T
R  i s  A  o r  G ,  K  i s  G  o r  T ,  Y  i s  C  o r  I . "
S E Q U E N C E  D E S C R I P T I O N : S E Q  I D  N O : 61:
J S - 1 0 - 2 7 8 - 0 8 7 A - 6 1

```

Query Match	1.4%	Score 24	DB 1	Length 29	
Best Local Similarity	72.4%	Pred. No. 3.1e+02			
Matches 21	Conservative 6	Indels 2	Gaps 0		
QY	979	TTGGCAGTCGCTGGCGCCCTTCACAT	1007		
	:		:		

Db 29 TTCRYSNCTGCTGCTGCCCTWCTWCMT 1

```
RESULT 170
US-11-054-211-32/c
; Sequence 32, Application US/11054211
; Publication No. US20050170461A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
;          Habata, Yugo
;          Kawamata, Yuji
;          Hosoya, Masaki
;          Fujii, Ryo
;          Fukusumi, Shoji
;          Kitada, Chieko
; TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIXE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/054,211
; FILING DATE: 08-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/716,147
; FILING DATE: 17-Nov-2000
; APPLICATION NUMBER: US/08/776,971
; FILING DATE: 06-Feb-1997
; APPLICATION NUMBER: PCT/JP96/03821
; FILING DATE: 28-Dec-1996
; APPLICATION NUMBER: JP 7/343371
; FILING DATE: 28-Dec-1995
; APPLICATION NUMBER: JP 8/59419
; FILING DATE: 15-Mar-1996
; APPLICATION NUMBER: JP 8/211805
; FILING DATE: 12-Aug-1996
; APPLICATION NUMBER: JP 8/246573
; FILING DATE: 18-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-11-054-211-32
```

```
Query Match 1.4%; Score 24; DB 1; Length 29;
Best Local Similarity 72.4%; Pred. No. 3.1e+02;
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

QY 979 TTGGCATTGCTGCTGCCCTTCCACAT 1007  
|||||  
Db 29 TTCRYSNCTGCTGCTGCCCTWCTWCMT 1

```
RESULT 171
US-10-005-956-1215
; Sequence 1215, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1215
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1215
```

```
Query Match 1.3%; Score 23.6; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 2.6e+02;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1631 CTGTGTGACTCAACCAATCACT 1654  
|||||  
Db 1 CTGKTGACTCAACCAATCACT 24

```
RESULT 172
US-10-719-900-67260
; Sequence 67260, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67260
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-67260
```

```
Query Match 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 926 AAGTCTCTGCCAAGCGAAGGTGCT 950  
|||||  
Db 1 AAGTCTCTGCCAAGCGAAGGTGCT 25

```
RESULT 173
US-10-719-900-237659
; Sequence 237659, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
```

```

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237659
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-237659

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1027 ATCAACCCAGATCTCTTACTGAGA 1051
Db      1 ATCAACCCAGATCTCTTACTGAGA 25

RESULT 174
US-10-719-900-247410
; Sequence 247410, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-247410

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db      1 ATCTACTGCTGCTCAATGACAGGT 25

RESULT 175
US-10-719-900-253859
; Sequence 253859, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 253859
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-253859

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

Cy      1136 ATGACAGTTCCTCTGCGCTTCA 1160
Db      1 ATGACAGTTCCTCTGCGCTTCA 25

RESULT 176
US-10-719-900-890393
; Sequence 890393, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 890393
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-890393

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      880 TGGGCGAGTGAGATCCCGGGGACT 904
Db      1 TGGGCGAGTGAGATCCCGGGTACT 25

RESULT 177
US-10-809-189-67914
; Sequence 67914, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67914
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-67914

Query Match      1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      1255 TACAAAGTCAGCCGCTGAGACCA 1279
Db      1 TACAAAGTCAGCCGCTGAGACCA 25

RESULT 178
US-10-809-189-67926
; Sequence 67926, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67926
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-10-809-189-67926

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1147 CGTGGGCTTCAGCATGCTTCC 1171
Db 1 CGTGTGCTTCAGCATGCTTTC 25

RESULT 179
US-11-036-317-400602
/ Sequence 400602, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 400602
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-400602

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 302 AAATGCTTTGGGAGCTGCTTA 326
Db 1 AAATGCTTTGGGAGCTGCTTA 25

RESULT 180
US-11-036-317-444773
/ Sequence 444773, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 444773
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-444773

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1062 GCAGGTCTACTGCGCCATCATGTGG 1086
Db 1 GCAGGTCTACTGCGCCAGCATGTGG 25

RESULT 181
US-11-036-317-466837
/ Sequence 466837, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 466837
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-466837

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 567 TATCTACTCATGACGGCTGTGGCC 591
Db 1 TATCTACTCATGACGCTGTGGCC 25

RESULT 182
US-11-060-756-169932
/ Sequence 169932, Application US/11060756
/ Publication No. US20050221354A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William Martin
/ TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
/ FILE REFERENCE: AM101083 (031896-042000)
/ CURRENT APPLICATION NUMBER: US/11/060,756
/ CURRENT FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 303284
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 169932
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: probe
US-11-060-756-169932

Query Match
Best Local Similarity 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.8e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1104 CATGTACACCCATCATCTACTGC 1128
Db 1 CATGTACATCCATCATCTACTGC 25
```

RESULT 183  
US-09-930-512-4/c  
; Sequence 4, Application US/09893512  
; Publication No. US20030017530A1  
; GENERAL INFORMATION:  
; APPLICANT: OMAN, CHRISTER  
; TITLE OF INVENTION: HEPHAELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4  
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/061,789  
; PRIOR FILING DATE: 1997-10-14  
; PRIOR APPLICATION NUMBER: 60/081,958  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 09/170,069  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-930-512-4

Query Match 1.3%; Score 23.4; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 3.5e+02;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATTCGCTGCTGCTTCCACAT 1007  
DB 29 TTCRYSTCTGCTGCTGCTGCTTCTCMT 1

RESULT 184  
US-10-799-736-4/c  
; Sequence 4, Application US/10799736  
; Publication No. US20050118675A1  
; GENERAL INFORMATION:  
; APPLICANT: OMAN, CHRISTER  
; TITLE OF INVENTION: HEPHAELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4  
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING  
; CURRENT FILING DATE: 2004-03-15  
; PRIOR APPLICATION NUMBER: US/10/799,736  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 60/061,789  
; PRIOR FILING DATE: 1997-10-14  
; PRIOR APPLICATION NUMBER: 60/081,958  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 09/170,069  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-799-736-4

Query Match 1.3%; Score 23.4; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 3.5e+02;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATTCGCTGCTGCTTCCACAT 1007  
DB 29 TTCRYSTCTGCTGCTGCTGCTTCTCMT 1

RESULT 185

US-10-005-956-1128/c  
; Sequence 1128, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1128  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-005-956-1128

Query Match 1.3%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1675 AATATAAGTTCGACACAGCTTTT 1697  
DB 23 AATATAAGTTCGACACAGCTTTT 1

RESULT 186  
US-10-310-914A-386270/c  
; Sequence 386270, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuazac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386270  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386270

Query Match 1.3%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1460 CCCCACCTGCTTGAACCTGCTT 1482  
DB 23 CCCCACCTGCTTGAACCTGCTT 1

RESULT 187  
US-10-310-914A-386274/c  
; Sequence 386274, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuazac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT FILING DATE: 2002-12-06

```

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386274
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386274

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      154 GACTCTGCTGACAGAGGGGGTTG 176
DB      23 GACTCTGCTGACAGAGGGGGTTG 1

RESULT 188
US-10-310-914A-386275/c
; Sequence 386275, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386275
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386275

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      154 GACTCTGCTGACAGAGGGGGTTG 176
DB      23 GACTCTGCTGACAGAGGGGGTTG 1

RESULT 189
US-10-310-914A-386284/c
; Sequence 386284, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386284
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386284

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1530 CTCACACTGGGAGCTTGCAGAAAG 1552
DB      23 CTCACACTGGGAGCTTGCAGAAAG 1
```

```

RESULT 190
US-10-310-914A-386298/c
; Sequence 386298, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386298
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386298

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      187 GTAGCTTTACGCTAGCTTCGA 209
DB      23 GTAGCTTTACGCTAGCTTCGA 1

RESULT 191
US-09-930-503-34/c
; Sequence 34, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; TITLE OF INVENTION: ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930.503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-34

Query Match      1.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1105 ATGTACAAACCCATCATCTACTG 1127
DB      24 ATGTACAAACCCATCATCTACTG 2

RESULT 192
US-11-036-317-490648
; Sequence 490648, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
```

```
FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 480648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-490648

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 970 GTGTGACCTTCCGATCTGCTGG 993
Db 2 GTGTGACCTTCCGATCTGCTGG 25

RESULT 193
US-11-060-756-34830
; Sequence 34830, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34830
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34830

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1102 ACCATGTACAACCCATCATCTAC 1125
Db 2 ACCATGTACAATCCCATCATCTAC 25

RESULT 194
US-10-005-956-1130/c
; Sequence 1130, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1130
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-10-005-956-1130

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1373 CACGAGTGAAGTCCAGACCAT 1394
Db 22 CACGAGTGAAGTCCAGACCAT 1

RESULT 195
US-10-005-956-1301/c
; Sequence 1301, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1301
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1301

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 673 TGAGTCTGAGCTCTCTGCTGG 694
Db 22 TGAGTCTGAGCTCTCTGCTGG 1

RESULT 196
US-10-310-914A-386285/c
; Sequence 386285, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Yvazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386285
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386285

Query Match
Best Local Similarity 1.2%; Score 22; DB 1; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1535 ACTGGGACTTGCAAAAAGGCTC 1556
Db 22 ACTGGGACTTGCAAAAAGGCTC 1
```

```
RESULT 197
US-10-310-914A-386297/c
; Sequence 386297, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386297
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386297

Query Match          1.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 GCGCCAGCGCCGACCCACAGCA 155
Db      22 GCGCCAGCGCCGACCCACAGCA 1

RESULT 198
US-10-310-914A-386305/c
; Sequence 386305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386305
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386305

Query Match          1.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1552 GGGTCAGTATGGGTAGGGAAA 1573
Db      22 GGGTCAGTATGGGTAGGGAAA 1

RESULT 199
US-10-809-67908
; Sequence 67908, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
```

```
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67908

Query Match          1.2%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1051 AAGTTATCCAGCAGGCTTACC 1072
Db      4 AAGTTATCCAGCAGGCTTACC 25

RESULT 200
US-10-719-900-146775
; Sequence 146775, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 146775
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-146775

Query Match          1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1388 AGACCATGACGAGAGCTTCAGCTT 1412
Db      1 AGACCATGACGAGAGCTTCAGCTT 25

RESULT 201
US-10-719-900-237660
; Sequence 237660, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237660
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-237660

Query Match          1.2%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1027 ATCAACCAAGATCTCTACTGAAGA 1051
```



Db 1 ATCAACCCAGATGCTCTACCTTAGA 25

## RESULT 202

US-10-719-900-455081  
; Sequence 455081, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 455081  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-455081

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 910 GACCGCTACCAAGCAAGTCTCTG 934  
Db 1 GACCGTTACCATGAGCAAGTCTCTG 25

## RESULT 203

US-10-719-900-890394  
; Sequence 890394, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; PRIOR FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 890394  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-890394

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 880 TGGGCCAGTGAATCCCGGGGACT 904  
Db 1 TGGGCCAGTGAATCCCGGGGACT 25

## RESULT 204

US-10-809-189-67912  
; Sequence 67912, Application US/10809189  
; Publication No. US20050048531A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/10/809,189  
; CURRENT FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US/09/396,196  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67912  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-809-189-67912

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 907 TCTGACCGCTACCAAGCAAGTCT 931  
Db 1 TCTGACCGTTACCATGAGCAAGTCT 25

## RESULT 205

US-10-809-189-67913  
; Sequence 67913, Application US/10809189  
; Publication No. US20050048531A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/10/809,189  
; CURRENT FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US/09/396,196  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67913  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-809-189-67913

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 913 CGCTACCAAGCAAGTCTCTGCCA 937  
Db 1 CGTTACCATGAGCAAGTCTCTGCCA 25

## RESULT 206

US-11-060-756-34801  
; Sequence 34801, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34801  
; LENGTH: 25

TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34801

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1110 CAACCCATCATCTACTGCTGCTCA 1134  
DB 1 CAATCCATCATCTACTGCTGCTCA 25

## RESULT 207

US-11-060-756-34809  
Sequence 34809, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34809  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34809

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 ACCCATCATCTACTGCTGCTCA 1136  
DB 1 ATCCATCATCTACTGCTGCTCA 25

RESULT 208  
US-11-060-756-34810  
Sequence 34810, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34810  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34810

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1111 AACCCATCATCTACTGCTGCTCA 1135  
DB 1 AATCCATCATCTACTGCTGCTCA 25

RESULT 209  
US-11-060-756-34831

Sequence 34831, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34831  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34831

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1098 CTCACCATGTACACCCCATCATC 1122  
DB 1 CTCACCATGTACATCCATCATC 25

RESULT 210  
US-11-060-756-36931  
Sequence 36931, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 36931  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-36931

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1105 ATGTACAACCCATCATCTACTGCT 1129  
DB 1 ATGTACAATCCATCATCTACTGCT 25

RESULT 211  
US-11-060-756-36932  
Sequence 36932, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 36932  
LENGTH: 25  
TYPE: DNA

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORGANISM: probe  
US-11-060-756-36932

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1104 CATCTACATCCCATCTCATCTACGTC 1128  
DB 1 CATCTACATCCCATCTCATCTACGTC 25

RESULT 212  
US-11-060-756-232071  
Sequence 232071, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 232071  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-232071

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 GCTGGCCATGAGCTCCACCATGTAC 1110  
DB 1 GCTGGCCATGAGCTCCACCATGTAC 25

RESULT 213  
US-11-060-756-260556  
Sequence 260556, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 260556  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-260556

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1085 GGCTGGCCATGAGCTCCACCATGTA 1109  
DB 1 GGCTGGCCATGAGCTCCACCATGTA 25

RESULT 214  
US-11-060-756-270235  
Sequence 270235, Application US/11060756

Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 270235  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-270235

Query Match 1.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 3.9e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1094 TGAGCTTCACCATGTACACCCCAT 1118  
DB 1 TGAGCTTCACCATGTACACCCCAT 25

RESULT 215  
US-08-796-570A-8/c  
Sequence 8, Application US/08796570A  
Publication No. US20020009771A1  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: G Protein Coupled Receptor Proteins,  
TITLE OF INVENTION: Their Production And Use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/796,570A  
FILING DATE: 06-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: Japan 8-021562  
FILING DATE: 2-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I.  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47147  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid Synthetic  
MOLECULE TYPE: DNA  
US-08-796-570A-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;

Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0

```

Qy      979  TTGGCATTCTGCTGAGCTGCCCTTCAC 1005
          |||:||||||| |||::|||
Db      27   TTGGCMTCTGCTGSGNTGCCYYWCNAC 1

```

RESULT 216  
IIS-09-929-

```

1 Sequence 6, Application US/09929752
2 Publication No. US20030113909NA1
3 GENERAL INFORMATION:
4 APPLICANT: Hinuma, Shuji
5          Fujii, Ryo
6          Kawamura, Yui
7 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
8 PRODUCTION AND USE THEREOF
9 NUMBER OF SEQUENCES: 11
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
12 STREET: 130 Water Street
13 CITY: Boston
14 STATE: MA
15 COUNTRY: USA
16 ZIP: 02109
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patentn. Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/929,752
24 FILING DATE: 14-Aug-2001
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/555,905
27 FILING DATE: <unknown>
28 APPLICATION NUMBER: JP 7-215798
29 FILING DATE: 24-AUG-1995
30 APPLICATION NUMBER: JP 6-326611
31 FILING DATE: 28-DEC-1994
32 APPLICATION NUMBER: JP 7-007177
33 FILING DATE: 20-JAN-1995
34 APPLICATION NUMBER: JP 7-051186
35 FILING DATE: 16-MAR-1995
36 APPLICATION NUMBER: JP 7-224544
37 FILING DATE: 10-AUG-1995
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Conlin, David G.
40 REGISTRATION NUMBER: 27,026
41 REFERENCE/DOCKET NUMBER: 1550/45836
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: 617-523-3400
44 TELEFAX: 617-523-6440
45 INFORMATION FOR SEQ ID NO: 6:
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 27 base pairs
48 TYPE: nucleic acid
49 STRANDEDNESS: single
50 TOPOLOGY: linear
51 MOLECULE TYPE: other nucleic acid
52 DESCRIPTION: /desc = "synthetic DNA"
53 FEATURE:
54 NAME/KEY: misc_feature
55 LOCATION: 3
56 OTHER INFORMATION: /product= "may be A, T, C or G"
57 NAME/KEY: misc_feature
58 LOCATION: 12
59 OTHER INFORMATION: /product= "may be A, T, C or G"
60 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
61 US-09-929-752-6

```

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	979	TTGGCATCTGCTGAGTGGCCCTTCAC	1005
		:         ::	
Db	27	TTTGCCMCTCTGCTGGNTGCCYYWCNAC	1

## RESULT 217

```

US-10-044-592-21/c
Sequence 21, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 21
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(27)
OTHER INFORMATION: mixed synthetic primer described on pg. 95
NAME/KEY: misc feature
LOCATION: (3)..(3)
OTHER INFORMATION: A, G, C or T
NAME/KEY: misc feature
LOCATION: (12)..(12)
OTHER INFORMATION: A, G, C or T
US-10-044-592-21

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 4.3e+02;
Matches 20; Conservative 4; Mismatches 3; Indels

QY 979 TTGGCCATCTGCTGCTGCCCTCCAC 1005
DB 27 TTGGCMTCTGCTGANTGCTTCWNCAC 1

RESULT 218
US-10-067-477-8/c
Sequence 8, Application US/10067477
Publication No. US20020168720A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: G Protein Coupled Receptor Proteins,
TITLE OF INVENTION: Their Production And Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dile, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/067,477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/796,570  
FILING DATE: 06-FEB-1997  
APPLICATION NUMBER: Japan 8-021562  
FILING DATE: 2-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenestein, Ronald I.  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47147  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid Synthetic  
MOLECULE TYPE: DNA  
US-10-067-477-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTCAC 1005  
Db 27 TTGGCCMTCTGCTGNTGCCCYWCNAC 1

RESULT 219  
US-10-090-569-8/c  
Sequence 8, Application US/10090569  
Publication No. US20030008329A1  
GENERAL INFORMATION:  
APPLICANT: HINUMA, Shuji  
FUJII, Ryo  
FUKUSUMI, Shoji  
OHTAKI, Tetsuya  
HOSOYA, Masaki  
OHGI, Kazuhiro  
ONDA, Haruo  
TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PRODUCTION AND USE THEREOF  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/090,569  
FILING DATE: 04-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,650  
FILING DATE: 11-OCT-1995  
APPLICATION NUMBER: 7-134412  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 6-326610

FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-247599  
FILING DATE: 13-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid Synthetic DNA  
OTHER INFORMATION: N is A, G, C, or T  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-090-569-8

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCCCTTCAC 1005  
Db 27 TTGGCCMTCTGCTGNTGCCCYWCNAC 1

RESULT 220  
US-10-184-722-6/c  
Sequence 6, Application US/10184722  
Publication No. US20030092618A1  
GENERAL INFORMATION:  
APPLICANT: HINUMA, SHUJI  
APPLICANT: TATEMOTO, KAZUHIKO  
APPLICANT: HOSOYA, MASAKI  
APPLICANT: HABATA, YUGO  
APPLICANT: FUJII, RYO  
APPLICANT: KITADA, CHIKO  
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE  
FILE REFERENCE: 48970(342)  
CURRENT APPLICATION NUMBER: US/10/184,722  
CURRENT FILING DATE: 2002-06-27  
PRIOR APPLICATION NUMBER: US/09/255,518  
PRIOR FILING DATE: 1999-02-22  
PRIOR APPLICATION NUMBER: PCT/JP98/05805  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 9-353955  
PRIOR FILING DATE: 1997-12-24  
PRIOR APPLICATION NUMBER: 10-032577  
PRIOR FILING DATE: 1998-02-16  
PRIOR APPLICATION NUMBER: 10-220853  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 10-271645  
PRIOR FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
NAME/KEY: modified base  
LOCATION: (1)..(27)  
OTHER INFORMATION: "n" may be a, t, c, g  
US-10-184-722-6

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;



INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
FEATURE:  
OTHER INFORMATION: /note = "N is A, G, C, or T; w is A or T;  
R is A or G; K is G or T."  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-278-087A-2

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGGTGGCTTCCAC 1005  
DB 27 TTGGCATTGCTGGTGGCTTCCAC 1

RESULT 223  
US-11-054-211-30/C  
Sequence 30, Application US/11054211  
Publication No. US20050170461A1  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
Habata, Yugo  
Kawamata, Yuji  
Hosoya, Masaki  
Fuji, Ryo  
Kikusumi, Shoji  
Kikada, Chieko  
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIRE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PatsEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/054, 211  
FILING DATE: 08-Feb-2005  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/716,147  
FILING DATE: 17-Nov-2000  
APPLICATION NUMBER: US/08/776,971  
FILING DATE: 06-Feb-1997  
APPLICATION NUMBER: PCT/JP96/03821  
FILING DATE: 28-DEC-1996  
APPLICATION NUMBER: JP 7/343371  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: JP 8/59419  
FILING DATE: 15-MAR-1996  
APPLICATION NUMBER: JP 8/211805  
FILING DATE: 12-AUG-1996  
APPLICATION NUMBER: JP 8/246573  
FILING DATE: 18-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Conlin, David G.  
REGISTRATION NUMBER: 27,026  
REFERENCE/DOCKET NUMBER: 47176  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-11-054-211-30

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 4.3e+02;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCATTGCTGGTGGCTTCCAC 1005  
DB 27 TTGGCATTGCTGGTGGCTTCCAC 1

RESULT 224  
US-11-060-756-34818  
Sequence 34818, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
Mounie, William Martin  
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303264  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34818  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34818

Query Match 1.2%; Score 21.4; DB 1; Length 25;  
Best Local Similarity 95.7%; Pred. No. 4.2e+02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1114 CCCATCATCTACTGCTGCTCA 1136  
DB 2 CCCATCATCTACTGCTGCTCA 24

RESULT 225  
US-09-930-503-23  
Sequence 23, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-23

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGGTGCA 976  
|||||  
DB 1 TGATGATTGTCGTGGTGCA 21

RESULT 226

US-09-930-503-24  
Sequence 24, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-24

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCACTCTCTGCCAGCGCA 944  
|||||  
DB 1 GCACTCTCTGCCAGCGCA 21

RESULT 227

US-09-930-503-26/c  
Sequence 26, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-26

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGGTGCA 976  
|||||  
DB 21 TGATGATTGTCGTGGTGCA 1

RESULT 228

US-09-930-503-28/c  
Sequence 28, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-28

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TGCTGTGATTGGCTATGCAT 856  
|||||  
DB 21 TGCTGTGATTGGCTATGCAT 1

RESULT 229  
US-09-930-503-31/c  
Sequence 31, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-31

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TTGGCAGATCTACTCATG 579  
|||||  
DB 21 TTGGCAGATCTACTCATG 1



```
RESULT 230
US-09-930-503-33/c
; Sequence 33, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-33

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1567 AGGAAACATTCATCCTTG 1587
Db      21  AGGAAACATTCATCCTTG 1

RESULT 231
US-09-930-503-38/c
; Sequence 38, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-38

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1567 AGGAAACATTCATCCTTG 1587
Db      21  AGGAAACATTCATCCTTG 1

RESULT 232
US-09-930-503-40
; Sequence 40, Application US/09930503
```

```
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-40

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      205  TTGGAATGATTAACGTCCTC 225
Db      1    TTGGAATGATTAACGTCCTC 21

RESULT 233
US-09-930-503-42/c
; Sequence 42, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-42

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      956  TGATGATTCGCGGTGTGCA 976
Db      21  TGATGATTCGCGGTGTGCA 1

RESULT 234
US-09-930-503-43/c
; Sequence 43, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
```

```
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 43
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-43

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          924 GCAAGTCTCTGCCAAGCGCAA 944
Db          21 GCAAGTCTCTGCCAAGCGCAA 1

RESULT 235
US-09-930-503-45
/ Sequence 45, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 45
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-45

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          956 TGATGATTTGCTCGGTGTGCA 976
Db          1 TGATGATTTGCTCGGTGTGCA 21

RESULT 236
US-09-930-503-47
/ Sequence 47, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
```

```
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 47
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-47

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          836 TGCTGTGATTTGCTATGTCAT 856
Db          1 TGCTGTGATTTGCTATGTCAT 21

RESULT 237
US-09-930-503-50
/ Sequence 50, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-50

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          559 TTCCGACGATATCTACTCCATG 579
Db          1 TTCCGACGATATCTACTCCATG 21

RESULT 238
US-09-930-503-52
/ Sequence 52, Application US/09930503
/ Publication No. US20030060438A1
/ GENERAL INFORMATION:
/ APPLICANT: HENRY, JAMES
/ APPLICANT: CAHILL, CATHERINE
/ APPLICANT: YASHPAL, KIRAN
/ TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
/ FILE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: 39245-173913
/ CURRENT APPLICATION NUMBER: US/09/930,503
/ CURRENT FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/226,086
/ PRIOR FILING DATE: 2000-08-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 52
```

LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-52

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1051 AGTTATCCAGCGGTCTAC 1071  
DB 1 AAGTTATCCAGCGGTCTAC 21

RESULT 239  
US-09-930-503-53  
Sequence 53, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 53  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-53

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1105 ATGTACAACCCATCATCTAC 1125  
DB 1 ATGTACAACCCATCATCTAC 21

RESULT 240  
US-09-930-503-57  
Sequence 57, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 57  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-930-503-57

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1567 AGGAAACATTCATCTCTG 1587  
DB 1 AGGAAACATTCATCTCTG 21

RESULT 241  
US-09-930-503-59/c  
Sequence 59, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-59

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 TTGGAATGATACGTCCTC 225  
DB 21 TTGGAATGATACGTCCTC 1

RESULT 242  
US-10-005-956-347/c  
Sequence 347, Application US/10005956  
Publication No. US20030113726A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: D0053NP  
CURRENT APPLICATION NUMBER: US/10/005,956  
CURRENT FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: 60/251,015  
PRIOR FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: 60/263,678  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/273,037  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 1579  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 347  
LENGTH: 21  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-005-956-347

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1545 GCAAAAAGGTCAGTATGGT 1565
Db      21  GCAAAAAGGTCAGTATGGT 1

RESULT 243
US-10-005-956-404
; Sequence 404, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 404
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-404

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      252 CATCTCCACTAACCCTCGGA 272
Db      1  CATCTCCACTAACCCTCGGA 21

RESULT 244
US-10-005-956-407
; Sequence 407, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 407
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-407

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1360 TCCAACTGCTCTTCACGAACT 1380
Db      1  TCCAACTGCTCTTCACGAACT 21

RESULT 245
US-10-005-956-408

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 408, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 408
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-408

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1360 TCCAACTGCTCTTCACGAACT 1380
Db      1  TCCAACTGCTCTTCACGAACT 21

RESULT 246
US-10-005-956-409
; Sequence 409, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 409
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-409

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1360 TCCAACTGCTCTTCACGAACT 1380
Db      1  TCCAACTGCTCTTCACGAACT 21

RESULT 247
US-10-005-956-467/c
; Sequence 467, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
```

```

; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 467
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-467

```

```

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      372 GTGATCATCTTACCCACA 392
Db      21 GTGATCATCTTACCCACA 1

```

```

RESULT 248
US-10-005-956-473/C
; Sequence 473, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 473
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-473

```

```

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1499 ATTCCTTCATCTGGAACAT 1519
Db      21 ATTCCTTCATCTGGAACAT 1

```

```

RESULT 249
US-10-005-956-533
; Sequence 533, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02

```

```

; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 533
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-533

```

```

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1399 GAGAGCTTCAGCTTCCTCC 1419
Db      1 GAGAGCTTCAGCTTCCTCC 21

```

```

RESULT 250
US-10-005-956-534
; Sequence 534, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 534
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-534

```

```

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1399 GAGAGCTTCAGCTTCCTCC 1419
Db      1 GAGAGCTTCAGCTTCCTCC 21

```

```

RESULT 251
US-10-005-956-535
; Sequence 535, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 535
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-535

```

Query Match 1.2%: Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 GAGAGCTTCAGCTTCCTCC 1419  
 |||||  
 DB 1 GAGAGCTTCAGCTTCCTCC 21

RESULT 252  
 US-10-005-956-1212  
 ; Sequence 1212, Application US/10005956  
 ; Publication No. US20030113726A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
 ; FILE REFERENCE: D0053NP  
 ; CURRENT APPLICATION NUMBER: US/10/005,956  
 ; PRIOR FILING DATE: 2001-12-03  
 ; PRIOR APPLICATION NUMBER: 60/251,015  
 ; PRIOR FILING DATE: 2000-12-04  
 ; PRIOR APPLICATION NUMBER: 60/263,678  
 ; PRIOR FILING DATE: 2001-01-23  
 ; PRIOR APPLICATION NUMBER: 60/273,037  
 ; PRIOR FILING DATE: 2001-03-02  
 ; NUMBER OF SEQ ID NOS: 1579  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1212  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-005-956-1212

Query Match 1.2%: Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 CACAACGATGGTACTACGGC 513  
 |||||  
 DB 1 CACAACGATGGTACTACGGC 21

RESULT 253  
 US-10-005-956-1217  
 ; Sequence 1217, Application US/10005956  
 ; Publication No. US20030113726A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
 ; FILE REFERENCE: D0053NP  
 ; CURRENT APPLICATION NUMBER: US/10/005,956  
 ; PRIOR FILING DATE: 2001-12-03  
 ; PRIOR APPLICATION NUMBER: 60/251,015  
 ; PRIOR FILING DATE: 2000-12-04  
 ; PRIOR APPLICATION NUMBER: 60/263,678  
 ; PRIOR FILING DATE: 2001-01-23  
 ; PRIOR APPLICATION NUMBER: 60/273,037  
 ; PRIOR FILING DATE: 2001-03-02  
 ; NUMBER OF SEQ ID NOS: 1579  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1217  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-005-956-1217

Query Match 1.2%: Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1492 CATGGAATTCCTCATCTG 1512  
 |||||

DB 1 CATGGAATTCCTCATCTG 21

RESULT 254  
 US-10-310-914A-386280/c  
 ; Sequence 386280, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiller, Kuvatz  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087,0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 386280  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-386280

Query Match 1.2%: Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GCCCCAGGGCGCCAGCCACAGG 154  
 |||||  
 DB 21 GCCCCAGGGCGCCAGCCACAGG 1

RESULT 255  
 US-10-310-914A-386281/c  
 ; Sequence 386281, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiller, Kuvatz  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087,0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 386281  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-386281

Query Match 1.2%: Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1730 GTGACTTGGCTGCATGCGAG 1750  
 |||||  
 DB 21 GTGACTTGGCTGCATGCGAG 1

RESULT 256  
 US-10-310-914A-386282/c  
 ; Sequence 386282, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiller, Kuvatz  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087,0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO: 386282  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-386282

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1439 CAGGCGCTTGGCAGTGCAG 1459  
Db 21 CAGGCGCTTGGCAGTGCAG 1

RESULT 257  
US-10-310-914A-386299/C  
Sequence 386299, Application US/10310914A  
Publication No. US2006003222A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kruzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087,0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO: 386299  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-386299

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1682 GGTGCGACGAGCTTTCTCTCA 1702  
Db 21 GGTGCGACGAGCTTTCTCTCA 1

RESULT 258  
US-11-127-877-430  
Sequence 430, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: Patentin version 3.3  
SEQ ID NO: 430  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-430

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 290 AACCGCCTGGCAATTGTCC 310  
Db 1 AACCGCCTGGCAATTGTCC 21

RESULT 259  
US-11-127-877-431  
Sequence 431, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: Patentin version 3.3  
SEQ ID NO: 431  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-431

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 303 AATTGTCCTTGGGACGCTGC 323  
Db 1 AATTGTCCTTGGGACGCTGC 21

RESULT 260  
US-11-127-877-432  
Sequence 432, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: Patentin version 3.3  
SEQ ID NO: 432  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-432

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGTAGTGTGATC 378  
|||||  
Db 1 AACGTGTAGTGTGATC 21

RESULT 261  
US-11-127-877-433  
; Sequence 433, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 433  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-433

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGTAACCTTACC 483  
|||||  
Db 1 AATACAGTGTGTAACCTTACC 21

RESULT 262  
US-11-127-877-434  
; Sequence 434, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 434  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-434

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTACCTATGCTGTCAC 495  
|||||  
Db 1 AACTTACCTATGCTGTCAC 21

RESULT 263  
US-11-127-877-435  
; Sequence 435, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 435  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-435

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGTAACGACC 514  
|||||  
Db 1 ACAACGAATGTAACGACC 21

RESULT 264  
US-11-127-877-436  
; Sequence 436, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 436  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-436

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 AAGTCCACAACTTCTTCCC 546  
|||||  
Db 1 AAGTCCACAACTTCTTCCC 21

RESULT 265



```
US-11-127-877-437
; Sequence 437, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Pascal G.
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Spitstaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 437
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-437

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      643 ACAGCCACCAAGTGTGTCATC 663
Db      1 ACAGCCACCAAGTGTGTCATC 21

RESULT 266
US-11-127-877-438
; Sequence 438, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitstaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 438
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-438

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      649 ACCAAGTGTGTCATCTGTGTC 669
Db      1 ACCAAGTGTGTCATCTGTGTC 21

RESULT 267
US-11-127-877-439
; Sequence 439, Application US/11127877
; Publication No. US2005028756SA1
```

```
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitstaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-439

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGTGTCATCTGTGTCATC 672
Db      1 AAAGTGTGTCATCTGTGTCATC 21

RESULT 268
US-11-127-877-440
; Sequence 440, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitstaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 440
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-440

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      713 ACTCAACCAACGAGACCATGC 733
Db      1 ACTCAACCAACGAGACCATGC 21

RESULT 269
US-11-127-877-441
; Sequence 441, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
```

```

; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-441

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCGATCTGTGTGACCTGTC 817
Db 1 ACCGATCTGTGTGACCTGTC 21

RESULT 270
US-11-127-877-442
; Sequence 442, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 442
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-442

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 ACTGTGCTGATCTACTTCTCTC 831
Db 1 ACTGTGCTGATCTACTTCTCTC 21

RESULT 271
US-11-127-877-443
; Sequence 443, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
```

```

; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: US/11/127,877
; CURRENT APPLICATION NUMBER: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 443
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-443

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 ACACCGTAGTGGGATCAGAC 877
Db 1 ACACCGTAGTGGGATCAGAC 21

RESULT 272
US-11-127-877-444
; Sequence 444, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 444
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-444

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 ACACATATGGCGCAGTGAGATC 894
Db 1 ACACATATGGCGCAGTGAGATC 21

RESULT 273
US-11-127-877-445
; Sequence 445, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```

; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 445  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-445

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 876 ACTATGGGCGCCAGTGGATCCC 896  
Db 1 ACTATGGGCGCCAGTGGATCCC 21

RESULT 274  
US-11-127-877-446  
; Sequence 446, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 446  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-446

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 920 ACGAGCAAGTCTGCGCAGC 940  
Db 1 ACGAGCAAGTCTGCGCAGC 21

RESULT 275  
US-11-127-877-447  
; Sequence 447, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 447  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-447

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1025 ACATCAACCCAGATCTCTACC 1045  
Db 1 ACATCAACCCAGATCTCTACC 21

RESULT 276  
US-11-127-877-448  
; Sequence 448, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 448  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-448

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1043 ACCTGAAGAGTTATTCACG 1063  
Db 1 ACCTGAAGAGTTATTCACG 21

RESULT 277  
US-11-127-877-449  
; Sequence 449, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 449
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-449

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAAGTTATCCAGCAGGTC 1068
Db 1 AAGAAGTTATCCAGCAGGTC 21

RESULT 278
US-11-127-877-450
; Sequence 450, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 450
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-450

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCCTAC 1071
Db 1 AAGTTATCCAGCAGGTCCTAC 21

RESULT 279
US-11-127-877-451
; Sequence 451, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 451
; LENGTH: 21
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-451

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 AATGACAGGTTCCGCTCGGCGC 1155
Db 1 AATGACAGGTTCCGCTCGGCGC 21

RESULT 280
US-11-127-877-452
; Sequence 452, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 452
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-452

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 AATGAATCCACCCGGTATC 1234
Db 1 AATGAATCCACCCGGTATC 21

RESULT 281
US-11-127-877-453
; Sequence 453, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-453
```

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1363 AACTGCTCTTCACGAGATGAC 1363  
DB 1 AACTGCTCTTCACGAGATGAC 21

RESULT 282  
US-11-127-877-454  
; Sequence 454, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 454  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-454

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 AAGTACTCCAGACATGAC 1397  
DB 1 AAGTACTCCAGACATGAC 21

RESULT 283  
US-11-127-877-455  
; Sequence 455, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 455  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-455

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1387 AAGACATGACAGAGCTTC 1407  
DB 1 AAGACATGACAGAGCTTC 21

RESULT 284  
US-11-127-877-456  
; Sequence 456, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 456  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-456

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 ACCATGACAGAGCTTCAGC 1410  
DB 1 ACCATGACAGAGCTTCAGC 21

RESULT 285  
US-11-127-877-457  
; Sequence 457, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 457  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-457

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1396 ACAGAGCTTCAGCTTC 1416

Db 1 ACAGAGGCTTCACTTCTCC 21

RESULT 286  
US-11-127-877-458  
; Sequence 458, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 458  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-458

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 AATTCCTTCATCTGAACC 1517  
Db 1 AATTCCTTCATCTGAACC 21

RESULT 287  
US-11-127-877-459  
; Sequence 459, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 459  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-459

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 AACCATCAGAAACCTCTCAG 1534  
Db 1 AACCATCAGAAACCTCTCAG 21

RESULT 288  
US-11-127-877-460  
; Sequence 460, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 460  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-460

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AATCAGTGAAGTTGCTGAGC 1668  
Db 1 AATCAGTGAAGTTGCTGAGC 21

RESULT 289  
US-11-127-877-461  
; Sequence 461, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 461  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-461

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 ACTTGCTGATGAGTGAGTGC 1753  
Db 1 ACTTGCTGATGAGTGAGTGC 21

RESULT 290  
US-11-127-877-462

```
; Sequence 462, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 462
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-462
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 290 ACCACGCTGGCAATTGTCC 310
Db 1 AACCAAGCTGGCAATTGTCC 21
```

```
RESULT 291
US-11-127-877-463
; Sequence 463, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 463
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-463
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 303 AATTGTCTTTGGGACACTGC 323
Db 1 AATTGTCTTTGGGACACTGC 21
```

```
RESULT 292
US-11-127-877-464
; Sequence 464, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-464
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 358 AACGTGTAGTAGTGTGATC 378
Db 1 AACGTGTAGTAGTGTGATC 21
```

```
RESULT 293
US-11-127-877-465
; Sequence 465, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-465
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 463 AATACAGTGTGAACCTTACC 483
Db 1 AATACAGTGTGAACCTTACC 21
```

```
RESULT 294
US-11-127-877-466
; Sequence 466, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
```

```
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-466
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 475 AACTTCACTATGCTGTCAC 495
Db 1 AACTTCACTATGCTGTCAC 21
```

```
RESULT 295
US-11-127-877-467
; Sequence 467, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-467
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 494 ACAACGAATGGTACTACGACC 514
Db 1 ACAACGAATGGTACTACGACC 21
```

```
RESULT 296
US-11-127-877-468
; Sequence 468, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```

```
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 468
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-468
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 643 ACAGCCACCAAGTGTGTCATC 663
Db 1 ACAGCCACCAAGTGTGTCATC 21
```

```
RESULT 297
US-11-127-877-469
; Sequence 469, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 469
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-469
```

```
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 649 ACCAAAGTGTGTCATGTGTC 669
Db 1 ACCAAAGTGTGTCATGTGTC 21
```

```
RESULT 298
US-11-127-877-470
; Sequence 470, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```



;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-05-12  
;; PRIOR APPLICATION NUMBER: 60/603,948  
;; PRIOR FILING DATE: 2004-08-24  
;; NUMBER OF SEQ ID NOS: 590  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 470  
;; LENGTH: 21  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-127-877-470

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 AAGTGTGATCTGTGTCATC 672  
DB 1 AAGTGTGATCTGTGTCATC 21

RESULT 299  
US-11-127-877-471  
;; Sequence 471, Application US/11127877  
;; Publication No. US20050287565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Merchiers, Pascal G.  
;; APPLICANT: Hoffmann, Marcel  
;; APPLICANT: Spittaels, Koenraad F. F.  
;; APPLICANT: Laenen, Wendy  
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
;; TITLE OF INVENTION: Amyloid-Beta Protein Production  
;; FILE REFERENCE: P27,800-B USA  
;; CURRENT APPLICATION NUMBER: US/11/127,877  
;; PRIOR FILING DATE: 2005-05-12  
;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-05-12  
;; PRIOR APPLICATION NUMBER: 60/603,948  
;; PRIOR FILING DATE: 2004-08-24  
;; NUMBER OF SEQ ID NOS: 590  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 471  
;; LENGTH: 21  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-127-877-471

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 ACTCACCACAGAGACCATGC 733  
DB 1 ACTCACCACAGAGACCATGC 21

RESULT 300  
US-11-127-877-472  
;; Sequence 472, Application US/11127877  
;; Publication No. US20050287565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Merchiers, Pascal G.  
;; APPLICANT: Hoffmann, Marcel  
;; APPLICANT: Spittaels, Koenraad F. F.  
;; APPLICANT: Laenen, Wendy  
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
;; TITLE OF INVENTION: Amyloid-Beta Protein Production  
;; FILE REFERENCE: P27,800-B USA  
;; CURRENT APPLICATION NUMBER: US/11/127,877  
;; PRIOR FILING DATE: 2005-05-12  
;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-05-12  
;; PRIOR APPLICATION NUMBER: 60/603,948

;; PRIOR FILING DATE: 2004-08-24  
;; NUMBER OF SEQ ID NOS: 590  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 472  
;; LENGTH: 21  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-127-877-472

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 ACCACATCTGTGTACTCTGC 817  
DB 1 ACCACATCTGTGTACTCTGC 21

RESULT 301  
US-11-127-877-473  
;; Sequence 473, Application US/11127877  
;; Publication No. US20050287565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Merchiers, Pascal G.  
;; APPLICANT: Hoffmann, Marcel  
;; APPLICANT: Spittaels, Koenraad F. F.  
;; APPLICANT: Laenen, Wendy  
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
;; TITLE OF INVENTION: Amyloid-Beta Protein Production  
;; FILE REFERENCE: P27,800-B USA  
;; CURRENT APPLICATION NUMBER: US/11/127,877  
;; PRIOR FILING DATE: 2005-05-12  
;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-05-12  
;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-08-24  
;; NUMBER OF SEQ ID NOS: 590  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 473  
;; LENGTH: 21  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-127-877-473

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTCTGC 831  
DB 1 ACTGTGCTGATCTACTCTGC 21

RESULT 302  
US-11-127-877-475  
;; Sequence 475, Application US/11127877  
;; Publication No. US20050287565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Merchiers, Pascal G.  
;; APPLICANT: Hoffmann, Marcel  
;; APPLICANT: Spittaels, Koenraad F. F.  
;; APPLICANT: Laenen, Wendy  
;; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
;; TITLE OF INVENTION: Amyloid-Beta Protein Production  
;; FILE REFERENCE: P27,800-B USA  
;; CURRENT APPLICATION NUMBER: US/11/127,877  
;; PRIOR FILING DATE: 2005-05-12  
;; PRIOR APPLICATION NUMBER: 60/570,352  
;; PRIOR FILING DATE: 2004-05-12  
;; PRIOR APPLICATION NUMBER: 60/603,948  
;; PRIOR FILING DATE: 2004-08-24  
;; NUMBER OF SEQ ID NOS: 590  
;; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 475
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-475

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      874 ACATATGGCCAGTGAGATCC 894
      |||
DB      1 ACATATGGCCAGTGAGATCC 21

RESULT 303
US-11-127-877-476
; Sequence 476, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 476
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-476

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      876 ACTATGGCCAGTGAGATCCC 896
      |||
DB      1 ACTATGGCCAGTGAGATCCC 21

RESULT 304
US-11-127-877-477
; Sequence 477, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 477
; LENGTH: 21
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-11-127-877-477

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      920 ACAGCAAGCTCTGTGCCAAGC 940
      |||
DB      1 ACAGCAAGCTCTGTGCCAAGC 21

RESULT 305
US-11-127-877-478
; Sequence 478, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 478
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-478

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1025 ACATCAACCCAGATCTCTACC 1045
      |||
DB      1 ACATCAACCCAGATCTCTACC 21

RESULT 306
US-11-127-877-479
; Sequence 479, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 479
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-479
```

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAAGAGTTATCCAGC 1063  
DB 1 ACCTGAAGAGTTATCCAGC 21

RESULT 307  
US-11-127-877-480  
; Sequence 480, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 480  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-480

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAGTTATCCAGCAGTC 1068  
DB 1 AAGAGTTATCCAGCAGTC 21

RESULT 308  
US-11-127-877-481  
; Sequence 481, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 481  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-481

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGCTTAC 1071  
DB 1 AAGTTATCCAGCAGCTTAC 21

RESULT 309  
US-11-127-877-484  
; Sequence 484, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 484  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-484

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AACGAGCTGGCAATTGTC 310  
DB 1 AACGAGCTGGCAATTGTC 21

RESULT 310  
US-11-127-877-485  
; Sequence 485, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 485  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-485

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AATTGTCCTTGGCAGCTGC 323  
|||||

Db 1 AATTGTCCTTGGGACAGCTGC 21

## RESULT 311

US-11-127-877-486  
; Sequence 486, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 486  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-486

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGGTAGTGATGATC 378

Db 1 AACCTGCTAGTGTGATC 21

RESULT 312  
US-11-127-877-487  
; Sequence 487, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 487  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-487

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGACTTAC 483

Db 1 AATACAGTGTGACTTAC 21

RESULT 313

US-11-127-877-488  
; Sequence 488, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 488  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-488

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACCTATGCTGCC 495

Db 1 AACTTCACCTATGCTGCC 21

RESULT 314  
US-11-127-877-489  
; Sequence 489, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 489  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-489

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGTACTACGCC 514

Db 1 ACAACGAATGTACTACGCC 21

RESULT 315

US-11-127-877-490  
; Sequence 490, Application US/11127877

```

; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-490

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 AAGTTCACAACTCTTCCC 546
DB 1 AAGTTCACAACTCTTCCC 21

RESULT 316
US-11-127-877-491
; Sequence 491, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 491
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-491

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 ACAGCCACCAAGTGTGATC 663
DB 1 ACAGCCACCAAGTGTGATC 21

RESULT 317
US-11-127-877-492
; Sequence 492, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
```

```

; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 492
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-492

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 ACCAAGTGTGATCTGTGTC 669
DB 1 ACCAAGTGTGATCTGTGTC 21

RESULT 318
US-11-127-877-493
; Sequence 493, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 493
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-493

Query Match
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No.3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 AAAGTGTGATCTGTGATC 672
DB 1 AAAGTGTGATCTGTGATC 21

RESULT 319
US-11-127-877-494
; Sequence 494, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
```

```

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 494
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-494

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      713 ACTCAACACAGAGACCATGC 733
Db      1 ACTCAACACAGAGACCATGC 21

RESULT 320
US-11-127-877-495
; Sequence 495, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 495
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-495

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      797 ACCACATCTGTGATCTGTC 817
Db      1 ACCACATCTGTGATCTGTC 21

RESULT 321
US-11-127-877-496
; Sequence 496, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
```

```

; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 496
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-496

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      811 ACTGTGCTGATCTACTTCCTC 831
Db      1 ACTGTGCTGATCTACTTCCTC 21

RESULT 322
US-11-127-877-497
; Sequence 497, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 497
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-497

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      857 ACACCGTAGTGGGATCACC 877
Db      1 ACACCGTAGTGGGATCACC 21

RESULT 323
US-11-127-877-498
; Sequence 498, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
```

; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 498  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-498

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 874 ACATATGGCCAGTGAGATC 894  
Db 1 ACATATGGCCAGTGAGATC 21

RESULT 324  
US-11-127-877-499  
; Sequence 499, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 499  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-499

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 876 ACTATGGCCAGTGATCCC 896  
Db 1 ACTATGGCCAGTGATCCC 21

RESULT 325  
US-11-127-877-500  
; Sequence 500, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24

; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 500  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-500

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 920 ACAGCAAGTCTGCCAAGC 940  
Db 1 ACAGCAAGTCTGCCAAGC 21

RESULT 326  
US-11-127-877-501  
; Sequence 501, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 501  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-501

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1025 ACATCAACCGATCTCACC 1045  
Db 1 ACATCAACCGATCTCACC 21

RESULT 327  
US-11-127-877-502  
; Sequence 502, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 502

LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-502

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAAGATTATCCAGC 1063  
DB 1 ACCTGAAGATTATCCAGC 21

RESULT 328  
US-11-127-877-503  
Sequence 503, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 503  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-503

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAAGTTATCCAGCAGGTC 1068  
DB 1 AAGAAGTTATCCAGCAGGTC 21

RESULT 329  
US-11-127-877-504  
Sequence 504, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 504  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens

US-11-127-877-504

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCAC 1071  
DB 1 AAGTTATCCAGCAGGTCAC 21

RESULT 330  
US-11-127-877-505  
Sequence 505, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 505  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-505

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 AATGACAGTTCGCTCGGC 1155  
DB 1 AATGACAGTTCGCTCGGC 21

RESULT 331  
US-11-127-877-506  
Sequence 506, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
TITLE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 506  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-506

Query Match 1.2%; Score 21; DB 1; Length 21;



Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0;

QY 1214 AATGAATCCACCCGGTATC 1234

Db 1 AATGAATCCACCCGGTATC 21

## RESULT 332

US-11-127-877-507  
; Sequence 507, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127, 877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 507  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-507

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1363 AACTGCTCTTCACGAGTGC 1383

Db 1 AACTGCTCTTCACGAGTGC 21

## RESULT 333

US-11-127-877-508  
; Sequence 508, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127, 877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 508  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-508

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 AAGTACTCAAGACCATGAC 1397

Db 1 AAGTACTCAAGACCATGAC 21

## RESULT 334

US-11-127-877-509  
; Sequence 509, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127, 877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 509  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-509

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 AAGCATGACAGAGCTTC 1407

Db 1 AAGCATGACAGAGCTTC 21

## RESULT 335

US-11-127-877-510  
; Sequence 510, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27, 800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127, 877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 510  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-510

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 ACCATGACAGAGCTTCAC 1410

Db 1 ACCATGACAGAGCTTCAC 21

```
RESULT 336
US-11-127-877-511
; Sequence 511, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 511
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-511
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1396 ACAGAGAGCTTCAGCTTCTCC 1416
Db 1 ACAGAGAGCTTCAGCTTCTCC 21
```

```
RESULT 337
US-11-127-877-512
; Sequence 512, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 512
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-512
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1497 AAATTCCTCATCTGGAACC 1517
Db 1 AAATTCCTCATCTGGAACC 21
```

RESULT 338

```
US-11-127-877-513
; Sequence 513, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 513
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-513
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1514 AACCATCAGAAACACCTCTAC 1534
Db 1 AACCATCAGAAACACCTCTAC 21
```

```
RESULT 339
US-11-127-877-514
; Sequence 514, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-514
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1648 AATCAGTGAACCTTGCTGAGC 1668
Db 1 AATCAGTGAACCTTGCTGAGC 21
```

```
RESULT 340
US-11-127-877-515
; Sequence 515, Application US/11127877
; Publication No. US20050287565A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 515
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-515

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1733 ACTTTGGCTGCATGCGAGTGC 1753
Db      1 ACTTTGGCTGCATGCGAGTGC 21

RESULT 341
US-11-127-877-516
; Sequence 516, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 516
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-516

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 AACCAAGCTGGCAAAATGTCC 310
Db      1 AACCAAGCTGGCAAAATGTCC 21

RESULT 342
US-11-127-877-517
; Sequence 517, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
```

```

; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 517
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-517

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 AATTGCTTTGGGAGCTGC 323
Db      1 AATTGCTTTGGGAGCTGC 21

RESULT 343
US-11-127-877-518
; Sequence 518, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 518
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-518

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      358 AACGTGTAGTGAATGATC 378
Db      1 AACGTGTAGTGAATGATC 21

RESULT 344
US-11-127-877-519
; Sequence 519, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spitlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
```

```

; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-519

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATGAGTGGTGAAGTCTCACC 483
DB 1 AATGAGTGGTGAAGTCTCACC 21

RESULT 345
US-11-127-877-520
; Sequence 520, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 520
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-520

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTCACCTATGCTGTGCAC 495
DB 1 AACTTCACCTATGCTGTGCAC 21

RESULT 346
US-11-127-877-521
; Sequence 521, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
```

```

; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 521
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-521

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 ACAACGAATGATCTACGACC 514
DB 1 ACAACGAATGATCTACGACC 21

RESULT 347
US-11-127-877-522
; Sequence 522, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-522

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 ACAGCCACCAAGTGTATC 663
DB 1 ACAGCCACCAAGTGTATC 21

RESULT 348
US-11-127-877-523
; Sequence 523, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
```

PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 523  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-523

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 649 ACCAAGTGTCTGTCTGTC 669  
Db 1 ACCAAGTGTCTGTCTGTC 21

RESULT 349  
US-11-127-877-524  
Sequence 524, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27,800-B USA  
CURRENT FILING DATE: 2005-05-12  
CURRENT APPLICATION NUMBER: US/11/127,877  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 524  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-524

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 652 AAAGTGTCTGTCTGTC 672  
Db 1 AAAGTGTCTGTCTGTC 21

RESULT 350  
US-11-127-877-525  
Sequence 525, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27,800-B USA  
CURRENT FILING DATE: 2005-05-12  
CURRENT APPLICATION NUMBER: US/11/127,877  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590

SOFTWARE: PatentIn version 3.3  
SEQ ID NO 525  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-525

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTCACCACAGACCATGC 733  
Db 1 ACTCACCACAGACCATGC 21

RESULT 351  
US-11-127-877-526  
Sequence 526, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27,800-B USA  
CURRENT FILING DATE: 2005-05-12  
CURRENT APPLICATION NUMBER: US/11/127,877  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 526  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-526

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGACTGTC 817  
Db 1 ACCACATCTGTGACTGTC 21

RESULT 352  
US-11-127-877-527  
Sequence 527, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27,800-B USA  
CURRENT FILING DATE: 2005-05-12  
CURRENT APPLICATION NUMBER: US/11/127,877  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 527  
LENGTH: 21

TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-527

Query Match  
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTCTC 831  
DB 1 ACTGTGCTGATCTACTCTC 21

RESULT 353  
US-11-127-877-528  
Sequence 528, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27, 800-B USA  
CURRENT APPLICATION NUMBER: US/11/127, 877  
PRIOR FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 528  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-528

Query Match  
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGATCAGAC 877  
DB 1 ACACCGTAGTGGGATCAGAC 21

RESULT 354  
US-11-127-877-529  
Sequence 529, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27, 800-B USA  
CURRENT APPLICATION NUMBER: US/11/127, 877  
PRIOR FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 529  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-529

Query Match  
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 ACATATGGGCCAGTGAGATC 894  
DB 1 ACATATGGGCCAGTGAGATC 21

RESULT 355  
US-11-127-877-530  
Sequence 530, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27, 800-B USA  
CURRENT APPLICATION NUMBER: US/11/127, 877  
PRIOR FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 530  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-530

Query Match  
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGGCCAGTGAGATCCC 896  
DB 1 ACTATGGGCCAGTGAGATCCC 21

RESULT 356  
US-11-127-877-531  
Sequence 531, Application US/11127877  
Publication No. US20050287565A1  
GENERAL INFORMATION:  
APPLICANT: Merchiers, Pascal G.  
APPLICANT: Hoffmann, Marcel  
APPLICANT: Spittaels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE REFERENCE: P27, 800-B USA  
CURRENT APPLICATION NUMBER: US/11/127, 877  
PRIOR FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 531  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-127-877-531

Query Match  
Best Local Similarity 1.2%; Score 21; DB 1; Length 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACGAGCAAGTCTCTGCCAAGC 940

DB 1 ACGAGCAAGTCTCTGCCAAGC 21

RESULT 357

US-11-127-877-532

; Sequence 532, Application US/11127877

; Publication No. US20050287565A1

; GENERAL INFORMATION:

; APPLICANT: Merchiers, Pascal G.

; APPLICANT: Hoffmann, Marcel

; APPLICANT: Spittaels, Koenraad F. F.

; APPLICANT: Laenen, Wendy

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

; FILE REFERENCE: P27,800-B USA

; CURRENT FILING DATE: 2005-05-12

; PRIOR FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: 60/570,352

; PRIOR FILING DATE: 2004-08-24

; NUMBER OF SEQ ID NOS: 590

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 532

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-127-877-532

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ACATCAACCCGAGTCTTACC 1045

DB 1 ACATCAACCCGAGTCTTACC 21

RESULT 358

US-11-127-877-533

; Sequence 533, Application US/11127877

; Publication No. US20050287565A1

; GENERAL INFORMATION:

; APPLICANT: Merchiers, Pascal G.

; APPLICANT: Hoffmann, Marcel

; APPLICANT: Spittaels, Koenraad F. F.

; APPLICANT: Laenen, Wendy

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

; FILE REFERENCE: P27,800-B USA

; CURRENT FILING DATE: 2005-05-12

; PRIOR FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: 60/570,352

; PRIOR FILING DATE: 2004-08-24

; NUMBER OF SEQ ID NOS: 590

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 533

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-127-877-533

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 ACCTGAGAGATTATTCAGC 1063

DB 1 ACCTGAGAGATTATTCAGC 21

RESULT 359

US-11-127-877-534

; Sequence 534, Application US/11127877

; Publication No. US20050287565A1

; GENERAL INFORMATION:

; APPLICANT: Merchiers, Pascal G.

; APPLICANT: Hoffmann, Marcel

; APPLICANT: Spittaels, Koenraad F. F.

; APPLICANT: Laenen, Wendy

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

; FILE REFERENCE: P27,800-B USA

; CURRENT FILING DATE: 2005-05-12

; PRIOR FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: 60/570,352

; PRIOR FILING DATE: 2004-08-24

; NUMBER OF SEQ ID NOS: 590

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 534

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-127-877-534

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1048 AAGAGTTATTCAGCAGTC 1068

DB 1 AAGAGTTATTCAGCAGTC 21

RESULT 360

US-11-127-877-535

; Sequence 535, Application US/11127877

; Publication No. US20050287565A1

; GENERAL INFORMATION:

; APPLICANT: Merchiers, Pascal G.

; APPLICANT: Hoffmann, Marcel

; APPLICANT: Spittaels, Koenraad F. F.

; APPLICANT: Laenen, Wendy

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

; FILE REFERENCE: P27,800-B USA

; CURRENT FILING DATE: 2005-05-12

; PRIOR FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: 60/570,352

; PRIOR FILING DATE: 2004-08-24

; NUMBER OF SEQ ID NOS: 590

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 535

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-127-877-535

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATTCAGCAGGTCTAC 1071

DB 1 AAGTTATTCAGCAGGTCTAC 21

```
RESULT 361
US-10-310-914A-386286/C
; Sequence 386286, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuaz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386286
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386286

Query Match          1.2%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      116 GCTTTAGAGAGACCTGAGCC 136
DB      21 GCTTTAGAGAGACCTGAGCC 1

RESULT 362
US-10-809-189-67919
; Sequence 67919, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809.189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396.196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-67919

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1382 ACTCGAGACATGACAGAGACT 1405
DB      2 ACTCGAGACATGACAGAGACT 25

RESULT 363
US-11-036-317-443229
; Sequence 443229, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
```

```
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536.639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-443229

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      843 GATTGGCTATGATACACCGTAGT 866
DB      1 GATTGGCTATGATACACGTGTGT 24

RESULT 364
US-11-060-756-34802
; Sequence 34802, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34802

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1051 AAGTTATCCAGCAGGTCTACCTG 1074
DB      2 AAGTTATCCAGCAGGTCTACTG 25

RESULT 365
US-11-060-756-36930
; Sequence 36930, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36930

Query Match          1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```



Qy 1108 TACACCCCATCTACTGCTGC 1131  
Db 2 TACATCCCATCTACTGCTTC 25

RESULT 366  
US-11-060-756-36933  
; Sequence 36933, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounes, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36933  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-36933

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1104 CATGTACACCCCATCTACTG 1127  
Db 2 CATGTACATCCCATCTACTG 25

RESULT 367  
US-11-060-756-36934  
; Sequence 36934, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounes, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36934  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-36934

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1106 TGTACACCCCATCTACTGCT 1129  
Db 1 TGTACATCCCATCTACTGCT 24

RESULT 368  
US-11-060-756-36935  
; Sequence 36935, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounes, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36935  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-36935

FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36935  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-36935

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1108 TACACCCCATCTACTGCTGC 1131  
Db 1 TACATCCCATCTACTGCTTC 24

RESULT 369  
US-11-060-756-233624  
; Sequence 233624, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounes, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233624  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-233624

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1053 GTTATCCAGCAGCTTACTGCTGC 1076  
Db 1 GTTATCCAGCAGCTTACTGCTGC 24

RESULT 370  
US-11-060-756-233625  
; Sequence 233625, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounes, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233625  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe  
US-11-060-756-233625

Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4.7e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1053 GTTATCCAGAGTCTACTGSC 1076  
Db 1 GTTCATCCAGCAGTCTACTGSC 24

RESULT 371  
US-10-005-956-1129/c  
Sequence 1129, Application US/10005956  
Publication No. US20030113726A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: D0053NP  
CURRENT APPLICATION NUMBER: US/10/005,956  
CURRENT FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: 60/251,015  
PRIOR FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: 60/263,678  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/273,037  
PRIOR FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 1579  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1129  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-005-956-1129

Query Match 1.2%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 3.8e+02;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1624 CCTCATGCTGTGACTCAAA 1644  
Db 21 CCTCATGCTGTGACTCAAA 1

RESULT 372  
US-10-278-087A-15/c  
Sequence 15, Application US/10278087A  
Publication No. US20030138817A1  
GENERAL INFORMATION:  
APPLICANT: Shuji Hinuma  
Yasunaki Ito  
Ryo Fujii  
TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edwards & Angell, LLP  
STREET: 101 Federal Street  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02209  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/278,087A  
FILING DATE: 31-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/461,436  
FILING DATE: 14-DEC-1999  
APPLICATION NUMBER: 09/038,572  
FILING DATE: 11-MAR-1998  
APPLICATION NUMBER: 08/513,974  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/JP95/01599

FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: 7-093989  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: 7-057186  
FILING DATE: 16-MAR-1995  
APPLICATION NUMBER: 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CONLIN, DAVID G.  
REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4444  
TELEFAX: 617-439-4170  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA  
FEATURE:  
OTHER INFORMATION: /note= "N is inosine; W is A or T;  
S is G or C; K is G or T; R is A or G."  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-278-087A-15

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
Best Local Similarity 70.8%; Pred. No. 4.6e+02;  
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCCCTTC 1002  
Db 24 TTGCGCATCTGCTGCTGCCCTTC 1

RESULT 373  
US-11-060-756-34807  
Sequence 34807, Application US/11060756  
Publication No. US20050221354A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: William Martin  
Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
TARGET GENES  
FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34807  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-34807

Query Match 1.2%; Score 20.4; DB 1; Length 25;  
Best Local Similarity 95.5%; Pred. No. 5e+02;

```
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1115 CCATCATCTACTGCTGCTCA 1136
Db 1 CCATCATCTACTGCTGCTCA 22

RESULT 374
US-10-719-956-382728
; Sequence 382728, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 382728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-382728

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1376 GAATGACTCCAGACCATGACAGA 1400
Db 1 GCAGCAACTCCAGACCATGACAGA 25

RESULT 375
US-10-719-900-33169
; Sequence 33169, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 33169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-33169

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1111 AACCCATCATCTACTGCTGCTCA 1135
Db 1 AACCCATCATCTACTGCTGCTCA 25

RESULT 376
US-10-719-900-146776
; Sequence 146776, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 146776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-146776

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1388 AGACCATGACGAGAGCTCAGCTT 1412
Db 1 AGACCATGACGAGAGCTCAGCTT 25

RESULT 377
US-10-719-900-152541
; Sequence 152541, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 152541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-152541

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1244 AGGCGAGTGTGTACAAGTCAGCG 1268
Db 1 AGGCGAGTGTGTACAAGTCAGCG 25

RESULT 378
US-10-719-900-455080
; Sequence 455080, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 455080
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-455080

Query Match 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 910 GACCGTACGACGACGAGTCTCTG 934  
 |||||  
 Db 1 GACCGTACCATGACGAAAGTCTCTG 25

RESULT 379  
 US-10-809-189-67918  
 ; Sequence 67918, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Miltmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; CURRENT FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67918  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-10-809-189-67918

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1375 CGAGTGACTCCAGACCATGACG 1399  
 |||||  
 Db 1 CGAGGCAACTCGAGACCATGACG 25

RESULT 380  
 US-10-809-189-67927  
 ; Sequence 67927, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Miltmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; CURRENT FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67927  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-10-809-189-67927

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1165 GCCTTCGCGTGCCTCCCTTCATCA 1189  
 |||||  
 Db 1 GCCTTCGCTGCTGCCCTTCATCA 25

RESULT 381  
 US-10-809-189-67930  
 ; Sequence 67930, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Miltmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; CURRENT FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67930  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-10-809-189-67930

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1231 TATCTCAGACCCGAGGAGTGT 1255  
 |||||  
 Db 1 TACTCCAGACCCGAGGAGTGT 25

RESULT 382  
 US-10-809-189-67931  
 ; Sequence 67931, Application US/10809189  
 ; Publication No. US20050048531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Miltmann  
 ; APPLICANT: David Mack  
 ; APPLICANT: David Lockhart  
 ; APPLICANT: Affymetrix, Inc.  
 ; TITLE OF INVENTION: Methods of Genetic Analysis  
 ; FILE REFERENCE: 3101.1  
 ; CURRENT APPLICATION NUMBER: US/10/809,189  
 ; CURRENT FILING DATE: 2004-03-25  
 ; PRIOR APPLICATION NUMBER: US/09/396,196  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: 60/100,678  
 ; PRIOR FILING DATE: 1998-09-17  
 ; NUMBER OF SEQ ID NOS: 127806  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67931  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: mus musculus  
 US-10-809-189-67931

Query Match 1.1%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 5.2e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1237 CAGACCCAGGCGAGTGTGTACAAG 1261  
 |||||  
 Db 1 CAGACCCAGGCGAGTGTGTACAAG 25

RESULT 383  
 US-10-956-157-170659  
 ; Sequence 170659, Application US/10956157  
 ; Publication No. US20050118625A1

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 170659
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-956-157-170659

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1386 CACAGCCATGACAGAGCTTCAGC 1410
Db 1 CACACCGCTCACAGAGCTTCAGC 25

RESULT 384
US-11-036-317-411229
; Sequence 411229, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-411229

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 493 CACACGAATGCTACTACGGCTCT 517
Db 1 CACACGCTGTGCTACTACGGCTCT 25

RESULT 385
US-11-036-317-413994
; Sequence 413994, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 413994
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Mus musculus
US-11-036-317-413994

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 CAGGCGCTGTCTCAAGTCAGCC 1267
Db 1 CAGGCGCGTGTCAAGTCAGCC 25

RESULT 386
US-11-060-756-27267
; Sequence 27267, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent version 3.2
; SEQ ID NO 27267
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-060-756-27267

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1005 CATCTTCTCCTCCTGCTCCTACATC 1029
Db 1 CATCTTCTCCTCCTGCTCCTACATC 25

RESULT 387
US-11-060-756-34789
; Sequence 34789, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent version 3.2
; SEQ ID NO 34789
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-060-756-34789

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CATCATCTACTGCTGCTCAATGAC 1140
Db 1 CATCATCTACTGCTGCTCAATGAC 25

RESULT 388
US-11-060-756-34795
; Sequence 34795, Application US/11060756
```

```
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34795

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1049 AGAAGTTATCCACAGGCTACCT 1073
Db      1 ACAAGTTCATCCACAGTCTACCT 25

RESULT 389
US-11-060-756-34800
; Sequence 34800, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-34800

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1117 ATCATCTACTGCTGCTCAATGACA 1141
Db      1 ATCATCTACTGCTGCTCAACACACA 25

RESULT 390
US-11-060-756-34880
; Sequence 34880, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34880
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
```

```
US-11-060-756-34880

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1115 CCATCATCTACTGCTGCTCAATGA 1139
Db      1 CCATCATCTACTGCTGCTCAATGA 25

RESULT 391
US-11-060-756-36619
; Sequence 36619, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36619

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1110 CAACCCCATCATCTACTGCTGCTC 1134
Db      1 CAACCCCATCATCTACTGCTGCTC 25

RESULT 392
US-11-060-756-36624
; Sequence 36624, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-36624

Query Match      1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1111 AACCCATCATCTACTGCTGCTCA 1135
Db      1 AACCCATCATCTACTGCTGCTCA 25

RESULT 393
US-11-060-756-36940
; Sequence 36940, Application US/11060756
; Publication No. US20050221354A1
```



```

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-123000

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 ATCTACTGCTGCTCAATGACAGGT 1144
Db 1 ATCTACTGCTGCTCAACACACAGGT 25

RESULT 399
US-11-060-756-146971
; Sequence 146971, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146971
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146971

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1049 AGAAGTTATCCAGCAGGTCTACCT 1073
Db 1 ACAAGTCAITCCAGCAAGTCTACCT 25

RESULT 400
US-11-060-756-146972
; Sequence 146972, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146972
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146972
```

```

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1049 AGAAGTTATCCAGCAGGTCTACCT 1073
Db 1 ACAAGTCAITCCAGCAAGTCTACCT 25

RESULT 401
US-11-136-527-151571
; Sequence 151571, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151571
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-151571

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1101 CACCATGTACACCCCATCATCTAC 1125
Db 1 CTCATCTACACCCCATCATCTAC 25

RESULT 402
US-11-136-527-151582
; Sequence 151582, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-151582

Query Match
Best Local Similarity 1.1%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 5.2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1100 CCACATGTACACCCCATCATCTA 1124
Db 1 CTCATCTACACCCCATCATCTA 25
```



```
RESULT 403
US-09-930-503-22
; Sequence 22, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-22

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1000 TTCCACATCTTCTCTCTCTCT 1019
DB      1 TTCCACATCTTCTCTCTCTCT 20

RESULT 404
US-09-930-503-25/c
; Sequence 25, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-25

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1012 TTCTCTCTGCGCTTACATCAA 1031
DB      20 TTCTCTCTGCGCTTACATCAA 1

RESULT 405
US-09-930-503-27/c
; Sequence 27, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-27
```

```
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPAL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-27

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 GTAGTGGGATCAGCACTATG 881
DB      20 GTAGTGGGATCAGCACTATG 1

RESULT 406
US-09-930-503-29/c
; Sequence 29, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-29

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      637 TCAGCCAGCCGACCAAGT 656
DB      20 TCAGCCAGCCGACCAAGT 1

RESULT 407
US-09-930-503-30/c
; Sequence 30, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-30
```

```
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-30

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      601 TACATGGCCATCATCATCC 620
Db      20 TACATGGCCATCATCATCC 1

RESULT 408
US-09-930-503-41/c
; Sequence 41, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-41

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1000 TTCCACATCTTCTCTCT 1019
Db      20 TTCCACATCTTCTCTCTCT 1

RESULT 409
US-09-930-503-44
; Sequence 44, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
```

```
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-44

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1012 TTCTCTCGCCCTACATCAA 1031
Db      1 TTCTCTCGCCCTACATCAA 20

RESULT 410
US-09-930-503-46
; Sequence 46, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-46

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 GTAGTGGGAATCACACTATG 881
Db      1 GTAGTGGGAATCACACTATG 20

RESULT 411
US-09-930-503-48
; Sequence 48, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
```

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-48

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 637 TCAGCCACAGCCACCAAGT 656  
Db 1 TCAGCCACAGCCACCAAGT 20

RESULT 412  
US-09-930-503-49  
Sequence 49, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CARILL, CATHERINE  
APPLICANT: VASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930,503  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-49

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 601 TACATGCCATCATCATCC 620  
Db 1 TACATGCCATCATCATCC 20

RESULT 413  
US-10-146-354A-34/C  
Sequence 34, Application US/10146354A  
Publication No. US20030054381A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: Seymour, Albert B.  
APPLICANT: Nelson, Darcy L.  
APPLICANT: Webb, Suzin M.  
APPLICANT: Affourtit, Jason P.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND  
FILE REFERENCE: PC10461AGPR  
CURRENT APPLICATION NUMBER: US/10/146,354A  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: 60/293,425  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 34  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer

FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)-(20)  
OTHER INFORMATION: artificial / primer  
US-10-146-354A-34

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 GGCACCTGTGTATGATGTG 374  
Db 20 GGCACCTGTGTATGATGTG 1

RESULT 414  
US-10-146-354A-46/C  
Sequence 46, Application US/10146354A  
Publication No. US20030054381A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: Seymour, Albert B.  
APPLICANT: Nelson, Darcy L.  
APPLICANT: Webb, Suzin M.  
APPLICANT: Affourtit, Jason P.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND  
FILE REFERENCE: PC10461AGPR  
CURRENT APPLICATION NUMBER: US/10/146,354A  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: 60/293,425  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
NAME/KEY: misc.feature  
LOCATION: (1)-(20)  
OTHER INFORMATION: artificial / primer  
US-10-146-354A-46

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1483 CCCTTCATGCATGGAATTC 1502  
Db 20 CCCTTCATGCATGGAATTC 1

RESULT 415  
US-10-146-354A-47  
Sequence 47, Application US/10146354A  
Publication No. US20030054381A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: Seymour, Albert B.  
APPLICANT: Nelson, Darcy L.  
APPLICANT: Webb, Suzin M.  
APPLICANT: Affourtit, Jason P.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND  
FILE REFERENCE: PC10461AGPR  
CURRENT APPLICATION NUMBER: US/10/146,354A  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: 60/293,425  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 46

```
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: artificial / primer
US-10-146-354A-47
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1417 TCCAAATGCTCTCTAGGC 1436
          |||||
Db       1 TCCAAATGCTCTCTAGGC 20
```

```
RESULT 416
US-10-146-354A-48/C
; Sequence 48, Application US/10146354A
; Publication No. US20030054381A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Seymour, Albert B.
; APPLICANT: Nelson, Darcy L.
; APPLICANT: Webb, Suzin M.
; APPLICANT: Affco, J. Jason P.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
; FILE REFERENCE: PC10461AGPR
; CURRENT FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/293,425
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: artificial / primer
US-10-146-354A-48
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1746 GCGAGTGCTCATTTGAGAT 1765
          |||||
Db       20 GCGAGTGCTCATTTGAGAT 1
```

```
RESULT 417
US-10-005-956-1213
; Sequence 1213, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
```

```
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1213
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1213
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      609 CATCATATCATCCCTCCAGC 628
          |||||
Db       1 CATCATATCATCCCTCCAGC 20
```

```
RESULT 418
US-10-005-956-1214
; Sequence 1214, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1214
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1214
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      915 CTACCAGAGCAAGTCTCTG 934
          |||||
Db       1 CTACCAGAGCAAGTCTCTG 20
```

```
RESULT 419
US-10-310-914A-386277/C
; Sequence 386277, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 386277
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
```

US-10-310-914A-386277

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 ATTTCTGGAAGTACCTTTGG 1739

Db 20 ATTCTGGAAGTACCTTTGG 1

RESULT 420

US-10-310-914A-386290/c  
; Sequence 386290, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kvuazac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A

CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3  
SEQ ID NO 386290

LENGTH: 20  
TYPE: RNA

ORGANISM: Human  
US-10-310-914A-386290

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 ATTCATTCTCGAAGTAC 1734

Db 20 ATTCATTCTCGAAGTAC 1

RESULT 421

US-10-310-914A-386294/c  
; Sequence 386294, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kvuazac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A

CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3  
SEQ ID NO 386294

LENGTH: 20  
TYPE: RNA

ORGANISM: Human  
US-10-310-914A-386294

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1552 GGGTCAGTATGGGTTAGGA 1571

Db 20 GGGTCAGTATGGGTTAGGA 1

RESULT 422

US-09-930-503-32/c  
; Sequence 32, Application US/09930503  
; Publication No. US20030060438A1

GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE

APPLICANT: YASHPAL, KIRAN  
APPLICANT: YASHPAL, KIRAN

TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF

FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930.503

CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086

PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32

LENGTH: 21  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-32

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTCCCAACTTCTT 542

Db 21 TGCAGTCCCAACTTCTT 2

RESULT 423

US-09-930-503-51  
; Sequence 51, Application US/09930503  
; Publication No. US20030060438A1  
; GENERAL INFORMATION:

APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE

APPLICANT: YASHPAL, KIRAN  
APPLICANT: YASHPAL, KIRAN

TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF

FILE REFERENCE: 39245-173913  
CURRENT APPLICATION NUMBER: US/09/930.503

CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 60/226,086

PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 51

LENGTH: 21  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-51

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTCCCAACTTCTT 542

Db 1 TGCAGTCCCAACTTCTT 20

RESULT 424

US-10-451-304-11  
; Sequence 11, Application US/10451304  
; Publication No. US20050079495A1  
; GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company LLC  
APPLICANT: Hall, Matthew D.

APPLICANT: McNulty, Shaun  
APPLICANT: Murray, James H.

```

; APPLICANT: Suman-Chauhan, Nirmala
; TITLE OF INVENTION: Modified Tachykinin Receptors
; FILE REFERENCE: A0000197
; CURRENT APPLICATION NUMBER: US/10/451,304
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: PCT/GB01/05404
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: UK 0031148.0
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
US-10-451-304-11
```

```

Query Match          1.1%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      438 CGCGAGGCTTCATGCGTGCAT 460
Db      1 CGCGAGGCTTCTATGGCTGCAT 23
```

```

RESULT 425
US-09-931-700-13/C
; Sequence 13, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202U4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid,
; OTHER INFORMATION: AM-R antisense probe (nucleotides 788-811)
US-09-931-700-13
```

```

Query Match          1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      980 TCGCATCTGTGCTGCTCCCTTCC 1003
```

```

Db      24 TTGTACATCTGTGCTGCTTACC 1
```

```

RESULT 426
US-09-930-503-35
; Sequence 35, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-35
```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      176 GTGTACGATGATGAGGCTT 194
Db      1 GTGTACGATGATGAGGCTT 19
```

```

RESULT 427
US-09-930-503-37/C
; Sequence 37, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-37
```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1548 AAAAGGTCAGTATGAGGTT 1566
Db      19 AAAAGGTCAGTATGAGGTT 1
```

```
RESULT 428
```

```
US-09-930-503-54/c
; Sequence 54, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-54

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      176 GTGTACAGATAGTAGGCTT 194
Db      19 GTGTACAGATAGTAGGCTT 1

RESULT 429
US-09-930-503-56
; Sequence 56, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-56

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1548 AAAAGGTCAGTAGGCTT 1566
Db      1 AAAAGGTCAGTAGGCTT 19

RESULT 430
US-10-005-956-81
; Sequence 81, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
```

```
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-81

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      534 CAACTTCTTCCCATCGCC 552
Db      1 CAACTTCTTCCCATCGCC 19

RESULT 431
US-10-005-956-85/c
; Sequence 85, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-85

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1626 TCATGCTGTGTGACTCAA 1644
Db      19 TCATGCTGTGTGACTCAA 1

RESULT 432
US-10-005-956-87/c
; Sequence 87, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
```

```
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-87
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1335 CACACCTCGTCCCTGGAC 1353
Db 19 CACACCTCGTCCCTGGAC 1
```

```
RESULT 433
US-10-005-956-145/c
; Sequence 145, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 145
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-145
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 663 CTGTGTCATCTGGTCCG 681
Db 19 CTGTGTCATCTGGTCCG 1
```

```
RESULT 434
US-10-005-956-149/c
; Sequence 149, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 19
```

```
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-149
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1529 CCTCACACTGGGACTTGCA 1547
Db 19 CCTCACACTGGGACTTGCA 1
```

```
RESULT 435
US-10-310-914A-386272/c
; Sequence 386272, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruszat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386272
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 167 AGGGGGTGTGTACAGAT 185
Db 19 AGGGGGTGTGTACAGAT 1
```

```
RESULT 436
US-10-310-914A-386273/c
; Sequence 386273, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kruszat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386273
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386273
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 167 AGGGGGTGTGTACAGAT 185
Db 19 AGGGGGTGTGTACAGAT 1
```

```
RESULT 437
US-10-310-914A-386300/c
```



```
; Sequence 386300, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386300
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386300

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1475 ACCTGCTCCTTCATGCA 1493
Db      19  ACCTGCTCCTTCATGCA 1

RESULT 438
US-10-310-914A-386304/C
; Sequence 386304, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386304
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386304

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 GCCCGACGCCGACCCACA 152
Db      19  GCCCGACGCCGACCCACA 1

RESULT 439
US-11-083-784-491124
; Sequence 491124, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714.333
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491124
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491124

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      401 GGACAGTGACGAACCTATT 419
Db      1  GGACAGTGACGAACCTATT 19

RESULT 440
US-11-083-784-491125
; Sequence 491125, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714.333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491125
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491125

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1655 GAACCTTGCGAGCCTGTA 1673
Db      1  GAACCTTGCGAGCCTGTA 19

RESULT 441
US-11-083-784-491126
; Sequence 491126, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
```

```
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491126

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      247 CCAACATCTCCACTAAC 265
          |||||:|:|||||:|
Db      1 CCAACACUCCACACUACA 19

RESULT 442
US-11-083-784-491127
; Sequence 491127, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491127
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491127

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      773 CGAACAGATTATGAGA 791
          |||||:|:|||||:|
Db      1 CGAACAGAUUUGAGAA 19

RESULT 443
US-11-083-784-491128
; Sequence 491128, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491128
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491128

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      76 AAAGAGTGTGCCCATAA 94
          |||||:|:|||||:|
Db      1 AAAGAGUGUCGCCCAUAA 19

RESULT 444
US-11-083-784-491129
; Sequence 491129, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491129

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      789 GAAAGTGATCCATCTGT 807
          |||||:|:|||||:|
Db      1 GAAAGUGACCAUCCUUGU 19

RESULT 445
US-11-083-784-491130
; Sequence 491130, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
/ APPLICANT: Leeke, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491130
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491130
```

```
Query Match 1.1%, Score 19, DB 1, Length 19,
Best Local Similarity 68.4%, Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 178 GTACAGATGATGAGCTTTA 196
Db 1 GUACAGAUAGUGGCUUUA 19
```

```
RESULT 446
US-11-083-784-491131
/ Sequence 491131, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmova, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leeke, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491131
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491131
```

```
Query Match 1.1%, Score 19, DB 1, Length 19,
Best Local Similarity 57.9%, Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 809 TGACTGTGCTGATCTACTT 827
Db 1 TGACUGUGGUGAUCUACU 19
```

```
RESULT 447
US-11-083-784-491132
/ Sequence 491132, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Dharmova, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leeke, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491132
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491132
```

```
Query Match 1.1%, Score 19, DB 1, Length 19,
Best Local Similarity 78.9%, Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1033 CCAGATCTCTACTGCTGAGA 1051
Db 1 CCAGATCTCTACTGCTGAGA 19
```

```
RESULT 448
US-11-083-784-491133
/ Sequence 491133, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmova, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leeke, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491133
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491133
```

```
Query Match 1.1%, Score 19, DB 1, Length 19,
Best Local Similarity 68.4%, Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 650 CCAAGTGTCTGCTGCTGCT 668
Db 1 CCAAGTGTCTGCTGCTGCT 19
```

```
RESULT 449
US-11-083-784-491134
```

```
; Sequence 491134, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491134
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491134
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 461 TCATACAGTGTGACTT 479
Db 1 UCAAUACAGUGUGAACU 19
```

```
RESULT 450
US-11-083-784-491135
; Sequence 491135, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491135
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 600 GTACATGGCCATCATCAT 618
Db 1 GUACAUGGCCANCAUACA 19
```

```
RESULT 451
US-11-083-784-491136
; Sequence 491136, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491136
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491136
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 398 TGAGGACGTGACGACTA 416
Db 1 UGAGGACAGUGACGACUA 19
```

```
RESULT 452
US-11-083-784-491137
; Sequence 491137, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491137
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491137
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 787 GAGAAAGTGACACATCT 805
```

Db 1 GAGAAAGUAGACCAUCU 19

RESULT 453

US-11-083-784-491138  
; Sequence 491138, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491138  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491138

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 578 TGACGGCTGGGCTTGA 596  
Db 1 UGACGGCUGGCGCCUUGA 19

RESULT 454

US-11-083-784-491139  
; Sequence 491139, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491139  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491139

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 777 CAAGATTATGAGAAAGTG 795  
Db 1 CAAGAUTUAGAGAAAGUG 19

RESULT 455

US-11-083-784-491140  
; Sequence 491140, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491140  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491140

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 766 GAGCATCCGAAACAATTT 784  
Db 1 GAGCAUCCGAAACAAGAUU 19

RESULT 456

US-11-083-784-491141  
; Sequence 491141, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491141  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491141

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 761 GGCCAGAGCATCCGACAA 779  
Db 1 GGCCAGAGCAUCCGACAA 19

## RESULT 457

US-11-083-784-491142  
; Sequence 491142, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491142  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491142

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 4.6e+02;  
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 106 CCTCTGTCTGCTTTGAA 124  
Db 1 CCTCTGTCTGCTTTGAA 19

## RESULT 458

US-11-083-784-491143  
; Sequence 491143, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491143  
; LENGTH: 19

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491143

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1473 TGACTGCTCTCCCTCATG 1491  
Db 1 TGACTGCTCTCCCTCATG 19

## RESULT 459

US-11-083-784-491144  
; Sequence 491144, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491144  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491144

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 47.4%; Pred. No. 4.6e+02;  
Matches 9; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1600 TCAATCTTCCCTATCTTT 1618  
Db 1 TCAATCTTCCCTATCTTT 19

## RESULT 460

US-11-083-784-491145  
; Sequence 491145, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 491145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491145

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      576 CATGACGCGCTGTGCGCCTT 594
      |||:|||||:|||||:|
Db      1 CAUGACGCGCTUGGCGCTUU 19

RESULT 461
US-11-083-784-491146
; Sequence 491146, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491146
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491146

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      395 GAATGACGACACTGACGAA 413
      |||:|||||:|||||:|
Db      1 GAATGACGACAGUGACGAA 19

RESULT 462
US-11-083-784-491147
; Sequence 491147, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491147
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491147

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      375 GATCATCTTAGCCGACAA 393
      |||:|||||:|||||:|
Db      1 GAUCAUCUUGCCGACCAA 19

RESULT 463
US-11-083-784-491148
; Sequence 491148, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491148
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491148

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1641 CAATCAATCTACTGAACT 1659
      |||:|||||:|||||:|
Db      1 CAATCAATCTACTGAACT 1659

RESULT 464
US-11-083-784-491149
; Sequence 491149, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
```

```

; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491149

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      447 CTCGATGGCTGCATTCAT 465
Db      1 CUCCAGGCGGCAUCCAU 19

```

```

RESULT 465
US-11-083-784-491150
; Sequence 491150, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491150

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      1742 GCAGCGAGTGTCTCTTTC 1760
Db      1 GCAUGCGAGGCUCAUUC 19

```

```

RESULT 466
US-11-083-784-491151
; Sequence 491151, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

```

```

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491151
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491151

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY      1415 CCTGCAATGCTCTCTCTA 1433
Db      1 CCUCCAUUGGCUCCUCA 19

```

```

RESULT 467
US-11-083-784-491152
; Sequence 491152, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491152
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491152

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY      1598 TCTCATTTCTTCTCTATCT 1616
Db      1 UCUCAUUCUUCUCCUUCU 19

```

```

RESULT 468
US-11-083-784-491153
; Sequence 491153, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```



```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134950S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491153
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491153

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1242 CCAGGCGCATGTGTACAA 1260
Db      1 CCAGGCGCATGTGTACAA 19

RESULT 469
US-11-083-784-491154
; Sequence 491154, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491154
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491154

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1031 ACCCAGTCTCTACCTGAA 1049
Db      1 ACCCAGTCTCTACCTGAA 19

RESULT 470
US-11-083-784-491155
; Sequence 491155, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491155
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491155

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GAGGCGCATGTTCAGCTTTC 73
Db      1 GAGGCGCATGTTCAGCTTTC 19

RESULT 471
US-11-083-784-491156
; Sequence 491156, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491156
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491156

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      356 GCAACGTGTGTAGTGTG 374
Db      1 GCAACGTGTGTAGTGTG 19

RESULT 472
US-11-083-784-491157
; Sequence 491157, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491157
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491157

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

QY 266 CCTCGAACCACCAATCAGT 284

Db 1 CCUCGAAACCCCAUCAGU 19

```

RESULT 473
US-11-083-784-491158
; Sequence 491158, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491158
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491158

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

QY 1699 CTCAGAGCCCAATGCAT 1717

Db 1 CUCAGAGCCCAUCAGU 19

RESULT 474

```

US-11-083-784-491159
; Sequence 491159, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491159

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

QY 1570 GAAACATTCCATCTTGA 1588

Db 1 GAAAGACUCCCAUCUUA 19

```

RESULT 475
US-11-083-784-491160
; Sequence 491160, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491160
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491160

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

QY 1376 GAAGTACTCCAGACCAT 1394

Db 1 GAAAGACUCCCAAGACAU 19

```
RESULT 476
US-11-083-784-491161
; Sequence 491161, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491161
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491161

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      35 TCCGAGACGTTTATTC 53
Db      1 UCCAGAGCGGUUAUUC 19

RESULT 477
US-11-083-784-491162
; Sequence 491162, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491162

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      102 CCACCTCTCTCTCTTT 120
Db      1 CCACCCCTCCGCGCUU 19

RESULT 478
US-11-083-784-491163
; Sequence 491163, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491163
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491163

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      764 CAGAGCATCCGACACAGAT 782
Db      1 CAGAGCAUCCGACACAGAU 19

RESULT 479
US-11-083-784-491164
; Sequence 491164, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491164
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491164

Query Match      1.1%; Score 19; DB 1; Length 19;
```



```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491168

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      737 GCAGAGTCGTGTCATGAT 755
Db      1 GCAGAGTCGTGTCATGAT 19

RESULT 484
US-11-083-784-491169
; Sequence 491169, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491169

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1660 TTGCTGAGCCTGTAAATA 1678
Db      1 UUGCUGAGCCUGUAAAUA 19

RESULT 485
US-11-083-784-491170
; Sequence 491170, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
```

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491170
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491170

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATCATCTGA 1656
Db      1 ACUCCAACCAATCATCTGA 19

RESULT 486
US-11-083-784-491171
; Sequence 491171, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491171

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      1596 AATCTCAATTCCTCCAT 1614
Db      1 AAUCUCAUUCUCCUUAU 19

RESULT 487
US-11-083-784-491172
; Sequence 491172, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2002-11-14
```

```
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491172
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491172
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 941 GCAAGGTGTCGCAAAATGAT 959
Db 1 GCAAGGUGGUCAAAAGAU 19
```

```
RESULT 488
US-11-083-784-491173
/ Sequence 491173, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491173
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491173
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 245 CCCCAACATCTCCACTAA 263
Db 1 CCCGAAACATCUCGACUAA 19
```

```
RESULT 489
US-11-083-784-491174
/ Sequence 491174, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
```

```
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491174
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491174
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 109 CCTGCTGCTTTAGAAAGA 127
Db 1 CCUGUCUGCUUAGAAAGA 19
```

```
RESULT 490
US-11-083-784-491175
/ Sequence 491175, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491175
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491175
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 32 GCATCAGAGCGTTTATA 50
Db 1 GCAUCGAGAGCGUUAUA 19
```

```
RESULT 491
US-11-083-784-491176
/ Sequence 491176, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

APPLICANT: Reynolds, Angelita

GENERAL INFORMATION:

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491180
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491180

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1360 TCCAACTGCTCTTTCACGAA 1378
      :||||:|:|:|:|:|:|
Db      1 UCCAAUCUCUCUCCACGAA 19

RESULT 496
US-11-083-784-491181
; Sequence 491181, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491181

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491182
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491182

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGTCATCTGTCTCA 670
      ||||:|:|:|:|:|:|
Db      1 AAAGUGUCAUCUGUGUCA 19

RESULT 498
US-11-083-784-491183
; Sequence 491183, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491183
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-491183

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      354 GGGCAAGTGTAGTAGTG 372
      |||||:|:|:|:|:|:|
Db      1 GGGCAAGCUGUGUAGUGAUG 19

RESULT 497
US-11-083-784-491182
; Sequence 491182, Application US/11083784
```



RESULT 499  
US-11-083-784-491184  
Sequence 491184, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491184  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491184

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 4.6e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATCAGAAACACCTCACA 1535  
Db 1 CAUCAGAAACACCCUCACA 19

RESULT 500  
US-11-083-784-491185  
Sequence 491185, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491185  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491185

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1026 CATCAACCCAGATCTTAC 1044  
||:|||||||:|:|:|

Db 1 CAUCAACCCAGATCTTAC 19

RESULT 501  
US-11-083-784-491186  
Sequence 491186, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491186  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491186

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 4.6e+02;  
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 806 GTGACTGTGCTGATCTA 824  
||:||||:|:|:|

Db 1 GUGGACUGGUGAUCUA 19

RESULT 502  
US-11-083-784-491187  
Sequence 491187, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491187  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491187

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

QY      1620 CCACCTCATGCTGTGTA 1638
          |||||:|:|:|:|:|
Db      1 CCACCTCAUGCTUGUGA 19

```

```

RESULT 503
US-11-083-784-491188
/ Sequence 491188, Application US/11083764
/ Publication No. US20050245475X1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khavrova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491188
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491188

```

[illegible]

```

RESULT 504
US-11-083-784-491189
? Sequence 491189, Application US/11083784
? Publication No. US20050245475A1
? GENERAL INFORMATION:
? APPLICANT: Dharmacon, Inc.
? APPLICANT: Khvorova, Anastasia
? APPLICANT: Reynolds, Angela
? APPLICANT: Leake, Devin
? APPLICANT: Marshall, William
? APPLICANT: Scaringe, Stephen
? TITLE OF INVENTION: Functional and Hyperfunctional siRNA
? FILE REFERENCE: 134990S
? CURRENT APPLICATION NUMBER: US/11/083,784
? PRIOR FILING DATE: 2005-03-18
? PRIOR APPLICATION NUMBER: US/10/714,333
? PRIOR FILING DATE: 2003-11-14
? PRIOR APPLICATION NUMBER: 60/502,050
? PRIOR FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 60/426,137
? PRIOR FILING DATE: 2002-11-14
? NUMBER OF SEQ ID NOS: 1591911
? SOFTWARE: Proprietary
? SEQ ID NO 491189
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Homo sapiens
US-11-083-784-491189

```

Query Match	1.1%	Score 19;	DB 1;	Length 19;
Best Local Similarity	94.7%	Pred. No. 4.6e+02;		
Matches	18;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	763	CGAGGCAATCCGAACACAGA	781	
DB	1	CGAGGCAATCCGAACACAGA	19	

```

RESULT 505
US-11-083-784-491190
/ Sequence 491190, Application US/11083784
/ Publication No. US20050245475M1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491190
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491190

```

Query Match	1.1%	Score 19	DB 1	Length 19
Best Local Similarity	68.4%	Pred. No. 4.6e+02		
Matches 13	Conservative 6	Mismatches 0	Indels 0	Gaps 0
QY	503	GGTACTACGCGCTGTCTA	521	
Db	1	GGTACTACGCGCTGTCUA	19	

```

US-11-083-784-491191
/ Sequence 491191, Application US/11083784
/ Publication NO. US2005024575A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIORITY FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491191
/ LENGTH: 19
/ TYPE: RNA
/

```

ORGANISM: Homo sapiens  
US-11-083-784-491191

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1215 AATGAATCCACCCCGTAT 1233  
DB 1 AAGGAAUCCACCCGGAU 19

RESULT 507  
US-11-083-784-491192

Sequence 491192, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491192  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491192

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 196 ACCGCTAGCTTGAATG 214  
DB 1 ACGCCUAGCUCGAAUUG 19

RESULT 508  
US-11-083-784-491193

Sequence 491193, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary

SEQ ID NO 491193  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491193

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 772 CCGACACAGATTATGAGA 790  
DB 1 CCGACACAGAUUUAUGGA 19

RESULT 509  
US-11-083-784-491194

Sequence 491194, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491194  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491194

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 4.6e+02;  
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 332 TCATTGCTGACTCTGT 350  
DB 1 UCAUUGUGUGACCUUGU 19

RESULT 510  
US-11-083-784-491195

Sequence 491195, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137

```

; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491195

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      33 CATCCAGAGCGTTATAT 51
Db      1 CAUCCAGAGCGUUUAUU 19

RESULT 511
US-11-083-784-491196
; Sequence 491196, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491196
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491196

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1631 CTGTGTGACTCAACCAAA 1649
Db      1 CTGUGUACUCAAACCAAA 19

RESULT 512
US-11-083-784-491197
; Sequence 491197, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491197

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1036 GATCTTACTGAGAGAGT 1054
Db      1 GATCUCUACCUAGAGAGU 19

RESULT 513
US-11-083-784-491198
; Sequence 491198, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491198

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      991 TGCTGCTTCCACATCT 1009
Db      1 UGGCTGCCUCCACACU 19

RESULT 514
US-11-083-784-491199
; Sequence 491199, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```

; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491199
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491199
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      769 CATCGAACAAGATTATG 787
Db      1 CAUCCGAACAGAUUUAUG 19
```

```
RESULT 515
US-11-083-784-491200
; Sequence 491200, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491200
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      753 GATCGAATGCCGACGACAT 771
Db      1 GAUCCGAUGGCCAGACCAU 19
```

```
RESULT 516
US-11-083-784-491201
; Sequence 491201, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491201
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491201
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      550 GCCGCTGCTTCGCCAGTA 568
Db      1 GCCGCTGCTTCGCCAGTA 19
```

```
RESULT 517
US-11-083-784-491202
; Sequence 491202, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491202
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      480 CACCTATGCTGTCCACAC 498
Db      1 CACCTAUGCTGCCACAC 19
```

```
RESULT 518
US-11-083-784-491203
; Sequence 491203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491203

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 479 TCACCTATGCTGTCACAA 497
Db 1 UCACCUAUGCUGUCCACAA 19

```

```

RESULT 519
US-11-083-784-491204
; Sequence 491204, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491204
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491204

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1384 TCACAAGCCATCAGACAGA 1402
Db 1 UCACAAGACCAGACAGAGA 19

```

```

RESULT 520
US-11-083-784-491205
; Sequence 491205, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491205
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491205

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1218 GAAATCCACCCGGATCTC 1236
Db 1 GAAAUCCACCCGGUAVUCC 19

```

```

RESULT 521
US-11-083-784-491206
; Sequence 491206, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491206

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1119 CATCTACTGCTGCTCAAT 1137
Db 1 CAUCUACUGCUGCCUCAAU 19

```

```

RESULT 522
US-11-083-784-491207

```

```
; Sequence 491207, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491207
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491207
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

Oy 504 GTACTACGGCTGTTCTNC 522

Db 1 GUACUACGGCCUCUCUAC 19

```
RESULT 523
US-11-083-784-491208
; Sequence 491208, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491208
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1601 CAATTCTTCCCTATCTTG 1619

Db 1 CAATUCUCCUACUUCUUG 19

```
RESULT 524
US-11-083-784-491209
; Sequence 491209, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491209
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491209
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

Oy 233 ACTCAGACTCTCCCAAA 251

Db 1 ACUCAGACUCUCCCAAA 19

```
RESULT 525
US-11-083-784-491210
; Sequence 491210, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491210
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491210
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

Oy 1747 CGAGTCTCATTTACAGAT 1765

Db 1 CGAGUGCUCAUUUCAGAAU 19

RESULT 526

US-11-083-784-491211  
; Sequence 491211, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491211  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491211

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1687 GACGACGCTTTCCTCAAGA 1705  
Db 1 GACGAGCUUUCUCCUACA 19

RESULT 527

US-11-083-784-491212  
; Sequence 491212, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491212  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491212

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1642 AAACCAATCTACTGAACCTT 1660  
Db 1 AAACCAATCTACTGAACCU 19

RESULT 528

US-11-083-784-491213  
; Sequence 491213, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491213  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491213

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1519 TCAGAAACACCTCTCAACT 1537  
Db 1 UCAGAAACACCCUCCACACU 19

RESULT 529

US-11-083-784-491214  
; Sequence 491214, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491214  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491214



Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
 Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 840 GGTGATGCTGATGCTAC 858  
 Db 1 GGUGAUGGCUAUGCAUAC 19

RESULT 530

US-11-083-784-491215  
 ; Sequence 491215, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 491215  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-491215

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 203 GCTTGAATGATGATGCT 221  
 Db 1 GCUUCGAAUGAUGAUAACGU 19

RESULT 531

US-11-083-784-491216  
 ; Sequence 491216, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 491216  
 ; LENGTH: 19

TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-083-784-491216

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
 Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy 543 TCCCATGCCGCGCTGCTTC 561  
 Db 1 UCCCAUCGCCGCGCUGUCUC 19

RESULT 532

US-11-083-784-491217  
 ; Sequence 491217, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 491217  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-083-784-491217

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
 Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 492 CCACACGAATGATGCTAC 510  
 Db 1 CCACACGAATGATGCTAC 19

RESULT 533

US-11-083-784-491218  
 ; Sequence 491218, Application US/11083784  
 ; Publication No. US20050245475A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911

```
; SOFTWARE: Proprietary
; SEQ ID NO 491218
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491218
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAGT 1292
          |||||:|||||:
Db       1 AGACCACCAUCUCCACAGU 19
```

```
RESULT 534
US-11-083-784-491219
```

```
; Sequence 491219, Application US/11083784
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 491219
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-491219
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      401 GGACAGTGCAGACTATT 419
          |||||:|||||:
Db       1 GGACAGUGAGCACTAUUU 19
```

```
RESULT 535
```

```
US-11-083-784-491220
```

```
; Sequence 491220, Application US/11083784
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491220
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491220
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      247 CCAAAGATCTCCACTACA 265
          |||||:|||||:
Db       1 CCAACACUCCACACUACA 19
```

```
RESULT 536
```

```
US-11-083-784-491221
```

```
; Sequence 491221, Application US/11083784
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

```
; PRIOR FILING DATE: 2003-11-14
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
```

```
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 491221
```

```
; LENGTH: 19
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-11-083-784-491221
```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      773 CGACCAAGATTATGAGA 791
          |||||:|||||:
Db       1 CGACCAAGAUUUAUGAGA 19
```

```
RESULT 537
```

```
US-11-083-784-491224
```

```
; Sequence 491224, Application US/11083784
; Publication No. US20050245475A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
```

;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO: 491224  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491224

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 789 GAAAGTGATCCATCTGT 807  
Db 1 GAAAGUGUACCAUCUCU 19

RESULT 538  
US-11-083-784-491225  
;; Sequence 491225, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; PRIOR FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO: 491225  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491225

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 4.6e+02;  
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 809 TGACTGCTACTACTT 827  
Db 1 UGACUGUGUCUACUCU 19

RESULT 539  
US-11-083-784-491226  
;; Sequence 491226, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US

;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO: 491226  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491226

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1033 CCAGATCTTACTGAAGA 1051  
Db 1 CCAGUUCUCUACUGAAGA 19

RESULT 540  
US-11-083-784-491227  
;; Sequence 491227, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; PRIOR FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO: 491227  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491227

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 650 CCAAGTGCTACTGTGT 668  
Db 1 CCAAGUGUCUACUCUGU 19

RESULT 541  
US-11-083-784-491229  
;; Sequence 491229, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William

```

/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491229
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491229

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      461 TCATATACAGTGTGTAAGCTT 479
      :|||:|||||:|||||:|
Db      1 UCAATUACAGUGGUGAACUU 19

```

```

RESULT 542
US-11-083-784-491231
/ Sequence 491231, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491231
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491231

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      600 GTACATGGCCATCATACAT 618
      :|||:|||||:|||||:|
Db      1 GUACATUGGCCAUCACUACAU 19

```

```

RESULT 543
US-11-083-784-491232
/ Sequence 491232, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia

```

```

/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491232
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491232

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      398 TGAGGACAGTGAGCAACTA 416
      :|||||:|||||:|
Db      1 UGAGGACAGUGACGACACUA 19

```

```

RESULT 544
US-11-083-784-491233
/ Sequence 491233, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmoon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491233
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491233

```

```

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      787 GAGAAAGTGTACACACTCT 805
      :|||||:|||||:|
Db      1 GAGAAAGTGTACACACTCT 19

```

```

RESULT 545
US-11-083-784-491234
/ Sequence 491234, Application US/11083784
/ Publication No. US20050245475A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491234

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Cy      777 CAAGATTTCAGGAAGTG 795
Db      1 CAAGAUUUUAGGAAGUG 19

RESULT 547
```

```

US-11-083-784-491237
; Sequence 491237, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491238

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      761 GGCAGAGCATCCGAACA 779
Db      1 GGCACAGCAUCCGAACA 19

RESULT 548
US-11-083-784-491238
; Sequence 491238, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491236

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Cy      777 CAAGATTTCAGGAAGTG 795
Db      1 CAAGAUUUUAGGAAGUG 19

RESULT 547
```

```

RESULT 549
US-11-083-784-491241
; Sequence 491241, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491241

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      576 CATGACGGCTGTGGCCTTT 594
      ||:|||||:|||||:
Db      1 CAUGACGGCTUGGCGCCUUD 19

```

```

RESULT 550
US-11-083-784-491244
; Sequence 491244, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491244
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491244

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      395 GAATGAGGACGTGACGAA 413
      ||:|||||:|||||:
Db      1 GAUGAGGACAGUGACGAA 19

```

```

RESULT 551
US-11-083-784-491245
; Sequence 491245, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491245

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      375 GATCATCTTAGCCACGAAA 393
      ||:|||||:|||||:
Db      1 GAUCATCTTAGCCACGAAA 19

```

```

RESULT 552
US-11-083-784-491248
; Sequence 491248, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491248

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;

```

Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 447 CTCGATGGCTGATCAAT 465  
Db 1 CUCCAGGCGUCGACUACAU 19

RESULT 553

US-11-083-784-491251

; Sequence 491251, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491251  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491251

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1031 ACCGAGTCTCTACTGGA 1049  
Db 1 ACCGAGUUCUACUACUGA 19

RESULT 554

US-11-083-784-491252

; Sequence 491252, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491252  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-11-083-784-491252

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 356 GCAAGCGGTAGTATGTCG 374  
Db 1 GCAAGCGUGUGACUACUG 19

RESULT 555

US-11-083-784-491256

; Sequence 491256, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491256  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491256

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 266 CTCGGAACCAATCACTT 284  
Db 1 CCUCGGAACCAACUACU 19

RESULT 556

US-11-083-784-491262

; Sequence 491262, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491262

LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491262

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 4.6e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 764 CAGAGATCCGACACAGAT 782  
DB 1 CAGAGCAUCCGACACAGAU 19

RESULT 557  
US-11-083-784-491263  
Sequence 491263, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491263  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491263

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 841 GTGATTGGCTATGCATACA 859  
DB 1 GTGATUGGCTATGCATACA 19

RESULT 558  
US-11-083-784-491264  
Sequence 491264, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491264  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491264

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 737 GCAGAGTGTGTGCATGAT 755  
DB 1 GCAGAGUCGUGGCAUGAU 19

RESULT 559  
US-11-083-784-491265  
Sequence 491265, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491265  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-491265

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCCCAACATCTCCACTAA 263  
DB 1 CCCCAACAUCCCAACUAA 19

RESULT 560  
US-11-083-784-491268  
Sequence 491268, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050



```
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491268
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491268
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      941 GCAAGTGCTGCAAAATGAT 959
Db      1 GCAAGUGUGUCAAAAUAGAU 19
```

```
RESULT 561
US-11-083-784-491269
; Sequence 491269, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491269
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      261 TAACACCTCGAACCCCAAT 279
Db      1 UAACACCTCCGAACCCCAAU 19
```

```
RESULT 562
US-11-083-784-491270
; Sequence 491270, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO: 491270
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-491270
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      583 GCTGTGGCTTGTGATAGT 601
Db      1 GCTUGGCGCCUUGAUGAU 19
```

```
RESULT 563
US-11-083-784-491271
; Sequence 491271, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 491271
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491271
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      482 CTTATGCTGTCCACAACGA 500
Db      1 CCUUGUGUGCCACAACGA 19
```

```
RESULT 564
US-11-083-784-491272
; Sequence 491272, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491272

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      786 TGAGAAAGTGTACCAATC 804
      :|||||:|:|||||:|
      1 UGAGAAAGUGAACCAATC 19

```

```

RESULT 565
US-11-083-784-491273
; Sequence 491273, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491273
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491273

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      652 AAAGTGTATCTGTCTCA 670
      |||||:|:|||||:|
      1 AAAGUGUUAUUCUGUGUCA 19

```

```

RESULT 566
US-11-083-784-491274
; Sequence 491274, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491274
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491274

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      354 GGGCAACGTGTGTATGATG 372
      |||||||:|:|||||:|
      1 GGGCAACGTGTGTATGATG 19

```

```

RESULT 567
US-11-083-784-491275
; Sequence 491275, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491275

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1026 CATCAACCCAGATCTCTAC 1044
      ||:|||||:|:|||||:|
      1 CAUCAAACCAAGAUUCUCUAC 19

```

```

RESULT 568
US-11-083-784-491276
; Sequence 491276, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.

```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491276

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 806 GTGTACTGTGCTGATCTA 824
DB 1 GUGUGACUGUGUCGACUUA 19

RESULT 569
US-11-083-784-491278
; Sequence 491278, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491278

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 763 CCAGAGCATCCGACACAGA 781
DB 1 CCAGAGCATCCGACACAGA 19

RESULT 570
US-11-083-784-491279
; Sequence 491279, Application US/11083784

```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491279

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 503 GGTACTACGGGCGCTTCTA 521
DB 1 GGUACUACGGCGCUCGUUUA 19

RESULT 571
US-11-083-784-491280
; Sequence 491280, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491280

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 332 TCATTGTGTGACTCTCT 350
DB 1 UCAUUGUGUGACCUUUA 19

```

```
RESULT 572
US-11-083-784-491281
; Sequence 491281, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491281
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491281
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      772 CCGAACAGATTATGAGA 790
          |||||:::|||||
Db      1 CCGAACAGAUUUNUGAGA 19

RESULT 573
US-11-083-784-491282
; Sequence 491282, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491282
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491282
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      1 GAUUCUACCUAGAGAGU 19
```

```
RESULT 574
US-11-083-784-491283
; Sequence 491283, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491283
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491283
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      991 TGGCTGCCCTTCACATCT 1009
          :|||:|||||:
Db      1 UGGCTGCCCUCCACACU 19

RESULT 575
US-11-083-784-491284
; Sequence 491284, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491284
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

QY 769 CATCCGAACAGATTATG 787  
|||:|||||:|:  
Db 1 CACCGAAGCAGAUUUAUG 19

## RESULT 576

US-11-083-784-491285  
; Sequence 491285, Application US//11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US//11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US//10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491285  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491285

Query Match  
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 753 GATCGAATGGCCAGACAT 771  
|||:|||||:|:  
Db 1 GAUCGAUUGCCAGAGCAU 19

RESULT 577  
US-11-083-784-491286  
; Sequence 491286, Application US//11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US//11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US//10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491286  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491286

Query Match  
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 550 GCCGCTGTTCGCCAGTA 568  
|||:|||||:|:  
Db 1 GCCCGUCUCUCCGCAUA 19

## RESULT 578

US-11-083-784-491287  
; Sequence 491287, Application US//11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US//11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US//10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491287  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-491287

Query Match  
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 480 CACCTATGCTTCACAC 498  
|||:|||||:|:  
Db 1 CACCUAUGCUGCCACAC 19

RESULT 579  
US-11-083-784-491288  
; Sequence 491288, Application US//11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US//11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US//10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491288  
; LENGTH: 19  
; TYPE: RNA

```
/ ORGANISM: Homo sapiens
US-11-083-784-491288
Query Match
  Query Local Similarity 1.1%; Score 19; DB 1; Length 19;
  Best Local Similarity 73.7%; Pred. No. 4.6e+02;
  Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 479 TCACCTATGCTGTCCACAA 497
   :|||:|||||:|||||:
Db 1 UCACCUAUGCUCGUCCACAA 19

RESULT 580
US-11-083-784-491291
/ Sequence 491291, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491291
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491291
Query Match
  Query Local Similarity 1.1%; Score 19; DB 1; Length 19;
  Best Local Similarity 68.4%; Pred. No. 4.6e+02;
  Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1119 CATCTACTGCTGCTCAAT 1137
   ||:|||||:|||||:
Db 1 CAUCUACUGUCGUCCUCAU 19

RESULT 581
US-11-083-784-491292
/ Sequence 491292, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
```

```
/ SEQ ID NO 491292
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491292
Query Match
  Query Local Similarity 1.1%; Score 19; DB 1; Length 19;
  Best Local Similarity 68.4%; Pred. No. 4.6e+02;
  Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 504 GTACTACGCGCTGTCTTAC 522
   ||:|||||:|||||:
Db 1 GUACUACGCGCUCGUCCUCA 19

RESULT 582
US-11-083-784-491294
/ Sequence 491294, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491294
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491294
Query Match
  Query Local Similarity 1.1%; Score 19; DB 1; Length 19;
  Best Local Similarity 84.2%; Pred. No. 4.6e+02;
  Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 233 ACTGAGACCTCTCCCAAA 251
   ||:|||||:|||||:
Db 1 ACUCAGACCUCCUCCCAAA 19

RESULT 583
US-11-083-784-491296
/ Sequence 491296, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
```

;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491296  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491296

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 840 GGTATTGGCTATGCTATC 858  
DB 1 GGUGAUGGCUAUGCAUAC 19

RESULT 584

US-11-083-784-491297  
; Sequence 491297, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 134990S  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491297  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491297

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 492 CCACACGATGTGCTATC 510  
DB 1 CCACACGACGAUGGUAUCUAC 19

RESULT 585

US-11-083-784-491298  
; Sequence 491298, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 134990S  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14

;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491298  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-491298

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 203 GCTTCGAATGATATACGT 221  
DB 1 GCUCGAAUGAUGAUAACGU 19

RESULT 586

US-11-101-244-491124  
; Sequence 491124, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 134990S  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; CURRENT FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491124  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-491124

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 401 GGACAGTACGACACTATTT 419  
DB 1 GGACAGGACGACGACUACUUV 19

RESULT 587

US-11-101-244-491125  
; Sequence 491125, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 134990S  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; CURRENT FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491125
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491125

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1655 GAACTTGTCTGAGCCTGTA 1673
Db 1 GAACUUGCUGAGCCUGUA 19

```

```

RESULT 588
US-11-101-244-491126
; Sequence 491126, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491126

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 247 CCAACATCTCCACTACA 265
Db 1 CCAACATCTCCACTACA 19

```

```

RESULT 589
US-11-101-244-491127
; Sequence 491127, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491127
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491127

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 773 CGAACAGATTATGAGAA 791
Db 1 CGAACAGATTATGAGAA 19

```

```

RESULT 590
US-11-101-244-491128
; Sequence 491128, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491128
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491128

```

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 76 AAAGAGTCTGCCATAA 94
Db 1 AAAGAGTCTGCCATAA 19

```

```

RESULT 591
US-11-101-244-491129
; Sequence 491129, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137

```



```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491129
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 789 GAAGGTGACCACTGCTGT 807
DB 1 GAAGUGUACCAUCUGU 19
```

## RESULT 592

```
US-11-101-244-491130
; Sequence 491130, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491130
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491130
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 178 GTACAGTACTAGGCTTTA 196
DB 1 GUACAGAGUGAGGCUUUA 19
```

## RESULT 593

```
US-11-101-244-491131
; Sequence 491131, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491131
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491131
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 809 TGACTGCTGATCTACTT 827
DB 1 UGACUGUCUGAUCUACU 19
```

## RESULT 594

```
US-11-101-244-491132
; Sequence 491132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491132
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1033 CCAGATCTTACCTGAGAA 1051
DB 1 CGAGUCUCUACCTGAGAA 19
```

## RESULT 595

```
US-11-101-244-491133
; Sequence 491133, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 491133
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491133

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      650 CCAAGTGTCTATCTGTGT 668
Db      1 CCAAGTGTCTATCTGTGT 19

RESULT 596
US-11-101-244-491134
; Sequence 491134, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491134
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491134

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      461 TCAATACAGTGTGAACCT 479
Db      1 UCAADACAGUGGUAACU 19

RESULT 597
US-11-101-244-491135
; Sequence 491135, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 491135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491135

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      600 GTACATGCCATCATACAT 618
Db      1 GUAACAGGCCAUAACAU 19

RESULT 598
US-11-101-244-491136
; Sequence 491136, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491136
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491136

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      398 TGAGCAGTGCAGCACTA 416
Db      1 UGAGCAGTGCAGCACTA 19

RESULT 599
US-11-101-244-491137
; Sequence 491137, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491137
```

LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491137

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 787 GAGAAAGTGATCCACATCT 805  
Db 1 GAGAAAGTGATCCACATCT 19

RESULT 600  
US-11-101-244-491138  
Sequence 491138, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491138  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491138

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 578 TGACGGCTGTGCGCTTTGA 596  
Db 1 TGACGGCTGTGCGCTTTGA 19

RESULT 601  
US-11-101-244-491139  
Sequence 491139, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491139  
LENGTH: 19

TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491139

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 777 CAAGATTATGAGAAAGTG 795  
Db 1 CAAGATTATGAGAAAGTG 19

RESULT 602  
US-11-101-244-491140  
Sequence 491140, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491140  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491140

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 766 GAGCATCCGAAACAAGATT 784  
Db 1 GAGCATCCGAAACAAGATT 19

RESULT 603  
US-11-101-244-491141  
Sequence 491141, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 491141  
LENGTH: 19  
TYPE: RNA

```
; ORGANISM: Homo sapiens
US-11-101-244-491141
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      761 GGGCAGAGCATCCGACAA 779
Db      1 GGGCAGAGCAUCCGACAA 19

RESULT 604
US-11-101-244-491142
; Sequence 491142, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491142
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491142

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      106 CCTCTGTCTGCTTAGAA 124
Db      1 CCUCUCUCUCUUGAGAA 19

RESULT 605
US-11-101-244-491143
; Sequence 491143, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-491143
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1473 TGACCTGCCTCCCTTCATG 1491
Db      1 UGACCCUGCCUCCUUCUUG 19

RESULT 606
US-11-101-244-491144
; Sequence 491144, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491144
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491144

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 4.6e+02;
Matches 9; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY      1600 TCAATTCCTCCCTATCTT 1618
Db      1 UCAUUCUUCUCCUUCUUCU 19

RESULT 607
US-11-101-244-491145
; Sequence 491145, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491145
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491145
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 576 CATGACGGCTGTGGCTTT 594  
||:|||||:|:|||||:  
Db 1 CAUGACGGCTUGGCTTUU 19

## RESULT 608

US-11-101-244-491146  
; Sequence 491146, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491146  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491146

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 4.6e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 395 GAATGAGACAGTACGAA 413  
||:|||||:|:|||||:  
Db 1 GAATGAGACAGTACGAA 19

## RESULT 609

US-11-101-244-491147  
; Sequence 491147, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491147  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491147

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GATCATCTTAGCCACAAA 393  
||:|||||:|:|||||:  
Db 1 GAUCAUCUAGCCACAAA 19

## RESULT 610

US-11-101-244-491148  
; Sequence 491148, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491148  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491148

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CAAACCAATCACTGA 1659  
||:|||||:|:|||||:  
Db 1 CAAACCAATCACTGA 19

## RESULT 611

US-11-101-244-491149  
; Sequence 491149, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491149  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491149

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity	68.4%	Pred. No. 4.6e+02	
Matches	13	Conservative	6
		Mismatches	0
		Indels	0
		Gaps	0
QY	447	CTCCATGGCTGCATTCAT	465
		: : : : : : : : : :	
Db	1	CUCCAUGGCTGCATTCAT	19

```

RESULT 612
US-11-101-244-491150
; Sequence 491150, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491150

```

```

RESULT 613
US-11-101-244-491151
; Sequence 491151, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491151
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491151

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;

```

	Matches	13;	Conservative	6;	Mismatches	0;	Indels	0;	Gaps	0;
OY		1415	CCTCCAAATGTCCTCTCCTA		1433					
			:    : : : : : :							
Db		1	CTUCCAAAGUGUCUCUCCUA		19					

```

RESULT 614
US-11-101-244-491152
; Sequence 491152, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491152
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491152

```

```

RESULT 615
US-11-101-244-491153
; Sequence 491153, Application US/11101244
; Publication No. US2005024679A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ. ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ. ID NO 491153
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491153

Query Match      1.3%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Indels 0; Gaps 0

```

Oy 1242 CCAGGCGAGTGTACAA 1260  
Db 1 CCAGGCGAGUGGUAACAA 19

## RESULT 616

US-11-101-244-491154  
; Sequence 491154, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491154  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491154

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1031 ACCGAGTCTTACTGAA 1049  
Db 1 ACCGAGUCUCUACCTGAA 19

## RESULT 617

US-11-101-244-491155  
; Sequence 491155, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491155  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491155

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 55 GAGCGCAGTTCAGCTTC 73  
Db 1 GAGCGCAGUGGUAACUUC 19

## RESULT 618

US-11-101-244-491156  
; Sequence 491156, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491156  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491156

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 356 GCAACGCGTAGCATGCTG 374  
Db 1 GCAACGUGGUAUGAUGUG 19

## RESULT 619

US-11-101-244-491157  
; Sequence 491157, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491157  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491157

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCUCGGAACCCCAUCCAGU 19

```
RESULT 620
US-11-101-244-491158
; Sequence 491158, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491158
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491158
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1699 CTCAGAGCCCATCTTGA 1717  
Db 1 CUCAGAGCCCAUCCAGU 19

```
RESULT 621
US-11-101-244-491159
; Sequence 491159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491159
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1570 GAAACATTCATCTTGA 1588  
Db 1 GAAACATTCATCTTGA 1588

Db 1 GAAACAUUCCAUCCUUGA 19

```
RESULT 622
US-11-101-244-491160
; Sequence 491160, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491160
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491160
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1376 GAAGTACTCCAGACCAT 1394  
Db 1 GAAGUAGUCCCAAGACCAU 19

```
RESULT 623
US-11-101-244-491161
; Sequence 491161, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491161
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491161
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 4.6e+02;  
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 35 TCACGAGCGTTATATTC 53  
Db 1 UCCAGAGCGUUAUUAUC 19



```
RESULT 624
US-11-101-244-491162
; Sequence 491162, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491162

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 102 CCACCTCTCTGTCGCTT 120
Db 1 CCACCCUCCUGUCUGCUU 19

RESULT 625
US-11-101-244-491163
; Sequence 491163, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491163
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491163

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 764 CAGAGCATCCGAAACAAGT 782
Db 1 CAGAGCAUCCGAAACAAGAU 19
```

```
RESULT 626
US-11-101-244-491164
; Sequence 491164, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491164
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491164

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1643 AACCAATCACTGAACCTT 1661
Db 1 AACCAAUCAUCGAAACUUU 19

RESULT 627
US-11-101-244-491165
; Sequence 491165, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491165
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491165

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1246 GGCAGTGTGTACAAAGTCA 1264
Db 1 GGCAGUGUGUACAAAGUCA 19
```

RESULT 628

```

US-11-101-244-491166
; Sequence 491166, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491166
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491166

```

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 68.4%; Pred. No. 4.6e+02;

Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 841 GTGATTGCTATGCATACA 859

Db 1 GUGAUGGCUAUGCAUCA 19

RESULT 629

```

US-11-101-244-491167
; Sequence 491167, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491167
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491167

```

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 78.9%; Pred. No. 4.6e+02;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1700 TCAAGAGCCCAATGCATTC 1718

Db 1 UCAAGAGCCCAATGCATTC 19

RESULT 630

US-11-101-244-491168

```

; Sequence 491168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491168

```

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 73.7%; Pred. No. 4.6e+02;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 737 GCAGAGTCGTGTCATGAT 755

Db 1 GCAGAGTCGTGTCATGAT 19

RESULT 631

```

US-11-101-244-491169
; Sequence 491169, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491169
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491169

```

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 68.4%; Pred. No. 4.6e+02;

Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1660 TTGCTGAGCCCTGTAAATA 1678

Db 1 TTGCTGAGCCCTGTAAATA 19

RESULT 632

US-11-101-244-491170

```

; Sequence 491170, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491170
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491170

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATCATCTGA 1656
Db      1 ACUCAACCAAUCACTGA 19

RESULT 633
US-11-101-244-491171
; Sequence 491171, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491171

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. NO. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      1596 AATCTCAATCTCTCCCTAT 1614
Db      1 AAUCUCAUUCUCCUCU 19

RESULT 634
US-11-101-244-491172
; Sequence 491172, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491172

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. NO. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      941 GCAAGTGTCGCAAAATGAT 959
Db      1 GCAAGUGUGUCAAAUUGAU 19

RESULT 635
US-11-101-244-491173
; Sequence 491173, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491173
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491173

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      245 CCCCAACATCTCCACTAA 263
Db      1 CCCCAACATCTCCACTAA 19

RESULT 636
US-11-101-244-491174
; Sequence 491174, Application US/11101244
; Publication No. US20050246794A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491174
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-491174

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      109 CCTGCTGCTTTAGACGA 127
Db      1 CCUGUCUCUUAGACGA 19

RESULT 637
US-11-101-244-491175
; Sequence 491175, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491175
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-491175

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491176
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-491176

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      583 GCTGTGCGCTTGATAGT 601
Db      1 GCUGUGGCUUUGAUGAGU 19
```

```
RESULT 639
US-11-101-244-491177
; Sequence 491177, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-11-101-244-491177

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      482 CCTATGCTGTCCACACGA 500
Db      1 CCUAVGCUUCCACACGA 19

RESULT 640
US-11-101-244-491178
; Sequence 491178, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491178
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 261 TAACACCTCGGAACCAAT 279
Db 1 UAACACCTCGGAACCAAU 19
```

```

RESULT 641
US-11-101-244-491179
; Sequence 491179, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491179
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1407 CAGCTCTCTCCCAATG 1425
Db 1 CAGCTCTCTCCCAUG 19
```

```

RESULT 642
US-11-101-244-491180
; Sequence 491180, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491180
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491180
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1360 TCCACCTGCTCTCAGAA 1378
Db 1 UCCACCTGCTCTCAGAA 19
```

```

RESULT 643
US-11-101-244-491181
; Sequence 491181, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491181
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 786 TGAGAAAGTGACACATC 804
Db 1 UGAGAAAGUGUACCAUCC 19
```

```

RESULT 644
US-11-101-244-491182
; Sequence 491182, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491182
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491182

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      652 AAAGTGTCTCTGTCTCA 670
Db      1 AAAGUGUCACUCUGUCA 19

```

```

RESULT 645
US-11-101-244-491183
; Sequence 491183, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491183
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491183

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      354 GGGCAACGTGTAGTAGT 372
Db      1 GGGCAACGTGTAGTAGT 19

```

```

RESULT 646
US-11-101-244-491184
; Sequence 491184, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491184

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1517 CATCAGAAACCCCTCACA 1535
Db      1 CATCAGAAACCCCTCACA 19

```

```

RESULT 647
US-11-101-244-491185
; Sequence 491185, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491185
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491185

```

```

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1026 CATCAACCCAGATCTCTAC 1044
Db      1 CATCAACCCAGATCTCTAC 19

```

```

RESULT 648
US-11-101-244-491186
; Sequence 491186, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491186
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491186

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      806 GTGTGACTGTGCTGATCTA 824
Db      1 GUGGACUGGUGCUGAUCUA 19

RESULT 649
US-11-101-244-491187
; Sequence 491187, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491187
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491187

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1620 CCACCTCATGCTGTGTGA 1638
Db      1 CCACCTCAGCUGCUGUGA 19

RESULT 650
US-11-101-244-491188
; Sequence 491188, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491188
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491188

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1572 AACATTCATCCTTGACT 1590
Db      1 AACATUCCAUCCUGAGU 19

RESULT 651
US-11-101-244-491189
; Sequence 491189, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491189
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491189

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      763 CCAGAGCATCGAACAAGA 781
Db      1 CCAGAGCAUCCGAACAAGA 19

RESULT 652
US-11-101-244-491190
; Sequence 491190, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491190

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      503 GGTACTACGGCCTGTCTA 521
Db      1 GGUACUACGCCCGUUCUA 19

RESULT 653
US-11-101-244-491191
; Sequence 491191, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491191
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491191

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1215 AATGAATCCACCGGTAT 1233
Db      1 AAUGAAUCCACCCGGUADU 19

RESULT 654
US-11-101-244-491192
; Sequence 491192, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491192
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491192

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      196 ACGCTAGCTTGAATG 214
Db      1 ACGCTAGCTUUGAUAUG 19

RESULT 655
US-11-101-244-491193
; Sequence 491193, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491193
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491193

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      772 CCGAACAGATTATGACA 790
Db      1 CCGAACAGAUUUAUGAGA 19

RESULT 656
US-11-101-244-491194
; Sequence 491194, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```



```

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491194
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491194
```

```

Query Match
Best Local Similarity 57.9%; Score 19; DB 1; Length 19;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      332 TCATTGTGTCGCTCTGT 350
Db      1 UCAGUGGUGGACCCUGU 19
```

```

RESULT 657
US-11-101-244-491195
; Sequence 491195, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491195
```

```

Query Match
Best Local Similarity 68.4%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      33 CATCCAGAGCGTTATAT 51
Db      1 CAUCGAGAGCGUUUAU 19
```

```

RESULT 658
US-11-101-244-491196
; Sequence 491196, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491196
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491196
```

```

Query Match
Best Local Similarity 78.9%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1631 CTGTGTGACTCAACAA 1649
Db      1 CUGUGGACUCGAAACCAA 19
```

```

RESULT 659
US-11-101-244-491197
; Sequence 491197, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491197
```

```

Query Match
Best Local Similarity 73.7%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1036 GATCTCTACTGAGAGT 1054
Db      1 GAUCUCUACCTGAGAGU 19
```

```

RESULT 660
US-11-101-244-491198
; Sequence 491198, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491198

Query Match
Best Local Similarity 68.4%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 991 TGGCTGCCCTTCCACATCT 1009
Db 1 UGGCUGCCCUCCACACUCU 19

RESULT 661
US-11-101-244-491199
; Sequence 491199, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491199
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491199

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 769 CATCCGACACAGATTATG 787
Db 1 CAUCCGACACAGAUUUUG 19

RESULT 662
US-11-101-244-491200
; Sequence 491200, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491200

Query Match
Best Local Similarity 84.2%; Score 19; DB 1; Length 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 753 GATCGAATGCCGACGACAT 771
Db 1 GAUCCGAUUGCCGACGACAU 19

RESULT 663
US-11-101-244-491201
; Sequence 491201, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491201
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491201

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 550 GCCGCTGCTTCGCCAGTA 568
Db 1 GCCGCTGCTTCGCCAGTA 19

RESULT 664
US-11-101-244-491202
; Sequence 491202, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491202  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-491202

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 480 CACCTATGCTGCCAAC 498  
Db 1 CACCUGCGUCCACAC 19

RESULT 665  
US-11-101-244-491203  
; Sequence 491203, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491203  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491203

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 479 TCACCTATGCTGCCAAC 497  
Db 1 UCACCGUCCGUCACCA 19

RESULT 666  
US-11-101-244-491204  
; Sequence 491204, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14

;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 491204  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-491204

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 4.6e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1384 TCACGACATGACAGAGA 1402  
Db 1 UCCAGACGAGACAGAGA 19

RESULT 667  
US-11-101-244-491205  
; Sequence 491205, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491205  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491205

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1218 GAATCCACCCGATATCTC 1236  
Db 1 GAATCCACCCGATATCTC 19

RESULT 668  
US-11-101-244-491206  
; Sequence 491206, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 491206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491206

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1119 CATCTACTGCTGCTCAT 1137
Db      1 CAUCUACUCGCGCCUCAU 19

RESULT 669
US-11-101-244-491207
; Sequence 491207, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491207
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491207

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      504 GTACTACGCGCTGTCTAC 522
Db      1 GUACTACGCGCTGUCUAC 19

RESULT 670
US-11-101-244-491208
; Sequence 491208, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

```

```

; SEQ ID NO 491208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491208

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1601 CAATCTCTCCCTATCTTGG 1619
Db      1 CAUUCUUCGCCUACUUCUUG 19

RESULT 671
US-11-101-244-491209
; Sequence 491209, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491209
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491209

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      233 ACTCAGACCTCTCCCCAAA 251
Db      1 ACTCAGACCTCTCCCCAAA 19

RESULT 672
US-11-101-244-491210
; Sequence 491210, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491210

```

```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491210

Query Match
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1747 CGAGTGCTCATTTGAGAT 1765
Db 1 CGAGTGCUCATUUCAGAU 19

RESULT 673
US-11-101-244-491211
; Sequence 491211, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491211
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491211

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1687 GACCAGCTTTCTCAAGA 1705
Db 1 GACCAGCUCUUCUCAAGA 19

RESULT 674
US-11-101-244-491212
; Sequence 491212, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491212
; LENGTH: 19
; TYPE: RNA
```

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491212

Query Match
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1642 AACCAATCAGTCACTT 1660
Db 1 AACCAAAUCCAGACCU 19

RESULT 675
US-11-101-244-491213
; Sequence 491213, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491213
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491213

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1519 TCAGAAACCTTCACACT 1537
Db 1 UCAGAAACACCCUCCACACU 19

RESULT 676
US-11-101-244-491214
; Sequence 491214, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491214
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
US-11-101-244-491214

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      840 GCGGATGCGCTATGCAATAC 858
DB      1 GGUAGUUGGCUAGCUAGUACU 19

RESULT 677
US-11-101-244-491215
; Sequence 491215, Application US//11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491215
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491215

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      203 GCTTCGAATGGATTAAGT 221
DB      1 GCUCGAAAGUAGUAAACGU 19

RESULT 678
US-11-101-244-491216
; Sequence 491216, Application US//11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491216
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-491216

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      543 TCCCATCGCCGCTGCTTC 561
DB      1 UCCCAUCCGCCGCGUCUUC 19

RESULT 679
US-11-101-244-491217
; Sequence 491217, Application US//11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491217
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491217

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      492 CCACACGAATGTAATCTAC 510
DB      1 CCACACGAAGUAGUACUAC 19

RESULT 680
US-11-101-244-491218
; Sequence 491218, Application US//11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491218
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491218
```

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1274 AGACCACCATCTCCACAGT 1292  
Db 1 AGACCACCAUUCACACAGU 19

RESULT 681  
US-11-101-244-491219  
; Sequence 491219, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491219  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491219

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 401 GGACAGTGCACCACTATT 419  
Db 1 GGACAGUGACGACUACU 19

RESULT 682  
US-11-101-244-491220  
; Sequence 491220, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491220  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491220

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 247 CCAACATCTCCACTACAA 265  
Db 1 CCAACAUUCUCCACUACA 19

RESULT 683  
US-11-101-244-491221  
; Sequence 491221, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491221  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491221

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 773 CGAACAGATTATGAGAA 791  
Db 1 CGAACAGAUUUNUGAGAA 19

RESULT 684  
US-11-101-244-491224  
; Sequence 491224, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491224  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491224

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 789 GAAAGTGACCATCTGCT 807  
Db 1 GAAAGUGUACCAUCUGU 19

RESULT 685

US-11-101-244-491225  
; Sequence 491225, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491225  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491225

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 4.6e+02;  
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 809 TGACTGTGCTGATCTACTT 827  
Db 1 UGACUGUGCUGAUCUACU 19

RESULT 686  
US-11-101-244-491226  
; Sequence 491226, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491226  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491226

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.6e+02;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1033 CCAGATCTCTACTGAAGA 1051  
Db 1 CCAGAUUCUACCUAGAAGA 19

RESULT 687

US-11-101-244-491227  
; Sequence 491227, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491227  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491227

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 650 CCAAGTGTGCTGCTGCT 668  
Db 1 CCAAGUGGUCUACUUGUGU 19

RESULT 688  
US-11-101-244-491229  
; Sequence 491229, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491229  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491229

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;



Oy 461 TCATACAGTGTGACT 479  
Db 1 UCAUACAGUGGUGAACU 19

## RESULT 689

US-11-101-244-491231  
Sequence 491231, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEO ID NOS: 1591911  
SOFTWARE: Proprietary  
SEO ID NO 491231  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491231

Query Match 1.1%, Score 19, DB 1, Length 19,  
Best Local Similarity 73.7%, Pred. No. 4.6e+02;  
Matches 14, Conservative 5, Mismatches 0, Indels 0, Gaps 0;

Oy 600 GTACATGCCATCATCAT 618  
Db 1 GUACAGUGGCCAUCACU 19

## RESULT 690

US-11-101-244-491232  
Sequence 491232, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEO ID NOS: 1591911  
SOFTWARE: Proprietary  
SEO ID NO 491232  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491232

Query Match 1.1%, Score 19, DB 1, Length 19,  
Best Local Similarity 84.2%, Pred. No. 4.6e+02;  
Matches 16, Conservative 3, Mismatches 0, Indels 0, Gaps 0;

Oy 398 TGAGACAGTGACGACTA 416  
Db 1 UGAGACAGUGACGACTA 19

## RESULT 691

US-11-101-244-491233  
Sequence 491233, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEO ID NOS: 1591911  
SOFTWARE: Proprietary  
SEO ID NO 491233  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491233

Query Match 1.1%, Score 19, DB 1, Length 19,  
Best Local Similarity 78.9%, Pred. No. 4.6e+02;  
Matches 15, Conservative 4, Mismatches 0, Indels 0, Gaps 0;

Oy 787 GAGAAAGTGACGACT 805  
Db 1 GAGAAAGUGACGACU 19

## RESULT 692

US-11-101-244-491234  
Sequence 491234, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEO ID NOS: 1591911  
SOFTWARE: Proprietary  
SEO ID NO 491234  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-491234

Query Match 1.1%, Score 19, DB 1, Length 19,  
Best Local Similarity 68.4%, Pred. No. 4.6e+02;  
Matches 13, Conservative 6, Mismatches 0, Indels 0, Gaps 0;

Oy 578 TGACGCTGTGCCTTGA 596

Db 1 UGACGGCUGGCGCCUUUGA 19

```

RESULT 693
US-11-101-244-491236
; Sequence 491236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491236

```

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 777 CAAGTTTATCGAAGAGTG 795  
 Db 1 CAAGAUVUUGAAGAAAGUG 19

```

RESULT 694
US-11-101-244-491237
; Sequence 491237, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491237
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491237

```

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 4.6e+02;  
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 766 GAGCATCCGAACAAGATT 784  
 |||||:|||||:|||||:|

Db 1 GAGCAUCCGACACAGAUUU 19

```

RESULT 695
US-11-101-244-491238
; Sequence 491238, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491238

```

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 761 GGCACAGCATCCGACAA 779  
 Db 1 GGCACAGCAUCCGACAA 19

```

RESULT 696
US-11-101-244-491241
; Sequence 491241, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491241

```

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 4.6e+02;  
 Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 576 CATGACGCGTGTGCGCTTT 594  
 Db 1 CAUGACGGCUGGCGCCUUU 19

```
RESULT 697
US-11-101-244-491244
; Sequence 491244, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491244
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491244

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 395 GAATGAGCAGTGACGAA 413
Db 1 GAATGAGCAGTGACGAA 19

RESULT 698
US-11-101-244-491245
; Sequence 491245, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491245

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 375 GATCATCTTAGCCACAAA 393
Db 1 GAUCAUCCUAGCCACAAA 19
```

```
RESULT 699
US-11-101-244-491248
; Sequence 491248, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491248

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 447 CTCGATGCTGATTCAT 465
Db 1 CUCCAUCCUGCAUCCAU 19

RESULT 700
US-11-101-244-491251
; Sequence 491251, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491251
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491251

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1031 ACCGATCTCTACTGAA 1049
Db 1 ACCGAGUCCUACUCCUAA 19
```

## RESULT 701

```
US-11-101-244-491252
; Sequence 491252, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491252
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491252
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

QY 356 GCAACGTGTAGTAGTGTG 374

DB 1 GCAACGUGUGAUGUGUG 19

## RESULT 702

```
US-11-101-244-491256
; Sequence 491256, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491256
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491256
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 266 CCTGGAGACCCATCAGTT 284

DB 1 CCUCGAGACCCAAUACAGU 19

## RESULT 703

## US-11-101-244-491262

```
; Sequence 491262, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491262
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491262
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 764 CAGAGCATCCGACCAAGAT 782

DB 1 CAGAGCAUCCGACCAAGAU 19

## RESULT 704

```
US-11-101-244-491263
; Sequence 491263, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491263
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

QY 841 GTGATTGGCTATGCATACA 859

DB 1 GUGAUUGGCUAUGCAUACA 19

## RESULT 705

US-11-101-244-491264

```

; Sequence 491264, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491264

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      737 GCAGAGTCGTGTGCATGAT 755
Db      1 GCAGAGTCGUGGCAUGAU 19

RESULT 706
US-11-101-244-491265
; Sequence 491265, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491265
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491265

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      245 CCCCAACATCTCCACTPA 263
Db      1 CCCCAACACUCGCCACUA 19

RESULT 707
US-11-101-244-491268
; Sequence 491268, Application US/11101244

```

```

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491268
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491268

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      941 GCAGAGTCGTCAAAATGAT 959
Db      1 GCAGAGTCGCGAACAUGAU 19

RESULT 708
US-11-101-244-491269
; Sequence 491269, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491269

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      261 TAACACCTCGAACCACAT 279
Db      1 TAACACCTCGAACCACAU 19

RESULT 709
US-11-101-244-491270
; Sequence 491270, Application US/11101244
; Publication No. US20050246794A1

```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491270
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-11-101-244-491270

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      583 GCTGTGCGCTTTGATAGCT 601
DB      1 GCUGUGGCUUUGAUGGU 19

RESULT 710
US-11-101-244-491271
/ Sequence 491271, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491271
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-11-101-244-491271

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491272
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-11-101-244-491272

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      786 TGAGAAAGTGATCCACATC 804
DB      1 UGAGAAAGUGUACCAACUC 19

RESULT 712
US-11-101-244-491273
/ Sequence 491273, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491273
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-11-101-244-491273

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 66.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      652 AAAGTGCACTGTGTCA 670
DB      1 AAAGUGUACAUUGUUGCA 19

RESULT 713
US-11-101-244-491274
/ Sequence 491274, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491274
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491274
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      354 GGGCACTGCTAGTANG 372
Db      1 GGGCACTGCTAGTANG 19
```

```

RESULT 714
US-11-101-244-491275
; Sequence 491275, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491275
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491275
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1026 CATCAACCCAGATCTTAC 1044
Db      1 CAUCAACCCAGATCTTAC 19
```

```

RESULT 715
US-11-101-244-491276
; Sequence 491276, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491276
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 4.6e+02;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      806 GTGACCTGCTGATCTA 824
Db      1 GTGACCTGCTGATCTA 19
```

```

RESULT 716
US-11-101-244-491278
; Sequence 491278, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491278
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      763 CCAGGATCCGAACAGA 781
Db      1 CCAGGATCCGAACAGA 19
```

```

RESULT 717
US-11-101-244-491279
; Sequence 491279, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491279

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      503 GGTACTACGCGCTGTTCTA 521
DB      1 GGUACUACGCGCCUGUUCUA 19

RESULT 718
US-11-101-244-491280
; Sequence 491280, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491280

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 4.6e+02;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      332 TCATTGTGTGACCTCTGT 350
DB      1 UCNUUGUGUGACUCUCU 19

RESULT 719
US-11-101-244-491281
; Sequence 491281, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491281
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491281

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      772 CCGAACCAAGATTATGAGA 790
DB      1 CCGAACCAAGAUUUAUGAGA 19

RESULT 720
US-11-101-244-491282
; Sequence 491282, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491282
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491282

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1036 GATCTCTACCTGAGAGACT 1054
DB      1 GAUUCUACCUAGAGAGAU 19

RESULT 721
US-11-101-244-491283
; Sequence 491283, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```



```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491283
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491283

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      991 TGCGTGCCTTCCACATCT 1009
Db      1 UGCGUGCCCUCCACAUUCU 19

RESULT 722
US-11-101-244-491284
; Sequence 491284, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491284

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      769 CATCGAACAAGATTATG 787
Db      1 CAUCCGAACAAGAUUUAUG 19

RESULT 723
US-11-101-244-491285
; Sequence 491285, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491285

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      753 GATCGAATGCCAGAGCAT 771
Db      1 GAUCCGAUCCGACAGCAU 19

RESULT 724
US-11-101-244-491286
; Sequence 491286, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491286

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      550 GCCGCTGTCTTCCGACGTA 568
Db      1 GCCGCTGTCTTCCGACGTA 19

RESULT 725
US-11-101-244-491287
; Sequence 491287, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491287
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491287

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      480 CACCTATGCTGTCCACAA 498
Db      1 CACCUAUGCUGUCCACAAC 19

RESULT 726
US-11-101-244-491288
; Sequence 491288, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491288
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491288

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      479 TCACCTATGCTGTCCACA 497
Db      1 UCACCUAUGCUGUCCACAA 19

RESULT 727
US-11-101-244-491291
; Sequence 491291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491291

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1119 CATCTACTGCTGCTCAAT 1137
Db      1 CAUCUACUGCUGCUCUCAAU 19

RESULT 728
US-11-101-244-491292
; Sequence 491292, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491292
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491292

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      504 GTACTACGGCCTGTCTAC 522
Db      1 GUACUACGGCUGUUCUAC 19

RESULT 729
US-11-101-244-491294
; Sequence 491294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491294
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 233 ACTGAGACCTCTCCCAA 251
Db 1 ACUCAGACCTCCTCCCAA 19
```

```
RESULT 730
US-11-101-244-491296
; Sequence 491296, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491296
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491296
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 840 GGTGATTGCTATGCATAC 858
Db 1 GGUGAUGGCUAUGCAUAC 19
```

```
RESULT 731
US-11-101-244-491297
; Sequence 491297, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491297
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491297
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 492 CCACACGAATGCTACTAC 510
Db 1 CCACACGAATGCTACTAC 19
```

```
RESULT 732
US-11-101-244-491298
; Sequence 491298, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491298
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491298
```

```
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 203 GCTTCGAATGATTAACGT 221
Db 1 GCTTCGAATGATTAACGU 19
```

```
RESULT 733
US-11-127-877-153
; Sequence 153, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koentraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
```

```
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 153
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-153

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 GTTCACACACTTCTTCCC 546
Db 1 GTTCACACACTTCTTCCC 19

RESULT 734
US-11-127-877-154
; Sequence 154, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 154
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-154

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 799 CACATCTGTGACATGTGC 817
Db 1 CACATCTGTGACATGTGC 19

RESULT 735
US-11-127-877-155
; Sequence 155, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 155
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-155

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATCAACCCAGATCTTACC 1045
Db 1 ATCAACCCAGATCTTACC 19

RESULT 736
US-11-127-877-156
; Sequence 156, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 156
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-156

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGACAGGTCGCTGGGC 1155
Db 1 TGACAGGTCGCTGGGC 19

RESULT 737
US-11-127-877-474
; Sequence 474, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 474
; LENGTH: 19
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-474

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      857 ACACCGTAGTGGGAAATCAG 875
Db      1 ACACCGTAGTGGGAAATCAG 19

RESULT 738
US-10-310-914A-51927
; Sequence 51927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Shiller, Kwuzat
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51927
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-51927

Query Match      1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1308 GGAGGAGCCAGAGGAGCGCCCC 1329
Db      1 GAAGGAGCCAGAGGAGCGCCCC 22

RESULT 739
US-10-310-914A-746504/c
; Sequence 746504, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Shiller, Kwuzat
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 746504
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-746504

Query Match      1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1299 GGCCGAGGAGGAGGAGCGAGNG 1320
Db      23 GGCCGAGGAGGAGGAGCGAGNG 2

RESULT 740
US-10-770-726-10079/c

; Sequence 10079, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10079
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-10079

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1049 AGAAGTTATCCAGCAGATC 1068
Db      20 AGAAGTTATCCAGCAGATC 1

RESULT 741
US-10-770-726-10445/c
; Sequence 10445, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770.726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10445
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-10445

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1049 AGAAGTTATCCAGCAGATC 1068
Db      20 AGAAGTTATCCAGCAGATC 1

RESULT 742
US-10-310-914A-1313224/c
; Sequence 1313224, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Shiller, Kwuzat
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313224
```

LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1313224

Query Match 1.0%; Score 18.4; DB 1; Length 23;  
Best Local Similarity 95.0%; Pred. No. 6.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1265 GCCGCTGAGAGACCAATC 1284  
DB 21 GCCGCTGAGAGACCAATC 2

RESULT 743  
US-10-310-914A-1313247/c  
Sequence 1313247, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kyuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1313247  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1313247

Query Match 1.0%; Score 18.4; DB 1; Length 23;  
Best Local Similarity 95.0%; Pred. No. 6.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1265 GCCGCTGAGAGACCAATC 1284  
DB 20 GCCGCTGAGAGACCAATC 1

RESULT 744  
US-09-930-503-39  
Sequence 39, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
FILE REFERENCE: 39245-173913  
CURRENT FILING DATE: 2001-08-16  
CURRENT APPLICATION NUMBER: US/09/930,503  
PRIOR APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 39  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-39

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055

DB 1 TCTTACTGAGAGAGTT 18

RESULT 745  
US-09-930-503-58/c  
Sequence 58, Application US/09930503  
Publication No. US20030060438A1  
GENERAL INFORMATION:  
APPLICANT: HENRY, JAMES  
APPLICANT: CAHILL, CATHERINE  
APPLICANT: YASHPAL, KIRAN  
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
FILE REFERENCE: 39245-173913  
CURRENT FILING DATE: 2001-08-16  
CURRENT APPLICATION NUMBER: 60/226,086  
PRIOR FILING DATE: 2000-08-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-58

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055  
DB 18 TCTTACTGAGAGAGTT 1

RESULT 746  
US-10-146-354A-32/c  
Sequence 32, Application US/10146354A  
Publication No. US20030054381A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc.  
APPLICANT: Nelson, Darcy L.  
APPLICANT: Webb, Suzin M.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND  
TITLE OF INVENTION: USES IN DIAGNOSIS AND TREATMENT OF DISEASES  
FILE REFERENCE: PCI0461AGPR  
CURRENT FILING DATE: 2002-08-15  
CURRENT APPLICATION NUMBER: US/10/146,354A  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
NAME/KEY: misc feature  
LOCATION: (1)-(18)  
OTHER INFORMATION: artificial / primer  
US-10-146-354A-32

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 CGCGAGTTCAGCTTCAA 75  
Db 18 CGCGAGTTCAGCTTCAA 1

RESULT 747  
US-10-005-956-1124/c  
; Sequence 1124, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1124  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-005-956-1124

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 581 CGGCTGTGCGCTTGATA 598  
Db 18 CGGCTGTGCGCTTGATA 1

RESULT 748  
US-10-005-956-1218  
; Sequence 1218, Application US/10005956  
; Publication No. US20030113726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005,956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1218  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-005-956-1218

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1301 CCCACGAGAGAGCCAG 1318  
Db 1 CCCACGAGAGAGCCAG 18

RESULT 749  
US-10-310-914A-386268/c

; Sequence 386268, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386268  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386268

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 CTTTCACCTCCTCTCT 115  
Db 18 CTTTCACCTCCTCTCT 1

RESULT 750  
US-10-310-914A-386291/c  
; Sequence 386291, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386291  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386291

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 ACCCTCCTGTCTGCTTA 121  
Db 18 ACCCTCCTGTCTGCTTA 1

RESULT 751  
US-10-310-914A-386293/c  
; Sequence 386293, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386293  
; LENGTH: 18  
; TYPE: RNA

```

; ORGANISM: Human
US-10-310-914A-386293

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1639 CTCGAACCAATGACTGA 1656
DB      18 CTCGAACCAATGACTGA 1

RESULT 752
US-10-310-914A-1157285/c
; Sequence 1157285, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1157285
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1157285

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1287 CACACTGCTGGGGGCCCA 1304
DB      18 CACAGTGTGGGGGCCCA 1

RESULT 753
US-10-310-914A-386292/c
; Sequence 386292, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386292
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386292

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      116 GCTTAGAAGAACCTGTA 133
DB      18 GCTTAGAAGAACCTGTA 1

RESULT 754
US-11-083-784-491261
; Sequence 491261, Application US/11083784
```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491261

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      197 CGCCTAGCTTGAAATG 214
DB      2 CGCCUAGCUCGAAAUUG 19

RESULT 755
US-11-101-244-491261
; Sequence 491261, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491261

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      197 CGCCTAGCTTGAAATG 214
DB      2 CGCCUAGCUCGAAAUUG 19

RESULT 756
US-10-310-914A-1305132/c
```



```
; Sequence 1305132, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuznet
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1305132
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1305132
```

```
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1403 GCTTCAGCTTCTCCTCCA 1420
Db 21 GCTTCAGCTTCTCCTCCA 4
```

```
RESULT 757
US-10-005-956-1303
; Sequence 1303, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005.956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1303
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1303
```

```
Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1681 AGGTGGAGCCAGCTTTTCC 1699
Db 1 AGGTGGAGCCAGCTTTTCC 19
```

```
RESULT 758
US-10-201-187-44/c
; Sequence 44, Application US/10201187
; Publication No. US20030104478A1
; GENERAL INFORMATION:
; APPLICANT: Witcamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
```

```
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Natural Ligand of G Protein Coupled Receptor ChemR23 and Uses The
; FILE REFERENCE: 9409/2045
; CURRENT APPLICATION NUMBER: US/10/201.187
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US09/905,253
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-201-187-44
```

```
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 669 CATCTGGGTCCTGGCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1
```

```
RESULT 759
US-10-603-566-38/c
; Sequence 38, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Witcamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603.566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-603-566-38
```

```
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 669 CATCTGGGTCCTGGCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1
```

```
RESULT 760
US-10-893-485-38/c
; Sequence 38, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergae, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentlief, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerink
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-10-893-485-38

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGGTCCTGGCTCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTCTT 1

RESULT 761
US-10-310-914A-322519
; Sequence 322519, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 322519
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-322519

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 129 CTTGAGCCCGGCGCCAGCC 149
||:|||||
```

```
Db 1 CTTGAGCCCGGCGCCAGCC 21

RESULT 762
US-11-134-811-38/c
; Sequence 38, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergae, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentlief, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerink
; FILE REFERENCE: 9409/2043
; CURRENT APPLICATION NUMBER: US/11/134,811
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: Synthetic primer
US-11-134-811-38

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CATCTGGGTCCTGGCTCTCTCT 689
Db 21 CATCTGGGTCCTGGCTCTTCT 1

RESULT 763
US-10-310-914A-467163/c
; Sequence 467163, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467163
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-467163

Query Match
Best Local Similarity 1.0%; Score 17.8; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 882 GGCCAGTGAATCCCCGGGGA 902  
Db 21 GGCCAGGAGGTCCCCGGGGA 1

## RESULT 764

US-10-310-914A-467164/c  
; Sequence 467164, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 467164  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-467164

Query Match 1.0%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 882 GGCCAGTGAATCCCCGGGGA 902  
Db 21 GGCCAGGAGGTCCCCGGGGA 1

## RESULT 765

US-10-310-914A-965080/c  
; Sequence 965080, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 965080  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-965080

Query Match 1.0%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 7e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 997 CCCTTCACATCTCTCTCTC 1017  
Db 22 CCCTTCACATCTCTCTCTC 2

## RESULT 766

US-10-310-914A-1184635  
; Sequence 1184635, Application US/10310914A  
; Publication No. US2006003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1184635  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1184635

Query Match 1.0%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 61.9%; Pred. No. 7e+02;  
Matches 13; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 532 CACACTCTTCCCATGCC 552  
Db 1 CACACCTUUCUCCCAVCCCC 21

## RESULT 767

US-10-005-956-82/c  
; Sequence 82, Application US/10005956  
; Publication No. US2003013726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005.956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 82  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-005-956-82

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 663 CTGTGTCATCTGGGTCTG 681  
Db 19 CTGTGTCATGAGGTCTCTG 1

## RESULT 768

US-10-005-956-86/c  
; Sequence 86, Application US/10005956  
; Publication No. US2003013726A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: D0053NP  
; CURRENT APPLICATION NUMBER: US/10/005.956  
; CURRENT FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/251,015  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: 60/263,678  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/273,037  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 1579  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86  
; LENGTH: 19

```
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-86

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1529 CCTCAGCTGGAGCTTGA 1547
Db      19  CCTCAGCTAGGACTTGA 1

RESULT 769
US-10-005-956-144
; Sequence 144, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 144
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-144

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      534 CAACCTCTTCCCGCAGCC 552
Db      1  CAACCTCTTCCCGCAGCC 19

RESULT 770
US-10-005-956-148/C
; Sequence 148, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 148
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-148

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1626 TCATGCTGTGACTCAAA 1644
Db      19  TCATGCTGTGACTCAAA 1

RESULT 771
US-10-005-956-150/C
; Sequence 150, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 150
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-150

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1335 CACACCTGTGCTCCTGAGC 1353
Db      19  CACACCTCATCCCTGAGC 1
```

```
RESULT 772
US-10-310-914A-88048/C
; Sequence 88048, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shilet, Kyuzet
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88048
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-88048
```

```
Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      167 AGGGGGGTGTGTACAGAT 185
Db      19  AGGGGGGTGTGTGACAGAT 1
```

```
RESULT 773
US-10-310-914A-1153363
; Sequence 1153363, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1398402
; SOFTWARE: Patent version 3.3
; SEQ ID NO 1153363
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1153363
```

```

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      675 GGTCTGGCTCTCTGCTG 693
      |||:|||||:|||||:
Db      1 GGUCCGCGCUCUCCUGCTG 19
```

```

RESULT 774
US-11-083-784-49660
; Sequence 49660, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49660
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49660
```

```

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1109 ACAACCCCATCATCTACTG 1127
      |||:|||||:|||||:
Db      1 ACAUCCCAUCCAUCCUACTG 19
```

```

RESULT 775
US-11-083-784-103957
; Sequence 103957, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 103957
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-103957
```

```

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.2e+02;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      668 TCATCTGGCTCTGCTCT 686
      |||:|||||:|||||:
Db      1 UCAUCUGGUCUGGCUUU 19
```

```

RESULT 776
US-11-083-784-490753
; Sequence 490753, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-490753
```

```

Query Match          1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1104 CATGTACACCCCATCATC 1122
      |||:|||||:|||||:
Db      1 CAUGUACAUCUCCAUCC 19
```

```

RESULT 777
US-11-083-784-490758
; Sequence 490758, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```



```
/ Sequence 491368, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491368
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491368
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1104 CATGACACCCCATCTATC 1122
Db 1 GACGACAUCCCAUCACUAC 19
```

```
RESULT 782
US-11-083-784-491376
/ Sequence 491376, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491376
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491376
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1106 TGTTACACCCCATCTATCTA 1124
Db 1 UGDACAUCGCCAUCACUACUA 19
```

```
RESULT 783
US-11-083-784-491384
/ Sequence 491384, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491384
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491384
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1107 GTACACACCCCATCTATCTAC 1125
Db 1 GUACCAUCCCAUCACUACUAC 19
```

```
RESULT 784
US-11-083-784-491392
/ Sequence 491392, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491392
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-491392
```

```
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 6.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1109 ACAACCCCATCTACTG 1127
```

Db 1 ACAUCCCAUCUACUG 19

## RESULT 785

US-11-083-784-854916  
; Sequence 854916, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 854916  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-854916

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 61.2%; Pred. No. 6.2e+02;  
Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 106 CCTCTGTCGCTTTAGAA 124  
Db 1 CCUCCUCUCGCUAAGAA 19

## RESULT 786

US-11-083-784-877764/C  
; Sequence 877764, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 877764  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-877764

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 6.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1402 AGCTTCAGCTTCTCTCCA 1420  
Db 19 AGCTTCAGCATCTCTCCA 1

## RESULT 787

US-11-083-784-946470/C  
; Sequence 946470, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 946470  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-946470

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1722 TTCTGGAAGTGACTTGAC 1740  
Db 19 TTCTGGAAGTGACTTGAC 1

## RESULT 788

US-11-083-784-1141173  
; Sequence 1141173, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1141173  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1141173



Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 6.2e+02;  
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

479 TCACCTAGCTGTCCACA 497  
:||||:||||:||||:  
Db 1 UCACCUAGCUGUCACAGA 19

## RESULT 789

US-11-083-784-1245667/c  
; Sequence 1245667, Application US/11083784  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1245667  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1245667

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

652 AAAGTGTCTCTGTCTCA 670  
:||||:||||:||||:  
Db 19 AAAGTGTCTCTGTCTCA 1

## RESULT 790

US-11-101-244-49660  
; Sequence 49660, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 49660  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-49660

US-11-101-244-49660

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1109 ACAACCCATCATCTACTG 1127  
:||||:||||:||||:  
Db 1 ACAUCCCAUCCUACUG 19

## RESULT 791

US-11-101-244-103957  
; Sequence 103957, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 103957  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-103957

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 6.2e+02;  
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

668 TCATCTGGGTCGCGGCT 686  
:||||:||||:||||:  
Db 1 UCAUCCGGGUCUCCU 19

## RESULT 792

US-11-101-244-490753  
; Sequence 490753, Application US/1101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 490753  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-490753

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1104 CATGTACACCCCATCATC 1122  
||:|||||:||||:|  
Db 1 CAUGUACAUCUCCAUCAUC 19

RESULT 793  
US-11-101-244-490758  
; Sequence 490758, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 490758  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-490758

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 6.2e+02;  
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1106 TGTACACCCCATCATCTTA 1124  
||:|||||:||||:|  
Db 1 UGUACAUCUCCAUCAUC 19

RESULT 794  
US-11-101-244-490759  
; Sequence 490759, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 490759  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-490759

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1107 GTACACCCCATCATCTAC 1125  
||:|||||:||||:|  
Db 1 GTCACAUCCCAUCUAC 19

RESULT 795  
US-11-101-244-490763  
; Sequence 490763, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 490763  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-490763

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1109 ACAACCCCATCATCTACTG 1127  
||:|||||:||||:|  
Db 1 ACAUCCCAUCUAC 19

RESULT 796  
US-11-101-244-491328  
; Sequence 491328, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491328  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491328

Query Match 1.0%; Score 17.4; DB 1; Length 19;

Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 562 GCCAGTACTTACTCCATCA 580  
Db 1 GCCAGCAUCUACUCCAUCA 19

RESULT 797

US-11-101-244-491368  
; Sequence 491368, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491368  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491368

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1104 CATGTACACCCCATCATC 1122  
Db 1 CAUGUACAUCUCCAUCAUC 19

RESULT 798  
US-11-101-244-491376  
; Sequence 491376, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491376  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491376

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 6.2e+02;

Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1106 TGTAACAACCCCATCATCTA 1124  
Db 1 UGUACAUCUCCAUCAUCA 19

RESULT 799

US-11-101-244-491384  
; Sequence 491384, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491384  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491384

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1107 GTACACCCCATCATCTAC 1125  
Db 1 GUACAUCUCCAUCAUCA 19

RESULT 800  
US-11-101-244-491392  
; Sequence 491392, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 134990S  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 491392  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-491392

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 6.2e+02;  
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

OY      1109 ACAACCCCATCATCTACTG 1127
          ||||| ||||: ||: ||: |
Db      1 ACAAUCCCAUCAUUCUACUG 19

```

```

RESULT: 80
US-11-101-244-854916
; Sequence: 854916, Application: US/11101244
; Publication No.: US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134930US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 854916
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-854916

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	63.2%;	Pred. No. 6.2e+02;		
Matches 12;	Conservative 6;	Mismatches 1;	Indels 0;	Gaps 0;

Dy 106 CCTCCTGTCTGCTTAGAA 124  
||:||:||:||::||||  
Db 1 CCUCCUGUCUGCUUAGAA 19

```

RESULT 802
US-11-101-244-877764/c
; Sequence 877764, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PENDING FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 877764
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-877764

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. No. 6.2e+02;		
Matches	18;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

```

Oy      1402 AGCTTCAGCTTCTCTCCA 1420
          |||||
Db      19 AGCTTCAGCATCTCTCCA 1

```

```

RESULT 803
US-11-101-244-946470/c
? Sequence 946470, Application US/11101244
? Publication No. US2005024679A1
? GENERAL INFORMATION:
? APPLICANT: Dharmacon, Inc.
? APPLICANT: Khvorova, Anastasia
? APPLICANT: Reynolds, Angela
? APPLICANT: Leake, Devin
? APPLICANT: Marshall, William
? APPLICANT: Scaringe, Stephen
? TITLE OF INVENTION: Functional and Hyperfunctional siRNA
? FILE REFERENCE: 13499US
? CURRENT APPLICATION NUMBER: US/11/101,244
? CURRENT FILING DATE: 2005-04-07
? PRIOR APPLICATION NUMBER: 60/502,050
? PRIOR FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 60/426,137
? PRIOR FILING DATE: 2002-11-14
? NUMBER OF SEQ ID NOS: 1591911
? SOFTWARE: Proprietary
? SEQ ID NO 946470
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Homo sapiens
US-11-101-244-946470

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. No. 6.2e+02;		
Matches 18;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1722 TTCTGGAAGTGACTTTGGC 1740  
|||||  
Db 19 TTCTGGAAGTGACCTTGGC 1

```

RESULT 804
US-11-101-244-1141173
Sequence 1141173, Application US/11101244
Publication No. US20050246794d1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1141173
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1141173

```

Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	68.4%;	Pred. No. 6.2e+02;		
Matches 13; Conservative	5;	Mismatches 1;	Indels 0;	Gaps 0;
479	TCACCTATGCTGTCCACA	497		

479 TCACCTATGCTGTCACAA 497

Db 1 UCACCUAUGCUCGACAGAA 19

RESULT 805  
US-11-101-244-1245667/c  
; Sequence 1245667, Application US/11101244  
; Publication NO. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1245667  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1245667

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 652 AAAGTGATCTGTGTCA 670  
Db 19 AAAGTGATCTGTGTCA 1

RESULT 806  
US-10-310-914A-515099  
; Sequence 515099, Application US/10310914A  
; Publication NO. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 515099  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-515099

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 57.9%; Pred. No. 7.1e+02;  
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 663 CTGTGTCATCTGGCTCCTG 681  
Db 3 CUGUGUCUCUCGCGUCUG 21

RESULT 807  
US-10-310-914A-1308283/c  
; Sequence 1308283, Application US/10310914A  
; Publication NO. US20060003322A1

; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 1308283  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1308283

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 7.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 365 TAGTGATGTGATCATCTT 383  
Db 19 TAGTGATGTGATCATCTT 1

RESULT 808  
US-10-310-914A-138766/c  
; Sequence 138766, Application US/10310914A  
; Publication NO. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 138766  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-138766

Query Match 1.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 986 TCTGCTGGCTGCCCTTC 1002  
Db 17 TCTGCTGGCTGCCCTTC 1

RESULT 809  
US-10-310-914A-822037/c  
; Sequence 822037, Application US/10310914A  
; Publication NO. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 822037  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-822037

Query Match 1.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 CAGTCCACACTCTCT 541  
DB 18 CAAGTCCACACTCTCT 2

## RESULT 810

US-11-083-784-128453  
Sequence 128453, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 134990S  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 128453  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-128453

Query Match 1.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGTCTCTGCCAA 938  
DB 1 GAGCAAGTCTCTGCCAA 17

## RESULT 811

US-11-083-784-128543  
Sequence 128543, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 134990S  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 128543  
LENGTH: 19

TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-128543

Query Match 1.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGTCTCTGCCAA 938  
DB 1 GAGCAAGTCTCTGCCAA 17

RESULT 812  
US-11-083-784-1265096  
Sequence 1265096, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 134990S  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1265096  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1265096

Query Match 1.0%; Score 17; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1533 ACACGGGACTCTGCCAA 1549  
DB 3 ACACGGGACTCTGCCAA 19

## RESULT 813

US-11-101-244-128453  
Sequence 128453, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 134990S  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: US/11/01,244  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 128453

LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-128453

Query Match  
 Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGCTCTGCGCAA 938  
 Db 1 GAGCAAGCTCTGCGCAA 17

RESULT 814  
 US-11-101-244-128543  
 Sequence 128543, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:

APPLICANT: Dharmacom, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO 128543  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-128543

Query Match  
 Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 922 GAGCAAGCTCTGCGCAA 938  
 Db 1 GAGCAAGCTCTGCGCAA 17

RESULT 815  
 US-11-101-244-1265096  
 Sequence 1265096, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacom, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO 1265096  
 LENGTH: 19

TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-1265096

Query Match  
 Best Local Similarity 82.4%; Pred. No. 6.7e+02;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1533 ACACCTGGGACTTGCCAAA 1549  
 Db 3 ACACCTGGGACTTGCCAAA 19

RESULT 816  
 US-10-310-914A-160462/c  
 Sequence 160462, Application US/10310914A  
 Publication No. US20060003322A1  
 GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac  
 APPLICANT: Shlier, Krizat  
 TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 FILE REFERENCE: 06087,0200,CPUS01  
 CURRENT APPLICATION NUMBER: US/10/310,914A  
 CURRENT FILING DATE: 2002-12-06  
 NUMBER OF SEQ ID NOS: 1388402  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 160462  
 LENGTH: 20  
 TYPE: RNA  
 ORGANISM: Human  
 US-10-310-914A-160462

Query Match  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1326 CCCCAGGCCACACCTT 1342  
 Db 17 CCCCAGGCCACACCTT 1

RESULT 817  
 US-10-023-066A-25/c  
 Sequence 25, Application US/10023066A  
 Publication No. US20030056242A1  
 GENERAL INFORMATION:  
 APPLICANT: E. I. DU PONT DE NEMOURS AND  
 COMPANY  
 TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR  
 INCREASING THE LYSINE AND  
 THREONINE CONTENT OF THE SEEDS OF  
 PLANTS  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E. I. DU PONT DE NEMOURS  
 AND COMPANY  
 STREET: 1007 MARKET STREET  
 CITY: WILMINGTON  
 STATE: DELAWARE  
 COUNTRY: U.S.A.  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MICROSOFT WORD VERSION 2.0C  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/023,066A  
 FILING DATE: 29-Apr-2002  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BARBARA C. SIEGELL





SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-10-023-066A-43

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 19 CTTGAGCTTCTCTCCA 3

## RESULT 820

US-10-804-678-25/C  
Sequence 25, Application US/10804678  
Publication No. US2005005330A1  
GENERAL INFORMATION:  
APPLICANT: EPELBAUM, SABINE URSULA  
FALCO, SAVERIO CARL  
MCDEVITT, RAYMOND ERVIN, III  
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR  
INCREASING THE LYSINE CONTENT OF  
THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT OFFICE 97  
SOFTWARE: MICROSOFT WINDOWS 95  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/804,678  
FILING DATE: 19-Mar-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,304  
FILING DATE: 27-Mar-1998  
APPLICATION NUMBER: 08/824,627  
FILING DATE: MARCH 27, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CHRISTENBURY, LYNNE M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1037-F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
82"  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-804-678-25

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 19 CTTGAGCTTCTCTCCA 3

## RESULT 821

US-10-804-678-41/C  
Sequence 41, Application US/10804678  
Publication No. US2005005330A1  
GENERAL INFORMATION:  
APPLICANT: EPELBAUM, SABINE URSULA  
FALCO, SAVERIO CARL  
MCDEVITT, RAYMOND ERVIN, III  
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR  
INCREASING THE LYSINE CONTENT OF  
THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT OFFICE 97  
SOFTWARE: MICROSOFT WINDOWS 95  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/804,678  
FILING DATE: 19-Mar-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,304  
FILING DATE: 27-Mar-1998  
APPLICATION NUMBER: 08/824,627  
FILING DATE: MARCH 27, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CHRISTENBURY, LYNNE M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: BB-1037-F  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..21  
OTHER INFORMATION: /product= "synthetic  
oligonucleotide"  
/standard\_name= "SM  
86"  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-804-678-41

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 19 CTTGAGCTTCTCTCCA 3



US-10-310-914A-460312

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 7.5e+02;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 130 CTGAGCCCCAGCGCCAGCC 149  
|:|||||:|||||  
Db 1 CUUAGCCCCAGCGCCAGCC 20

RESULT 826

US-10-310-914A-1145210  
; Sequence 1145210, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1145210  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1145210

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 70.0%; Pred. No. 7.5e+02;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 978 CTTGCCATCTGCTGCTGC 997  
|:|||||:|||||  
Db 1 CUGGCCACCTGCGCGCC 20

RESULT 827

US-10-770-726-10314/C  
; Sequence 10314, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; TITLE OF INVENTION: CANCERS  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770.726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10314  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNA1  
US-10-770-726-10314

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1049 AGAAGTTATCCACAGCTC 1068  
|:|||||:|||||  
Db 21 AAAAGTTATCAAGCAGCTC 2

RESULT 828

US-10-310-914A-43024/C  
; Sequence 43024, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 43024  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-43024

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 134 GCCCAGCGCCAGCCAGCAG 153  
|:|||||:|||||  
Db 21 GCCCAGCGCCAGCCAGCAG 2

RESULT 829

US-10-310-914A-151367  
; Sequence 151367, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 151367  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-151367

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 65.0%; Pred. No. 7.9e+02;  
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 980 TCGCCATCTGCTGCTGCC 999  
|:|||||:|||||  
Db 2 UCCCCUCUGCGUGCC 21

RESULT 830

US-10-310-914A-201071/C  
; Sequence 201071, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 201071  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human

US-10-310-914A-201071

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1295 TGGGGGCCCGAGGAG 1314

DB 21 TGGGGGCCCGAGGAG 2

RESULT 831

US-10-310-914A-412673/C  
; Sequence 412673, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 412673  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-412673

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1604 TTCTTCCTATCTTCCAC 1623

DB 21 TTCTTCCTATCTTCCAC 2

RESULT 832

US-10-310-914A-444744/C  
; Sequence 444744, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 444744  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-444744

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGGTTAGGAAACATTCCA 1561

DB 21 GGGTTAGGAAACATTCCA 2

RESULT 833

US-10-310-914A-800870  
; Sequence 800870, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 800870  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-800870

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 80.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 640 GCCACGCGCAGCAAGTGT 659

DB 1 GCCACGCGCAGCAAGTGT 20

RESULT 834

US-10-310-914A-843549  
; Sequence 843549, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 843549  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-843549

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 80.0%; Pred. No. 7.9e+02;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 715 TCACACACGAGACCATGCC 734

DB 2 TCACACACGAGACCATGCC 21

RESULT 835

US-10-138-674-2971/C  
; Sequence 2971, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MEHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2971  
; LENGTH: 18

```

; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCGGCGCTGTCAGC 1

RESULT 836
US-10-287-949A-2971/c
; Sequence 2971, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2971
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCGGCGCTGTCAGC 1

RESULT 837
US-10-951-303-2971/c
; Sequence 2971, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MHHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2971
; LENGTH: 18
; TYPE: RNA
```

```

; ORGANISM: Mus musculus
US-10-951-303-2971

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTCAGC 641
DB 18 CCAGCCGGCGCTGTCAGC 1

RESULT 838
US-10-310-914A-336642/c
; Sequence 336642, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 336642
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-336642

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 AGGTCAGTATGGGTAG 1568
DB 18 AGGTCATATAGGTTAG 1

RESULT 839
US-10-310-914A-999588
; Sequence 999588, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 999588
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-999588

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 18;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1453 GGTGACAGCCCACTGCC 1470
DB 1 GGUGACAGCCCACTGCC 18

RESULT 840
US-10-310-914A-1071407
; Sequence 1071407, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1071407
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1071407

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 7e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1448 TGGCAGGTGACGCCCCCA 1465
Db      1 UGCAGAGGGGAGCCCCCA 18

RESULT 841
US-10-310-914A-1378476
; Sequence 1378476, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378476
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1378476

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1233 TCTCCAGACCCAGGCGAG 1250
Db      1 UCUGCAGACCCAGGCGAG 18

RESULT 842
US-10-310-914A-687663
; Sequence 687663, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 687663
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-687663
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      890 AGATCCCGGGAGCTCCT 907
Db      2 AGCTCCCGGGAGCTCCU 19

RESULT 843
US-10-310-914A-1378477
; Sequence 1378477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1378477
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1378477

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1233 TCTCCAGACCCAGGCGAG 1250
Db      1 UCUGCAGACCCAGGCGAG 18

RESULT 844
US-10-310-914A-1384285/C
; Sequence 1384285, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1384285
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1384285

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1006 ATCTTCTCTCTCTGCCC 1023
Db      19 ACCTTCTCTCTCTGCCC 2

RESULT 845
US-11-083-784-49684
; Sequence 49684, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49684
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-49684

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1114 CCCATCATCTACTGCTGC 1131
Db 1 CCCAUCACUACUCGUCUC 18
```

```

RESULT 846
US-11-083-784-209546/C
; Sequence 209546, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 209546
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-209546
```

```

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1001 TCCACATCTCTCTCC 1018
Db 18 TCCACCTCTCTCTCTCC 1
```

RESULT 847

```

US-11-083-784-405179/C
; Sequence 405179, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 405179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-405179

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1405 TTCAGCTTCTCTCCAT 1422
Db 19 TTCAGCTTCTCTCCAT 2
```

```

RESULT 848
US-11-083-784-427206
; Sequence 427206, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 427206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-427206
```

```

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1550 AAGGTCAGTATGGTTA 1567
Db 2 AAGGTCAGTATGGTTA 19
```

```
RESULT 849
US-11-083-784-491396
; Sequence 491396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491396

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.5e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1095 GAGCTCCACCCATGTRCAA 1112
Db      1 GAGCTCCACCAUGUCAA 18

RESULT 850
US-11-083-784-521114
; Sequence 521114, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521114
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-521114

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1048 AAGAAGTTATCCAGCAG 1065
Db      2 AAGAAGUUUACCAAGAG 19

RESULT 851
US-11-083-784-531574
; Sequence 531574, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531574

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1274 AGACCACTCTCCAGCAG 1291
Db      1 AGACUACCAUCCACAG 18

RESULT 852
US-11-083-784-531575
; Sequence 531575, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531575

Query Match      0.9%; Score 16.4; DB 1; Length 19;
```



Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291  
Db 1 AGACUACCAUCUCCACAG 18

## RESULT 853

US-11-083-784-531674  
; Sequence 531674, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacom, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 531674  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-531674

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291  
Db 1 AGACUACCAUCUCCACAG 18

## RESULT 854

US-11-083-784-531675  
; Sequence 531675, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacom, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 531675  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-11-083-784-531675

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291  
Db 1 AGACUACCAUCUCCACAG 18

## RESULT 855

US-11-083-784-531774  
; Sequence 531774, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacom, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 531774  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-531774

Query Match  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCAACCATCTCCACAG 1291  
Db 1 AGACUACCAUCUCCACAG 18

## RESULT 856

US-11-083-784-531775  
; Sequence 531775, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacom, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 531775

```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531775

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACAG 18

```

```

RESULT 857
US-11-083-784-531872
; Sequence 531872, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531872
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531872

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACAG 18

```

```

RESULT 858
US-11-083-784-531873
; Sequence 531873, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

```

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531873

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACAG 18

```

```

RESULT 859
US-11-083-784-531972
; Sequence 531972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-531972

```

```

Query Match
Best Local Similarity 83.3%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1274 AGACCAACATCTCCACAG 1291
Db 1 AGACUACCAUCCACAG 18

```

```

RESULT 860
US-11-083-784-531973
; Sequence 531973, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050

```

PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 531973  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-531973

Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291  
DB 1 AGACUACCAUCUCCACAG 18

RESULT 861  
US-11-083-784-532071  
Sequence 532071, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 532071  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-532071

Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291  
DB 1 AGACUACCAUCUCCACAG 18

RESULT 862  
US-11-083-784-532072  
Sequence 532072, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 532072  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-532072

Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1274 AGACCACCATCTCCACAG 1291  
DB 1 AGACUACCAUCUCCACAG 18

RESULT 863  
US-11-083-784-578805/C  
Sequence 578805, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 578805  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-578805

Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 7.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1720 ATTTCGGAAGTGACTTT 1737  
DB 19 ATTTCGGAAGTGACTTT 2

RESULT 864  
US-11-083-784-723652  
Sequence 723652, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 723652
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-723652

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      392 AAAGATGAGACAGTGA 409
Db      2 AAAGAUGAGAACAGUGA 19

```

```

RESULT 865
US-11-083-784-723752
Sequence 723752, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 723752
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-723752

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      392 AAAGATGAGACAGTGA 409
Db      2 AAAGAUGAGAACAGUGA 19

```

```

RESULT 866
US-11-083-784-911949
Sequence 911949, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin

```

```

APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 911949
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-911949

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1643 AACCAATCAGTCACTT 1660
Db      2 AACCAAAUCACUGAAAU 19

```

```

RESULT 867
US-11-083-784-928479/c
Sequence 928479, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO: 928479
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-928479

```

```

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1007 TCTTCTCTCTGCGCTT 1024
Db      19 TCTTCTCTCTCTGCGCTT 2

```

```

RESULT 868
US-11-083-784-1141172
Sequence 1141172, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.

```

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1141172

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 480 CACCTATGCTGTCCACAA 497
Db 1 CACCUAUCGUCGUCGACGA 18

RESULT 869
US-11-083-784-1259943/c
; Sequence 1259943, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1259943
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1259943

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 650 CCAAGTGTGATCTGTG 667
Db 19 CCAAGTGTGATCTGTG 2

RESULT 870
US-11-083-784-1473036/c
; Sequence 1473036, Application US/11083784

```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1473036
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1473036

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1417 TCCATGTGCTCTCTAG 1434
Db 19 TCCATGTGCTCTCTAG 2

RESULT 871
US-11-083-784-1484938
; Sequence 1484938, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1484938
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1484938

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 7.5e+02;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 657 GGTGATGTGTCATCTG 674
Db 1 GGTGATGTGTCATCTG 18

```

```
RESULT 872
US-11-101-244-49684
; Sequence 49684, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 49684
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-49684

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY      1114 CCCATCATCTACTGCTGC 1131
DB      1  CCCAUCACUCCUACUCGCUUC 18

RESULT 873
US-11-101-244-209546/C
; Sequence 209546, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 209546
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-209546

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1001 TCCACATCTTCTCCCTCC 1018
DB      18  TCCACCTCTTCTCTCTCC 1

RESULT 874
```

```
US-11-101-244-405179/C
; Sequence 405179, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 405179
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-405179

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1405 TTCAGCTTCTCTCCAT 1422
DB      19  TTCAGCTTCTCTCCATT 2

RESULT 875
US-11-101-244-427206
; Sequence 427206, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 427206
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-427206

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY      1550 AAGGCTCAGTATGGGTTA 1567
DB      2   AAGGCGUCAUUAUGGCUUA 19

RESULT 876
US-11-101-244-491396
```

```
/ Sequence 491396, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491396
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491396

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1095 GAGCTCCACCATGTACAA 1112
Db 1 GAGCTCAACCAUGUACAA 18

RESULT 877
US-11-101-244-521114
/ Sequence 521114, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 521114
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-521114

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531574
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531574

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1274 AGACCACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18

RESULT 879
US-11-101-244-531575
/ Sequence 531575, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 531575
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-531575

Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 878
US-11-101-244-531574
/ Sequence 531574, Application US/11101244
```

```
RESULT 880
US-11-101-244-531674
/ Sequence 531674, Application US/11101244
/ Publication No. US20050246794A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531674
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531674

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCUCCACAG 18

RESULT 881
US-11-101-244-531675
; Sequence 531675, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531675
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531675

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCUCCACAG 18

RESULT 882
US-11-101-244-531774
; Sequence 531774, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531774

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCUCCACAG 18

RESULT 883
US-11-101-244-531775
; Sequence 531775, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 531775
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-531775

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCCUCCACAG 18

RESULT 884
US-11-101-244-531872
; Sequence 531872, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```



```
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 531872
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-531872
```

```
Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```
RESULT 885
US-11-101-244-531873
Sequence 531873, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 531873
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-531873
```

```
Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```
RESULT 886
US-11-101-244-531972
Sequence 531972, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
```

```
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 531972
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-531972
```

```
Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```
RESULT 887
US-11-101-244-531973
Sequence 531973, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 531973
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-531973
```

```
Query Match
Best Local Similarity 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1274 AGACCAACCATCTCCACAG 1291
Db 1 AGACUACCAUCUCCACAG 18
```

```
RESULT 888
US-11-101-244-532071
Sequence 532071, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 532071
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-532071
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCUCCACAG 18
```

```
RESULT 889
US-11-101-244-532072
; Sequence 532072, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 532072
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-532072
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1274 AGACCACCATCTCCACAG 1291
Db      1 AGACUACCAUCUCCACAG 18
```

```
RESULT 890
US-11-101-244-578805/c
; Sequence 578805, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 578805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-578805
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1720 ATTTCTGGAAGTACTTT 1737
Db      19 ATTTCTGGAAGTACTT 2
```

```
RESULT 891
US-11-101-244-723652
; Sequence 723652, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 723652
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-723652
```

```
Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      392 AAAGATGAGACAGTGA 409
Db      2 AAAGATGAGACAGTGA 19
```

```
RESULT 892
US-11-101-244-723752
; Sequence 723752, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacom, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 723752
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-723752
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      392 AAGAGATGAGCAGCTGA 409
      |||||:|||||:|||||
Db      2 AAGAAUGAGAACAGUGA 19
```

```

RESULT 893
US-11-101-244-911949
; Sequence 911949, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 911949
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-911949
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      1643 AACCAATCACTGAAGCTT 1660
      |||||:|||||:|||||
Db      2 AACCAAAUCACUGAAAUU 19
```

```

RESULT 894
US-11-101-244-928479/c
; Sequence 928479, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 928479
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-928479
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1007 TCTTCTCTCTCGCCCT 1024
      |||||:|||||:|||||
Db      19 TCTTCTCTCTCGCCCT 2
```

```

RESULT 895
US-11-101-244-1141172
; Sequence 1141172, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1141172
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1141172
```

```

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.5e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      480 CACCTATGCTGTCACAA 497
      |||||:|||||:|||||
Db      1 CACCUAUGCTUGCCACAGA 18
```

```

RESULT 896
US-11-101-244-1259943/c
; Sequence 1259943, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1259943
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1259943

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      650 CCAAGTGTCTCTCTGTG 667
      |||||
DB      19 CCAAGTGTCTCTCTGTG 2

RESULT 897
US-11-101-244-1473036/c
; Sequence 1473036, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1473036
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1473036

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1417 TCCATGTGCTTCTCTAG 1434
      |||||
DB      19 TCCATGTGCTTCTCTAG 2

RESULT 898
US-11-101-244-1484938
; Sequence 1484938, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1484938
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1484938

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 7.5e+02;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY      657 GGTCTGTGTCTCTCTG 674
      |||:|:|:|:|:|:|
DB      1 GGGCAUCUGUCUACUCG 18

RESULT 899
US-09-967-669-87/c
; Sequence 87, Application US/09967669
; Publication No. US2003092650A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Frier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: RTS-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-87

Query Match          0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      963 TGTGTGTGTGTGACCTT 980
      |||||
DB      18 TGTGTGTGTGTGACCTT 1

RESULT 900
US-10-996-951-3
; Sequence 3, Application US/10996951
; Publication No. US20050255493A1
; GENERAL INFORMATION:
; APPLICANT: Macaulay, Valentine Moya
; APPLICANT: Schall, Muhammad
; TITLE OF INVENTION: MOLECULAR TARGETING OF THE IGF-1 RECEPTOR
; FILE REFERENCE: 351044-0011
; CURRENT APPLICATION NUMBER: US/10/996,951
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/GB03/02306
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 0212303.2
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
```

```
FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-996-951-3
Query Match      0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1409 GCCTTCCTCCCAATGTC 1426
DB      3 GCCTTCCTCCCAATGTC 20

RESULT 901
US-10-310-914A-157159
; Sequence 157159, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivzuc
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157159
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-157159

Query Match      0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 8e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      125 GGACCTGAGCCCGCAGGC 142
DB      3 GGACCTGAGCCCGCAGGC 20

RESULT 902
US-10-310-914A-428826
; Sequence 428826, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivzuc
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 428826
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-428826

Query Match      0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 8e+02;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1231 TATTCGAGACCCGAGGC 1248
DB      3 UATCUCGAGACCCGAGGC 20

RESULT 903
US-10-310-914A-677516
```

```
; Sequence 677516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivzuc
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677516
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-677516

Query Match      0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1305 CGAGAGGAGCCGAGGA 1322
DB      3 CAAGAGGAGCCGAGGA 20

RESULT 904
US-10-310-914A-1236794/c
; Sequence 1236794, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivzuc
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1236794
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1236794

Query Match      0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1690 CAGCTTTCTCTCAAGAGC 1707
DB      19 CAGCTTTCTCTCAAGAGC 2

RESULT 905
US-09-780-164-770
; Sequence 770, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Biact, Larry
; APPLICANT: Mswigen, Jim
; TITLE OF INVENTION: Method and Reagent for the inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 770
```

; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-164-770

Query Match 0.9%; Score 16; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 7.1e+02;  
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 801 CATCTGNGTACGTGTG 816  
Db 2 CAUCUGUGACUGUG 17

RESULT 906  
US-11-083-784-523603/c  
; Sequence 523603, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 523603  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-523603

Query Match 0.9%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CACATCTTCTCTCTCC 1018  
Db 16 CACATCTTCTCTCTCC 1

RESULT 907  
US-11-083-784-1146200/c  
; Sequence 1146200, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1146200  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1146200

Query Match 0.9%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CTTCACATCTTCTTC 1014  
Db 17 CTTCACATCTTCTTC 2

RESULT 908  
US-11-101-244-523603/c  
; Sequence 523603, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 523603  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-523603

Query Match 0.9%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 CACATCTTCTCTCTCC 1018  
Db 16 CACATCTTCTCTCTCC 1

RESULT 909  
US-11-101-244-1146200/c  
; Sequence 1146200, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary  
SEQ ID NO 1146200  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-1146200

Query Match 0.9%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CTTCCACATCTTCTTC 1014  
|||  
DB 17 CTTCCACATCTTCTTC 2

RESULT 910  
US-10-370-860A-10/c  
Sequence 10, Application US/10370860A  
Publication No. US20030219791A1  
GENERAL INFORMATION:  
APPLICANT: NOVO NORDISK A/S  
APPLICANT: Wahl, Philip  
APPLICANT: No. US20030219791A1by, Peder Lisby  
APPLICANT: Grondahl, Christen  
APPLICANT: Stenmcke, Vibeke Westphal  
TITLE OF INVENTION: A transducer of Mas Signalling  
FILE REFERENCE: 6475.200-US  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/231,670  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: PA 2002 00277  
PRIOR FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/934,948  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: PCT/DK01/00550  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: PA 2000 01259  
PRIOR FILING DATE: 2000-08-25  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-370-860A-10

Query Match 0.9%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGGCTCTCCGTGCGC 695  
|||  
DB 16 TGGCTCTCTGCTGCGC 1

RESULT 911  
US-10-370-860A-12  
Sequence 12, Application US/10370860A  
Publication No. US20030219791A1  
GENERAL INFORMATION:  
APPLICANT: NOVO NORDISK A/S  
APPLICANT: Wahl, Philip  
APPLICANT: No. US20030219791A1by, Peder Lisby  
APPLICANT: Grondahl, Christen  
APPLICANT: Stenmcke, Vibeke Westphal  
TITLE OF INVENTION: A transducer of Mas Signalling  
FILE REFERENCE: 6475.200-US  
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/231,670  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: PA 2002 00277  
PRIOR FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/934,948  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: PCT/DK01/00550  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: PA 2000 01259  
PRIOR FILING DATE: 2000-08-25  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-370-860A-12

Query Match 0.9%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGGCTCTCCGTGCGC 695  
|||  
DB 5 TGGCTCTCTGCTGCGC 20

RESULT 912  
US-10-310-914A-157270  
Sequence 157270, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyuzet  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 157270  
LENGTH: 20  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-157270

Query Match 0.9%; Score 16; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 8.6e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGACCTGAGCCCGAG 140  
|||  
DB 4 GGACCTGAGCCCGAG 19

RESULT 913  
US-10-310-914A-454995  
Sequence 454995, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyuzet  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 454995

```

; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-454995

Query Match          0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1449 GCGAGGTGACGCCCC 1464
       |||||.....|
DB      2   GGCAGGTGACGCCCC 17

RESULT 914
US-10-206-693-14/c
; Sequence 14, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA interference mediated inhibition of Nogo and Nogo Receptor Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-206-693-14

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCACATCTTCTCCTCT 1019
       |||||.....|
DB      19 TCCTCCTCTTCTCCTCT 1

RESULT 915
US-10-206-693-240
; Sequence 240, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA interference mediated inhibition of Nogo and Nogo Receptor Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT APPLICATION NUMBER: US/10/206,693
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-693-240

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 47.4%; Pred. No. 8.4e+02;
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCACATCTTCTCCTCT 1019
       |||||.....|

```

```

Db          1 UCCUCUCUCUCUCUCUCUCU 19

RESULT 916
US-10-310-914A-151357
; Sequence 151357, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 151357
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-151357

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY          981 CGCCATCTGCTGCGTCC 999
      |||:|:|:|:|:|:|:|:|
Db          1 CCCCCUCUCUCGCGCUCGCC 19

RESULT 917
US-10-310-914A-232218/c
; Sequence 232218, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 232218
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-232218

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          672 CTGGGTCCTGAGCTCTCTG 690
      |||:|:|:|:|:|:|:|:|
Db          19 CCGGGTCCTGAGCTCTCTCTG 1

RESULT 918
US-10-310-914A-360899
; Sequence 360899, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 360899
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-360899

```



NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 360899  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-360899

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 676 GTCTGCTCTCTCCGTCTG 694  
Db 1 GCCCUGGCTCUGGCTGCG 19

## RESULT 919

US-10-310-914A-432064  
Sequence 432064, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 432064  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-432064

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 8.4e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 92 AAAAGCCTCCACCTCC 110  
Db 1 AAAAGCCTCCACCTCC 19

## RESULT 920

US-10-310-914A-542218  
Sequence 542218, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 542218  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-542218

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 8.4e+02;  
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 821 TCTACTTCTCCCTCCCTGCT 839  
Db 1 UCUGCUCUCCTCCCTCCCTG 19

## RESULT 921

US-10-310-914A-846052/C  
Sequence 846052, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 846052  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-846052

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1306 GAGGAGGAGCCAGAGGACG 1324  
Db 19 GAGGAGGAGCCAGAGGACG 1

## RESULT 922

US-10-310-914A-855297  
Sequence 855297, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 855297  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-855297

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 8.4e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1284 CTCGACGCTGCTGGGCGCC 1302  
Db 1 CUCGCCAGUGUGUGGCGCC 19

## RESULT 923

US-10-310-914A-1016265/C  
Sequence 1016265, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402

```
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1016265
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1016265

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1350 GGACCTGACTCCACTGCC 1368
DB 19 GGCCCTGACTCCCACTGCC 1

RESULT 924
US-10-310-914A-1023203
/ Sequence 1023203, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1023203
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1023203

Query Match
Best Local Similarity 52.6%; Score 15.8; DB 1; Length 19;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1003 CACATCTTCTCTCTCTCTGC 1021
DB 1 CACUUCUUCUUCUUCUUCUCC 19

RESULT 925
US-10-310-914A-1026538
/ Sequence 1026538, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1026538
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1026538

Query Match
Best Local Similarity 84.2%; Score 15.8; DB 1; Length 19;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1260 ACTCAGCCCGCTCGAGACC 1278
DB 1 AGCCAGCCCGCTCGAGACC 19
```

```
RESULT 926
US-10-310-914A-1078351/c
/ Sequence 1078351, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1078351
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1078351

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 240 CCTCTCCCAACATCTCC 258
DB 19 CCTCTCCCAACTCTCTCC 1

RESULT 927
US-10-310-914A-1105562/c
/ Sequence 1105562, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1105562
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1105562

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 324 CTACACGCTCATTTGTGTG 342
DB 19 CTACATGCTTATTTGTGTG 1

RESULT 928
US-10-310-914A-1138736/c
/ Sequence 1138736, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
```

SEQ ID NO 1138736  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-914A-1138736

Query Match  
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1383 CTCGAGACATGACAGAG 1401  
Db 19 CTCGAGATCAAGACAGAG 1

RESULT 929  
US-10-914A-1153367  
Sequence 1153367, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kiyazat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087,0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1153367  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-914A-1153367

Query Match  
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 673 TGGGTCTGCTCTCTCTGC 691  
Db 1 UAGGUCGCGCUCUCUCGC 19

RESULT 930  
US-11-014-373-235/c  
Sequence 235, Application US/11014373  
Publication No. US20050196781A1  
GENERAL INFORMATION:  
APPLICANT: Robin, Howard  
TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION  
FILE REFERENCE: 400/241 MBH04-1067  
CURRENT APPLICATION NUMBER: US/11/014,373  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: PCT/US 04/16390  
PRIOR FILING DATE: 2004-05-24  
PRIOR APPLICATION NUMBER: US 10/826,966  
PRIOR FILING DATE: 2004-04-16  
PRIOR APPLICATION NUMBER: US 10/757,803  
PRIOR FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US 10/720,448  
PRIOR FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US 10/693,059  
PRIOR FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT/US03/05346  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT/US03/05028  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 678  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 235  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Target Sequence/siNA sense region  
US-11-014-373-235

Query Match  
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCCAGCGCGGCGGCGG 26  
Db 19 AGCCAGCGCGGCGGCGG 1

RESULT 931  
US-11-014-373-512  
Sequence 512, Application US/11014373  
Publication No. US20050196781A1  
GENERAL INFORMATION:

APPLICANT: McSwiggen, James  
APPLICANT: Robin, Howard  
TITLE OF INVENTION: RNA INTERFERENCE MEDIATED INHIBITION OF STAT3 GENE EXPRESSION  
FILE REFERENCE: 400/241 MBH04-1067  
CURRENT APPLICATION NUMBER: US/11/014,373  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: PCT/US 04/16390  
PRIOR FILING DATE: 2004-05-24  
PRIOR APPLICATION NUMBER: US 10/826,966  
PRIOR FILING DATE: 2004-04-16  
PRIOR APPLICATION NUMBER: US 10/757,803  
PRIOR FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: US 10/720,448  
PRIOR FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US 10/693,059  
PRIOR FILING DATE: 2003-10-23  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT/US03/05346  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT/US03/05028  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 678  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 512  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Target Sequence/siNA sense region  
US-11-014-373-512

Query Match  
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCCAGCGCGGCGGCGG 26  
Db 1 AGCCAGCGCGGCGGCGG 19

RESULT 932  
US-11-083-784-2836  
; Sequence 2836, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 2836  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-2836

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 103 CACCTCTGCTGCTTGA 121  
Db 1 CACCCUCCUUCGCAUUA 19

RESULT 933  
US-11-083-784-49632  
; Sequence 49632, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 49632  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-49632

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 8.4e+02;  
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1104 CATGTACACCCATCATC 1122  
Db 1 CAUCUACAUCUCCAUCAUC 19

RESULT 934  
US-11-083-784-49652  
; Sequence 49652, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 49652  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-49652

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1106 TGTACACCCATCATCTA 1124  
Db 1 UCUCACAUCUCCAUCAUCA 19

RESULT 935  
US-11-083-784-96612  
; Sequence 96612, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 96612  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-96612

Query Match 0.9%; Score 15.8; DB 1; Length 19;

Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 447 CTCGATGGCTGCATTCAT 465  
|||:||||:||||:  
Db 1 CGCCATGGCUGCAUUGAAU 19

## RESULT 936

US-11-083-784-104234/c

; Sequence 104234, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 104234  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-11-083-784-104234

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCTCC 1018  
|||||:|||||:|||||:  
Db 19 TTCACATCTTCTCTCTCC 1

## RESULT 937

US-11-083-784-116911

; Sequence 116911, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 116911  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-11-083-784-116911

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGGCTGTCTACTG 524  
|||:||||:||||:|  
Db 1 ACUACGGGCGUCUCUACUG 19

## RESULT 938

US-11-083-784-116984

; Sequence 116984, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 116984  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-11-083-784-116984

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGGCTGTCTACTG 524  
|||:||||:||||:|  
Db 1 ACUACGGGCGUCUCUACUG 19

## RESULT 939

US-11-083-784-117020

; Sequence 117020, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117020

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117020
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCGCTGTCTACTG 524
      ||:|||||:|:|:|:|:|
DB      1 ACUACGGCGCUCGCUACUG 19
```

```
RESULT 940
US-11-083-784-117049
; Sequence 117049, Application US//11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117049
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117049
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCGCTGTCTACTG 524
      ||:|||||:|:|:|:|:|
DB      1 ACUACGGCGCUCGCUACUG 19
```

```
RESULT 941
US-11-083-784-117107
; Sequence 117107, Application US//11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```

```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117107
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117107
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCGCTGTCTACTG 524
      ||:|||||:|:|:~|:|
DB      1 ACUACGGCGCUCGCUACUG 19
```

```
RESULT 942
US-11-083-784-117181
; Sequence 117181, Application US//11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117181
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117181
```

```
Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      506 ACTACGGCGCTGTCTACTG 524
      ||:|||||:|:~|:|:|
DB      1 ACUACGGCGCUCGCUACUG 19
```

```
RESULT 943
US-11-083-784-117219
; Sequence 117219, Application US//11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US//11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
```

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117219

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCUCUCUACUG 19

RESULT 944
US-11-083-784-117250
; Sequence 117250, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 117250
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-117250

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTTCTACTG 524
Db      1 ACUACGGGCGUCUCUCUACUG 19

RESULT 945
US-11-083-784-155785
; Sequence 155785, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 155785
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-155785

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      650 CCAAGTGTCTATCTGTCT 668
Db      1 CCAAGGUGUCUCUCUGUGU 19

RESULT 946
US-11-083-784-190805
; Sequence 190805, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-190805

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 8.4e+02;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1002 CCACATCTTCTCTCTCTG 1020
Db      1 CCACAUUCUCUCUCUCUCUG 19

RESULT 947
US-11-083-784-190884
; Sequence 190884, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 190884  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-190884

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 52.6%; Pred. No. 8.4e+02;  
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1002 CCACATCTTCTTCCTCG 1020  
Db 1 CCACATCTTCTTCCTCG 19

RESULT 948  
US-11-083-784-198455  
Sequence 198455, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 198455  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-198455

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTACTG 524  
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 949  
US-11-083-784-198486  
Sequence 198486, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin

APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 198486  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-198486

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTACTG 524  
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 950  
US-11-083-784-198511  
Sequence 198511, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 198511  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-198511

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTACTG 524  
Db 1 ACUACGGCGCUCUCUACUG 19

RESULT 951  
US-11-083-784-198533  
Sequence 198533, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.



```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198533
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198533

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 506 ACTACGGCGCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

```

```

RESULT 952
US-11-083-784-198551
; Sequence 198551, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198551
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198551

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 506 ACTACGGCGCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

```

```

RESULT 953
US-11-083-784-198589
; Sequence 198589, Application US/11083784

```

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198589

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 506 ACTACGGCGCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

```

```

RESULT 954
US-11-083-784-198623
; Sequence 198623, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198623
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-198623

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 506 ACTACGGCGCTGTCTACTG 524
Db 1 ACUACGGCGCUCUCUACUG 19

```

RESULT 955  
US-11-083-784-198673  
; Sequence 198673, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 198673  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-198673

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCGCTGTCTACTG 524  
||:|||||:|:|:|:|:  
Db 1 ACUACGGCGCTGCGUCUACUG 19

RESULT 956  
US-11-083-784-198715  
; Sequence 198715, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 198715  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-198715

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCGCTGTCTACTG 524  
||:|||||:|:|:|:|:  
Db 1 ACUACGGCGCTGCGUCUACUG 19

Db 1 ACUACGGCGCTGCGUCUACUG 19

RESULT 957  
US-11-083-784-207465  
; Sequence 207465, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 207465  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-207465

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 986 TCTGCTGGCTGCGCCCTTCCA 1004  
||:|||||:|:|:|:|:  
Db 1 UCUCUGGCTGCGCCCUCA 19

RESULT 958  
US-11-083-784-222212  
; Sequence 222212, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 222212  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-222212

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 8.4e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 398 TGAGGACAGTGAAGACTA 416  
:|||||:|||||  
Db 1 UGAGGACAGUCCACCACTA 19

```

RESULT 959
US-11-083-784-225150
; Sequence 225150, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 225150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-225150

```

Query Match	0.9%	Score 15.8	DB 1	Length 19
Best Local Similarity	73.7%	Pred. No. 8.4e+02		
Matches 14, Conservative		3, Mismatches 2,	Indels 0,	Gaps 0

QY 75 AAAGAGTGTGCCATAA 93  
|||:|:|:|:  
Db 1 AAGAGAGTGTGACCAUAA 19

```

RESULT 960
US-11-083-784-256569/c
; Sequence 256569, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-256569

```

```

Query Match      0.94;   Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      984 CATGCTGCTGCTGCTTC 1002
      |||||
Db      19 CATGCTGCTGCTGCTTC 1

```

```

QY      984  CATCGCTGAGCTGCCTTC  1002
        ||||| ||||| |||||
Db      19  CATCTGCTGACTGCACCTTC  1

RESULT 961
US-11-083-784-256617/c
: Sequence 256617, Application US/11083784
: Publication No. US20050245475A1
: GENERAL INFORMATION:
: APPLICANT: Dharmacon, Inc.
: APPLICANT: Khvorovca, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional sRNA
: FILE REFERENCE: 13490US
: CURRENT APPLICATION NUMBER: US/11/083,784
: CURRENT FILING DATE: 2005-03-18
: PRIOR APPLICATION NUMBER: US/10/714,333
: PRIOR FILING DATE: 2003-11-14
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 256617
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-083-784-256617

```

Query Match	0.9%	Score 15.8	DB 1	Length 19
Best Local Similarity	89.5%	Pred. No. 8.4e+02		
Match 17, Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy 985 ATCTGCTGCGCTGCCCTTC 1003  
Db 19 ATCTGCTGACTGCACCTTC 1

```

RESULT 962
US-11-083-784-259212/C
Sequence 259212, Application US/11083784
Publication No. US2005024475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/7714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 259212
LENGTH: 19
TYPE: RNA

```

```
; ORGANISM: Homo sapiens
US-11-083-784-259212

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCCACATCTTCTTCTCC 1018
Db 19 TTCTCATCTTCTTCTCC 1

RESULT 963
US-11-083-784-275438/c
; Sequence 275438, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 275438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-275438

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 526 AAGTTCACACTTCTTCTC 544
Db 19 AACTTCACACATCTTCTC 1

RESULT 964
US-11-083-784-398635
; Sequence 398635, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 398635
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-398635

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1620 CCACCCCTCATGCTGTGTGA 1638
Db 1 CCACCCUAATCCGTGTGGA 19

RESULT 965
US-11-083-784-411203/c
; Sequence 411203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 411203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-411203

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCCACATCTTCTTCTCC 1018
Db 19 TTCTCATCTTCTTCTCC 1

RESULT 966
US-11-083-784-425415/c
; Sequence 425415, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 425415  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-425415

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCC 1018  
Db 19 TTCCTCATCTTCTCTCTCC 1

RESULT 967  
US-11-083-784-482386  
; Sequence 482386, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 482386  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-482386

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCTCTTCA 1004  
Db 1 UCUCUGGCUUCCUUCUA 19

RESULT 968  
US-11-083-784-482438  
; Sequence 482438, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14

;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 482438  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-482438

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCTCTTCA 1004  
Db 1 UCUCUGGCUUCCUUCUA 19

RESULT 969  
US-11-083-784-490736  
; Sequence 490736, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 490736  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-490736

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 447 CTCAGTGGCTGATTCAT 465  
Db 1 CUGCAUGGCUUCCUUCUA 19

RESULT 970  
US-11-083-784-490744  
; Sequence 490744, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784



```

; APPLICANT: leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491367

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 941 GCAGGCTGCTCAAAATGAT 959
Db 1 GAAAGCTGUCCAAAUGAU 19

RESULT 975
US-11-083-784-491377
; Sequence 491377, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Keynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491377
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491377

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 986 TCTGCTGCTGCGCTTCA 1004
Db 1 UCUGCTGCTGCGCTCAUCA 19

RESULT 976
US-11-083-784-504820
; Sequence 504820, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Keynolds, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 504820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-504820

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1089 GGCATGAGCTCCACATG 1107
Db 1 GGCACUACGCTCCACAU 19

RESULT 977
US-11-083-784-520347/C
; Sequence 520347, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Keynolds, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 520347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-520347

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 571 TACTCATGACGCGTGG 589
Db 1 TTCTCAATGACGCGTGG 1

RESULT 978
US-11-083-784-521051
```

```

; Sequence 521051, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 521051
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-521051

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1046 TGAAGAGTTTATCCGCA 1064
DB      1 UCAGAGAGUUAUCCGAA 19

```

```

RESULT 979
US-11-083-784-537233/C
; Sequence 537233, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 537233
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-537233

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      652 AAAGGTCATCTGTCGCA 670
DB      19 AAAGGTCATCTGTCATCA 1

```

```

RESULT 980
US-11-083-784-548572
; Sequence 548572, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 548572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-548572

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      774 GAACAAGTTTATGAGAA 792
DB      1 GCACAACAUUUAUGAGAA 19

```

```

RESULT 981
US-11-083-784-647566
; Sequence 647566, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647566
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-647566

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1713 GCATTCATTCTGGAAT 1731

```



Db 1 GCAAUUCAUUUCUGAAGU 19

## RESULT 982

US-11-083-784-647654  
; Sequence 647654, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 647654  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-647654

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1713 GCATTCATTCTTGTGAGT 1731

Db 1 GCAAUUCAUUUCUGAAGU 19

## RESULT 983

US-11-083-784-651197/c  
; Sequence 651197, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 651197  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-651197

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 801 CATCTGTGACTGTGCTG 819

Db 19 CATCTGGGTGGCTGTGCTG 1

## RESULT 984

US-11-083-784-692671/c  
; Sequence 692671, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 692671  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-692671

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 526 AAGTCCACAACCTCTTC 544

Db 19 AATTCACCACTTCTTC 1

## RESULT 985

US-11-083-784-809922/c  
; Sequence 809922, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 809922  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-809922

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 652 AAAGTGTCTATCTGTGCA 670  
DB 19 AATGTGTCTATCTGTGCA 1

## RESULT 986

US-11-083-784-835805  
Sequence 835805, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 835805  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-835805

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 576 CATGACGCTGTGCTCTT 594  
DB 1 CAUGAUGAUGGCGCCUU 19

RESULT 987  
US-11-083-784-895312/c  
Sequence 895312, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 895312  
LENGTH: 19

TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-895312

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1000 TTCACATCTTCTCTCC 1018  
DB 19 TTCACATCTTCTCTCC 1

RESULT 988  
US-11-083-784-946407/c  
Sequence 946407, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 946407  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-946407

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1720 ATTCTGGAAGTACTTG 1738  
DB 19 AATCTGGAAGTACTTG 1

RESULT 989  
US-11-083-784-951796/c  
Sequence 951796, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 951796
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-951796

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%;	Pred. No. 8.4e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy		568	ATCTACTCCATGACGGCTG	586
Db		19	ATATACTCCATGACGTCTG	1

RESULT 990  
US-11-083-784-973051

```

sequence 573051, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Pharmakon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 973051
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-973051

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	73.7%;	Pred. No. 8.4e+02;		
Matches 14;	Conservative	3;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy	247	CCAACATCTCCACTACA	265
		: : :	
Db	1	CCAACAUUCUCACTUACA	19

RESULT 991  
US-11-083-784-978358/c  
Sequence 978358, Application US/11083784  
Publication No. US20050245475X1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khavrova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional sIRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083.784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 978356

```

ORGANISM: Homo sapiens  
US-11-083-784-978358

Query Match	0.94;	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%;	Pred. No. 8.4e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      1080 CATGTGGCTGGCCATGAGC 1098
          ||| ||||| |||||
Db      19 CATATGGCTGTCATGAGC 1

```

RESULT 992  
US-11-083-784-1073668/c  
; Sequence 1073668, Application US/11083784

```

PUBLICATION NO: US20050243475AI
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 154990US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/7714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1073668
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1073668

```

Query Match	0.94;	Score 15.8;	DB 1;	length 19;
Best Local Similarity	89.5%;	Pred. No. 8.4e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1003	CACATCTTCTTCCTCCTGC	1021
Db	19	CACCTTCTTCTTCCTCCTCC	1

```

RESULT 993
US-11-083-784-1077487/c
: Sequence 1077487, Application US/11083784
: Publication No. US20050245475A1
: GENERAL INFORMATION:
: APPLICANT: Dharmacon, Inc.
: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 15499US
: CURRENT APPLICATION NUMBER: US/11/083, 784
: CURRENT FILING DATE: 2005-03-18
: PRIORITY APPLICATION NUMBER: US/10/774, 333

```

;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1077487  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-1077487

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1572 AATCATTCATCATTGAGT 1590  
Db 19 AATCATTCATCATTGAGT 1

RESULT 994  
US-11-083-784-1112807/c  
;; Sequence 1112807, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1112807  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-1112807

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAAGTCTCTCC 226  
Db 19 GAATGATTAAGTCTCTCC 1

RESULT 995  
US-11-083-784-1112871/c  
;; Sequence 1112871, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US

;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1112871  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-1112871

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 GAATGATTAAGTCTCTCC 226  
Db 19 GAATGATTAAGTCTCTCC 1

RESULT 996  
US-11-083-784-1115683/c  
;; Sequence 1115683, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; APPLICANT: Scaringe, Stephen  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/083,784  
;; CURRENT FILING DATE: 2005-03-18  
;; PRIOR APPLICATION NUMBER: US/10/714,333  
;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1115683  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-1115683

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1408 AGCTTCCTCCAAATGTGC 1426  
Db 19 AGCTTCCTCCAAATGTGC 1

RESULT 997  
US-11-083-784-1115733/c  
;; Sequence 1115733, Application US/11083784  
;; Publication No. US20050245475A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 115733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-115733

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1408 AGCTTCCTCCATGTC 1426
Db      19 AGCTTCACCCACCAATGTC 1

```

```

RESULT 998
US-11-083-784-1141062/c
; Sequence 1141062, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1141062

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCACATCTGCACTCTCC 1

```

```

RESULT 999
US-11-083-784-1145497/c
; Sequence 1145497, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1145497
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1145497

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCACATCTTCTCTCC 1

```

```

RESULT 1000
US-11-083-784-1159730/c
; Sequence 1159730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1159730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1159730

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCATCTCTCTCTCC 1

```

```

RESULT 1001
US-11-083-784-1257590/c
; Sequence 1257590, Application US/11083784
; Publication No. US20050245475A1

```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1257590
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1257590

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTTCCTCC 1018
DB      19  TTCCTCTTCTTCTCTCC 1

RESULT 1002
US-11-083-784-1323231
/ Sequence 1323231, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1323231
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1323231

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1356 GACCTCACTGCTCTTCA 1374
DB      1  GACCTGACCTGCTCTTCA 19

RESULT 1003
```

```
US-11-083-784-1350821/c
/ Sequence 1350821, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1350821
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1350821

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      652 AAAGTGATCTGTGTCA 670
DB      19  AATGTGATCTGTGTCA 1

RESULT 1004
US-11-083-784-1351424/c
/ Sequence 1351424, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1351424
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1351424

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      391 AAAAGATGAGGACATGA 409
DB      19  AAAATATGAGGACATGA 1
```

```
RESULT 1005
US-11-083-784-1370891/c
; Sequence 1370891, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1370891
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1370891

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      49 TATTCGAGCGCCGACTTCA 67
Db      19 TATTCGAGAGCCCTGTCA 1

RESULT 1006
US-11-083-784-1388942
; Sequence 1388942, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1388942
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1388942

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1116 CATCATCTACTGCTGCTTC 1134
Db      1 CAUCACUCACUCGCUCAUC 19

RESULT 1007
US-11-083-784-1513262/c
; Sequence 1513262, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513262
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513262

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1000 TTCACATCTTCTTCTCTCC 1018
Db      19 TTCGACCTCTTCTCTCTCC 1

RESULT 1008
US-11-083-784-1513264/c
; Sequence 1513264, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513264

Query Match      0.9%; Score 15.8; DB 1; Length 19;
```





Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 8.4e+02;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1104 CATGTACACCCCATCATC 1122  
Db 1 CAUCUACAUCCAUC 19

RESULT 1013

US-11-101-244-49652  
; Sequence 49652, Application US/11101244  
; Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 49652

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-49652

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1106 TGTACACCCCATCATCTA 1124  
Db 1 UCUCACAUCCAUCU 19

RESULT 1014

US-11-101-244-96612

; Sequence 96612, Application US/11101244

; Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 96612

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-96612

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 447 CTCGATGCTGCTTCAT 465  
Db 1 CGCCAUUGCUGCAUUGAU 19

RESULT 1015

US-11-101-244-104234/C

; Sequence 104234, Application US/11101244

; Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 104234

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-104234

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1000 TTCCACATCTTCTCCCTCC 1018  
Db 19 TTCACCTTCTCTTCTCC 1

RESULT 1016

US-11-101-244-116911

; Sequence 116911, Application US/11101244

; Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

PRIOR FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 116911

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-101-244-116911

Query Match 0.9%; Score 15.8; DB 1; Length 19;

Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524  
||:|||||:|:|:|:|:  
DB 1 ACUACGGGCGUCUCUACUG 19

RESULT 1017

US-11-101-244-116984  
; Sequence 116984, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 116984  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-116984

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524  
||:|||||:|:|:|:|:  
DB 1 ACUACGGGCGUCUCUACUG 19

RESULT 1018

US-11-101-244-117020  
; Sequence 117020, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117020  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117020

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;

Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524  
||:|||||:|:|:|:|:  
DB 1 ACUACGGGCGUCUCUACUG 19

RESULT 1019

US-11-101-244-117049  
; Sequence 117049, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117049  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117049

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524  
||:|||||:~:~:~:~:~:  
DB 1 ACUACGGGCGUCUCUACUG 19

RESULT 1020

US-11-101-244-117107  
; Sequence 117107, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117107  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117107

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 506 ACTACGGCGCTGTCTACTCG 524  
||:|||||:|:|:|:|:  
Db 1 ACUACGGCGCGUCUCUCACUG 19

## RESULT 1021

US-11-101-244-117181  
; Sequence 117181, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117181  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117181

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 506 ACTACGGCGCTGTCTACTCG 524  
||:|||||:|:|:|:|:  
Db 1 ACUACGGCGCGUCUCUCACUG 19

## RESULT 1022

US-11-101-244-117219  
; Sequence 117219, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117219  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117219

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 506 ACTACGGCGCTGTCTACTCG 524  
||:|||||:|:|:|:|:  
Db 1 ACUACGGCGCGUCUCUCACUG 19

## RESULT 1023

US-11-101-244-117250  
; Sequence 117250, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Khvorova, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 117250  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-117250

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 506 ACTACGGCGCTGTCTACTCG 524  
||:|||||:|:~|:|:|:|:  
Db 1 ACUACGGCGCGUCUCUCACUG 19

## RESULT 1024

US-11-101-244-155785  
; Sequence 155785, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 155785  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-155785

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 57.9%; Pred. No. 8.4e+02;  
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 CCAAGUGUGCCUCUCUGU 19

```

RESULT 1025
US-11-101-244-190805
; Sequence 190805, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-190805

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 8.4e+02;  
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1002 CCACATCTTCTTCCCTCG 1020  
 Db 1 CCACATCTTCTTCCCTCG 19

```

RESULT 1026
US-11-101-244-190884
; Sequence 190884, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 190884
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-190884

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 52.6%; Pred. No. 8.4e+02;  
 Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1002 CCACATCTTCTTCCCTCG 1020  
 Db 1 CCACATCTTCTTCCCTCG 19

Db 1 CCAAGUGUGCCUCUCUGU 19

```

RESULT 1027
US-11-101-244-198455
; Sequence 198455, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198455
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198455

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTTACTG 524  
 Db 1 ACUACGGGCGUCUCUACUG 19

```

RESULT 1028
US-11-101-244-198486
; Sequence 198486, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198486

```

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTCTTACTG 524  
 Db 1 ACUACGGGCGUCUCUACUG 19

```

RESULT 1029
US-11-101-244-198511
; Sequence 198511, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198511

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
|:|||||:|:|:|:|:|
Db 1 ACUACGGGCGUCUCUACUG 19

```

```

RESULT 1030
US-11-101-244-198533
; Sequence 198533, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198533
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198533

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
|:|||||:|:|:|:|:|
Db 1 ACUACGGGCGUCUCUACUG 19

```

```

RESULT 1031
US-11-101-244-198551
; Sequence 198551, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198551
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198551

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
|:|||||:|:|:|:|:|
Db 1 ACUACGGGCGUCUCUACUG 19

```

```

RESULT 1032
US-11-101-244-198589
; Sequence 198589, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198589

```

```

Query Match
Best Local Similarity 63.2%; Score 15.8; DB 1; Length 19;
Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 506 ACTACGGCCTGTTCTACTG 524
|:|||||:~:~:~:~:~:
Db 1 ACUACGGGCGUCUCUACUG 19

```

```

RESULT 1033
US-11-101-244-198623
; Sequence 198623, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198623
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198623

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTCTACTG 524
DB      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1034
US-11-101-244-198673
; Sequence 198673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198673
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198673

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTCTACTG 524
DB      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1035

```

```

US-11-101-244-198715
; Sequence 198715, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 198715
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-198715

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      506 ACTACGGCCTGTCTACTG 524
DB      1 ACUACGGGCGUCGUCUACUG 19

RESULT 1036
US-11-101-244-207465
; Sequence 207465, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 207465
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-207465

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      986 TCTGCTGGCTGCGCTTCCA 1004
DB      1 UCUCGCGGCGUCGUCUCAA 19

RESULT 1037
US-11-101-244-222212

```

```
; Sequence 222212, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222212
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-222212
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 398 TGAGGACGAGTGCACCACTA 416
Db 1 TGAGGACGAGTGCACCACTA 19
```

```
RESULT 1038
US-11-101-244-225150
; Sequence 225150, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 225150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-225150
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 75 AAAAGAGTCTGCCCATAA 93
Db 1 AAGGAGGUGCUGACCAUA 19
```

```
RESULT 1039
US-11-101-244-256569/c
; Sequence 256569, Application US/11101244
```

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-256569
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 984 CATCTGCTGGCTGCCCTTC 1002
Db 19 CATCTGCTGACTGCACCTTC 1
```

```
RESULT 1040
US-11-101-244-256617/c
; Sequence 256617, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 256617
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-256617
```

```
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 985 ATCTGCTGCTGCCCTTCC 1003
Db 19 ATCTGCTGACTGCACCTTC 1
```

```
RESULT 1041
US-11-101-244-259212/c
; Sequence 259212, Application US/11101244
; Publication No. US20050246794A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 259212
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-259212

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1000 TTCACATCTTCTCTCTCC 1018
DB      19  TTCTCATCTTCTTCTCATCC 1

RESULT 1042
US-11-101-244-275438/c
/ Sequence 275438, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 275438
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-275438

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      526 AAGTTCACAACTTCTTTC 544
DB      19  AACTTCACAACTCTTTC 1

RESULT 1043
US-11-101-244-398635
/ Sequence 398635, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 398635
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-398635

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      1620 CCACCTTCATCGCTGTGCA 1638
DB      1  CCACCCUAAUCCUGUGUGA 19

RESULT 1044
US-11-101-244-411203/c
/ Sequence 411203, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 411203
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-411203

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1000 TTCACATCTTCTCTCTCC 1018
DB      19  TTCTCATCTTCTTCTCATCC 1

RESULT 1045
US-11-101-244-425415/c
/ Sequence 425415, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```



```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 425415
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-425415

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1000 TTCCACATCTTCTCTCC 1018
DB      19  TTCCATCTTCTCTCTCC 1

```

```

RESULT 1046
US-11-101-244-482386
; Sequence 482386, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 482386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-482386

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      986 TCTGCTGGCTGCGCTTCCA 1004
DB      1  UCUGCGGCGUCCCUCCUA 19

```

```

RESULT 1047
US-11-101-244-482438
; Sequence 482438, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

```

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 482438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-482438

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      986 TCTGCTGGCTGCGCTTCCA 1004
DB      1  UCUGCGGCGUCCCUCCUA 19

```

```

RESULT 1048
US-11-101-244-490736
; Sequence 490736, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 490736
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-490736

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      447 CTCATGGCTGCGCTTCAAT 465
DB      1  CUGAUGGCGUCCCUCCAU 19

```

```

RESULT 1049
US-11-101-244-490744
; Sequence 490744, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

```

```
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 490744
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-490744

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      562 GCCAGTATCTACTCCATGA 580
Db      1 GUCAGCAUCUACUCCAUCA 19

RESULT 1050
US-11-101-244-490754
/ Sequence 490754, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 490754
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-490754

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1097 GCTCCACCATGTACACCC 1115
Db      1 GCUUCACCAUGUACAUC 19

RESULT 1051
US-11-101-244-491301
/ Sequence 491301, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
```

```
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ PRIOR FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491301
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491301

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1090 GCCATGAGCTCCACCATGT 1108
Db      1 GCAUGAGCUCUACCAUGU 19

RESULT 1052
US-11-101-244-491346
/ Sequence 491346, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 491346
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-491346

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1097 GCTCCACCATGTACACCC 1115
Db      1 GCUCAACCAUGUACAUC 19

RESULT 1053
US-11-101-244-491367
/ Sequence 491367, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491367
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-491367

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      941 GCAAGGTGTCACAAATGAT 959
Db      1 GAAAGGUTGCAAAAU 19

RESULT 1054
US-11-101-244-491377
; Sequence 491377, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491377
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-491377

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      986 TCTGCTGCTGCTCTTCA 1004
Db      1 UCUGCUGGCGCCCAUCA 19

RESULT 1055
US-11-101-244-504820
; Sequence 504820, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 504820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-504820

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.4e+02;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1089 GGCATGAGCTCCACCATG 1107
Db      1 GGCAUCAGCUCCAACAU 19

RESULT 1056
US-11-101-244-520347/c
; Sequence 520347, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 520347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-520347

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      571 TACTCATGACGCGTGTG 589
Db      19 TTCTCATGACGCGTGTG 1

RESULT 1057
US-11-101-244-521051
; Sequence 521051, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 521051
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-521051

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 8.4e+02;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1046 TGAAGAAATTATCCAGCA 1064  
: |||||:::|||||  
Db 1 UCAAGAGUUAUCCAGAA 19

```
RESULT 1058
US-11-101-244-537233/c
/ Sequence 537233, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 537233
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-537233

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 652 AAAGTCATCTGTGTCA 670  
: |||||:::|||||  
Db 19 AAAGTCATCTGTATCA 1

```
RESULT 1059
US-11-101-244-548572
/ Sequence 548572, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
```

```
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 548572
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-548572

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 8.4e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

Qy 774 GAACAAGATTATGAGAA 792  
: |||||:::|||||  
Db 1 GCAACACAUUUGAGAA 19

```
RESULT 1060
US-11-101-244-647566
/ Sequence 647566, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 647566
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-647566

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1713 GCATTCATTTCGAACT 1731  
: |||||:::|||||  
Db 1 GCAUUCAUUUCUGAAGU 19

```
RESULT 1061
US-11-101-244-647654
/ Sequence 647654, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
```

```

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647654
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-647654
```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY      1713 GCATTCATTCTGGAAGT 1731
Db      1 GCAUUCUAUUCUGAAGU 19
```

```

RESULT 1062
US-11-101-244-651197/c
; Sequence 651197, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 651197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-651197
```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      801 CATCTGTGACGTGCTG 819
Db      19 CATCTGCTGCTGCTGCTG 1
```

```

RESULT 1063
US-11-101-244-692671/c
; Sequence 692671, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 692671
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-692671
```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      526 AAGTCCACCACTCTTTC 544
Db      19 AATTCACCACTTCTTTC 1
```

```

RESULT 1064
US-11-101-244-809922/c
; Sequence 809922, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 809922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-809922
```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      652 AAAGTGCATCTGTGTC 670
Db      19 AATGTGTCACCTGTGTC 1
```

```

RESULT 1065
US-11-101-244-835805
; Sequence 835805, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

```

; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 835805
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-835805

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 8.4e+02;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      576 CATGACGGCTGTGACCTTT 594
Db      1 CAUGAUGAUGUGGACCUU 19

```

```

RESULT 1066
US-11-101-244-895312/C
; Sequence 895312, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 895312
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-895312

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1000 TTCACATCTTCTCTCC 1018
Db      19 TTCAGTCTTCTCTCC 1

```

```

RESULT 1067
US-11-101-244-946407/C
; Sequence 946407, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 946407
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-946407

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1720 ATTTCTGGAAGTACCTTG 1738
Db      19 AATTCTGGAAGTACCTTG 1

```

```

RESULT 1068
US-11-101-244-951796/C
; Sequence 951796, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 951796
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-951796

```

```

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      568 ATCTACTCATGACGCTG 586
Db      19 ATATCTCATGACGCTG 1

```

```

RESULT 1069
US-11-101-244-973051
; Sequence 973051, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137

```

;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 973051  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-973051

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 8.4e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 247 CCAACATCTCCACTACACA 265  
Db 1 CCAACACUCUCCACUCUACA 19

RESULT 1070  
US-11-101-244-978358/c  
;; Sequence 978358, Application US/11101244  
;; Publication No. US20050246794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; PRIOR FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 978358  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-978358

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1080 CATGTGCTGGCCATGAGC 1098  
Db 19 CATGTGCTGCTCATGAGC 1

RESULT 1071  
US-11-101-244-1073668/c  
;; Sequence 1073668, Application US/11101244  
;; Publication No. US20050246794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; PRIOR FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14

;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1073668  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-1073668

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1003 CACATCTCTTCCCTCCGTC 1021  
Db 19 CACTTCTTCTCTCTCTCC 1

RESULT 1072  
US-11-101-244-1077487/c  
;; Sequence 1077487, Application US/11101244  
;; Publication No. US20050246794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; PRIOR FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1077487  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-101-244-1077487

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1572 AAACATTCATCCTTGAGT 1590  
Db 19 AATCATTCATCATTTGAGT 1

RESULT 1073  
US-11-101-244-1112807/c  
;; Sequence 1112807, Application US/11101244  
;; Publication No. US20050246794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dharmacon, Inc.  
;; APPLICANT: Khvorova, Anastasia  
;; APPLICANT: Reynolds, Angela  
;; APPLICANT: Leake, Devin  
;; APPLICANT: Marshall, William  
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
;; FILE REFERENCE: 13499US  
;; CURRENT APPLICATION NUMBER: US/11/101,244  
;; PRIOR FILING DATE: 2005-04-07  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 1112807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1112807

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      208 GAATGATTAACGCTCTCC 226
Db      19 GAAGTGATTAACGCTCTCC 1

```

```

RESULT 1074
US-11-101-244-1112871/c
; Sequence 1112871, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1112871
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1112871

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      208 GAATGATTAACGCTCTCC 226
Db      19 GAAGTGATTAACGCTCTCC 1

```

```

RESULT 1075
US-11-101-244-1115683/c
; Sequence 1115683, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

```

```

; SEQ ID NO 1115683
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1115683

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1408 AGCTTCTCTCCATGTCG 1426
Db      19 AGCTTCAACCAATGTCG 1

```

```

RESULT 1076
US-11-101-244-1115733/c
; Sequence 1115733, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1115733
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1115733

```

```

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1408 AGCTTCTCTCCATGTCG 1426
Db      19 AGCTTCAACCAATGTCG 1

```

```

RESULT 1077
US-11-101-244-1141062/c
; Sequence 1141062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1141062

```



```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1141062

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCACATCTCTCTCTCTCC 1

RESULT 1078
US-11-101-244-1145497/c
; Sequence 1145497, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1145497
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1145497

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCACATATCTCTCTCTCC 1

RESULT 1079
US-11-101-244-1159730/c
; Sequence 1159730, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1159730
; LENGTH: 19
; TYPE: RNA
```

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1159730

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCCTCATCTCTCTCTCC 1

RESULT 1080
US-11-101-244-1257590/c
; Sequence 1257590, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257590
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1257590

Query Match          0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1000 TTCACATCTTCTCTCTCC 1018
Db      19   TTCCTCTTCTCTCTCTCC 1

RESULT 1081
US-11-101-244-1323231
; Sequence 1323231, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1323231
; LENGTH: 19
; TYPE: RNA
```

; ORGANISM: Homo sapiens  
US-11-101-244-1323231

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 8.4e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1356 GACCTCCAACTGCTCTCA 1374  
Db 1 GACCTGACCTGCTCTCA 19

RESULT 1082

US-11-101-244-1350821/c  
; Sequence 1350821, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1350821  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1350821

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 652 AAAGTGTCATCTGTCTCA 670  
Db 19 AATGTGTCATCTGTCTCA 1

RESULT 1083

US-11-101-244-1351424/c  
; Sequence 1351424, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1351424  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-11-101-244-1351424

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 391 AAAAGATGAGGAGGAGTCA 409  
Db 19 AAAATATGAGGAGGAGTCA 1

RESULT 1084

US-11-101-244-1370891/c  
; Sequence 1370891, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1370891  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1370891

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 8.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 TATTTGAGGCCAGTCTCA 67  
Db 19 TATTTGAGGCCAGTCTCA 1

RESULT 1085

US-11-101-244-1388942  
; Sequence 1388942, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1388942  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1388942

Query Match	0.9%;	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	57.9%;	Pred. No. 8.4e+02;		
Matches 11; Conservative	6;	Mismatches 2;	Indels	

Qy	1116	CATCATCTACTGCTGCCTC	1134
		::  ::  ::  ::  ::	
Db	1	CAUCAUCUACUGCUCAUC	19

```

RESULT 1086
US-11-101-244-1513262/C
Sequence 1513262, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIORITY APPLICATION NUMBER: 60/502,050
PRIORITY FILING DATE: 2003-09-10
PRIORITY APPLICATION NUMBER: 60/426,137
PRIORITY FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1513262
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1513262

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%;	Pred. No. 8.4e+02;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1000	TTCCACATCTTCTTCCTCC	1018
Db	19	TTGACCTCTTCTTCCTCC	1

```

RESULT 1087
US-11-101-244-1513264/c
; Sequence 1513264, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIORITY FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIORITY FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513264
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; OS-11-101-244-1513264

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%;	Pred. No. 8.4e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1000	TTCCACATCTTCTTCCTCC	1018
Db	19	TTGCACCTCTTCTTCCTCC	1

```

RESULT 1088
US-11-101-244-1564341/c
Sequence 1564341, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, David
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 15499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1564341
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1564341

```

Query Match	0.9%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%	Pred. No. 8.4e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1655	GAAC	TTGT	GAGC	CTGT	1673
Db	19	GAAC	TTGC	AGAC	CTTTA	1

```

RESULT 1089
US-11-101-244-1582659/c
; Sequence 1582659, Application US/11101244
; Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1582659
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1582659
Query Match
0.9% Score 15.8; DB 1; Length 19

```

Query Match	0.9%; Score 15.8; DB 1; Length 19;
-------------	------------------------------------

```
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1402 AGCTCAGCTTCCTCCCA 1420
Db 19 ATCTTCAGCATCTCTCCA 1

RESULT 1090
US-11-069-611-255/c
; Sequence 255, Application US/11069611
; Publication No. US2006058255A1
; GENERAL INFORMATION:
; APPLICANT: Chen, et al.
; TITLE OF INVENTION: RNAi Based Therapeutics for Allergic Rhinitis and Asthma
; FILE REFERENCE: 0492611-0614
; CURRENT APPLICATION NUMBER: US/11/069,611
; CURRENT FILING DATE: 2005-03-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mouse sequence
US-11-069-611-255

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 948 GGTCAAAATGATGATGTC 966
Db 19 GGTGAAATGATGATGTC 1

RESULT 1091
US-09-780-533A-1841
; Sequence 1841, Application US/09780533A
; Publication No. US2003006011A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowirita, Bharat
; APPLICANT: Haebberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1841
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1841

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.9e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 619 CCCCTCAGCCCGCGCT 635
Db 1 CCCGCCAGCCCGCGCT 17

RESULT 1092
US-09-848-754A-3109/c
; Sequence 3109, Application US/09848754A

; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3109
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3109

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1693 CTTTCTCAGAGCC 1709
Db 17 CTTTCTCAGAGCC 1

RESULT 1093
US-10-138-674-2435/c
; Sequence 2435, Application US/10138674
; Publication No. US2004007565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2435
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 716 CAACCAAGAGACCATG 732
Db 17 CAACCAAGAGACCATG 1

RESULT 1094
US-10-287-949A-2435/c
; Sequence 2435, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
```

SOFTWARE: Patentin version 3.0  
SEQ ID NO 2435  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Mus musculus  
US-10-287-949A-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCCAGAGACCATTG 732  
Db 17 CAACCCAGAGACCATTG 1

RESULT 1095  
US-10-712-672-1375  
Sequence 1375, Application US/10712672  
Publication No. US20040102413A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Chowrira, Bharat  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
FILE REFERENCE: MHB00-882-C (400/019)  
CURRENT APPLICATION NUMBER: US/10/712,672  
CURRENT FILING DATE: 2003-11-13  
PRIOR APPLICATION NUMBER: US/09/653,225  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: 60/197,769  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/150,713  
PRIOR FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 5586  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 1375  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-712-672-1375

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 7.9e+02;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1686 GGACGACGTTTCTCTCA 1702  
Db 1 GGCGCAGCUUUCUCA 17

RESULT 1096  
US-10-951-303-2435/c  
Sequence 2435, Application US/10951303  
Publication No. US20050227937A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Becabedo, Jaime  
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate  
FILE REFERENCE: MHB00-876-K (400/021)  
CURRENT APPLICATION NUMBER: US/10/951,303  
CURRENT FILING DATE: 2004-09-27  
PRIOR APPLICATION NUMBER: US/09/685,664  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08

PRIOR APPLICATION NUMBER: US 09/371,772  
PRIOR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8231  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2435  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Mus musculus  
US-10-951-303-2435

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 716 CAACCCAGAGACCATTG 732  
Db 17 CAACCCAGAGACCATTG 1

RESULT 1097  
US-09-850-948-19/c  
Sequence 19, Application US/09850948  
Publication No. US20030059770A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Jianxin  
APPLICANT: An, Songzhu  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer  
FILE REFERENCE: 018781-008300US  
CURRENT APPLICATION NUMBER: US/09/850,948  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:quantitative  
US-09-850-948-19

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 986 TCTGCTGGCTGCCCTTC 1002  
Db 18 TCTGCTGGCTGCCCTTC 2

RESULT 1098  
US-10-273-575-19/c  
Sequence 19, Application US/10273575  
Publication No. US20030108931A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Jianxin  
APPLICANT: An, Songzhu  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated with Cancer  
FILE REFERENCE: 018781-008300US  
CURRENT APPLICATION NUMBER: US/10/273,575  
CURRENT FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: US/09/850,948  
PRIOR FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:quantitative

```
; OTHER INFORMATION: RT-PCR primer OGR1 reverse
; US-10-273-575-19

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      986 TCTGCTGCTGCTCCCTTC 1002
      |||||
Db      18 TCTGCTGCTGCTCCCTTC 2

RESULT 1099
US-10-680-402-70
; Sequence 70; Application US/10680402
; Publication No. US20040147732A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPMY9, EXPRESSED
; FILE REFERENCE: D0045A CIP
; CURRENT APPLICATION NUMBER: US/10/680,402
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: U.S. 09/964,923
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: U.S. 60/235,709
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,775
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/309,625
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-680-402-70

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      309 CCTTTGGGCGAGCTGCCT 325
      |||||
Db      2 CCTTTGGGCGAGCTTCCT 18

RESULT 1100
US-10-310-914A-230274/C
; Sequence 230274; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 230274
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-230274

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 CCCCTCCAGCCCGGCT 635

; OTHER INFORMATION: RT-PCR primer OGR1 reverse
; US-10-273-575-19

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 CCCCTCCAGCCCGGCT 635
```

---

```
Db      18 CCCCTTCAGCCCGGCT 2

RESULT 1101
US-10-310-914A-677466
; Sequence 677466; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677466
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-677466

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1305 CGAGAGAGAGCCGAGG 1321
      |||||
Db      2 CAAGAGAGAGCCGAGG 18

RESULT 1102
US-10-310-914A-677474
; Sequence 677474; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 677474
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-677474

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1308 CGAGAGCCGAGGAGG 1324
      |||||
Db      1 GGAGAGCCGAGGAGG 17

RESULT 1103
US-10-310-914A-800869
; Sequence 800869; Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
```

;; CURRENT FILING DATE: 2002-12-06  
;; NUMBER OF SEQ ID NOS: 1388402  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 800869  
;; LENGTH: 18  
;; TYPE: RNA  
;; ORGANISM: Human  
US-10-310-914A-800869

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 88.2%; Pred. No. 8.5e+02;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 640 GCCACAGCCACCAAGT 656  
Db 1 GCCACACACCAAGU 17

RESULT 1104  
US-10-310-914A-888641/c  
;; Sequence 888641, Application US/10310914A  
;; Publication No. US2006003322A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Isaac  
;; APPLICANT: Shiller, Kuzat  
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
;; FILE REFERENCE: 06087.0200.CPUS01  
;; CURRENT APPLICATION NUMBER: US/10/310,914A  
;; CURRENT FILING DATE: 2002-12-06  
;; NUMBER OF SEQ ID NOS: 1388402  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 888641  
;; LENGTH: 18  
;; TYPE: RNA  
;; ORGANISM: Human  
US-10-310-914A-888641

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1304 ACGAGAGAGCCAGAG 1320  
Db 18 AGGAGAGAGCCAGAG 2

RESULT 1105  
US-10-310-914A-892826/c  
;; Sequence 892826, Application US/10310914A  
;; Publication No. US2006003322A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Isaac  
;; APPLICANT: Shiller, Kuzat  
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
;; FILE REFERENCE: 06087.0200.CPUS01  
;; CURRENT APPLICATION NUMBER: US/10/310,914A  
;; CURRENT FILING DATE: 2002-12-06  
;; NUMBER OF SEQ ID NOS: 1388402  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 892826  
;; LENGTH: 18  
;; TYPE: RNA  
;; ORGANISM: Human  
US-10-310-914A-892826

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CCTCCCTGCTGCTGA 844  
|||||

Db 18 CCTCCCTGCTGCTGA 2

RESULT 1106  
US-10-310-914A-1042518  
;; Sequence 1042518, Application US/10310914A  
;; Publication No. US2006003322A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Isaac  
;; APPLICANT: Shiller, Kuzat  
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
;; FILE REFERENCE: 06087.0200.CPUS01  
;; CURRENT APPLICATION NUMBER: US/10/310,914A  
;; CURRENT FILING DATE: 2002-12-06  
;; NUMBER OF SEQ ID NOS: 1388402  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 1042518  
;; LENGTH: 18  
;; TYPE: RNA  
;; ORGANISM: Human  
US-10-310-914A-1042518

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 70.6%; Pred. No. 8.5e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 519 CTACTGCAGTTCACA 535  
Db 1 CUACUGCAAGUCCAA 17

RESULT 1107  
US-10-310-914A-1145229  
;; Sequence 1145229, Application US/10310914A  
;; Publication No. US2006003322A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Isaac  
;; APPLICANT: Shiller, Kuzat  
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
;; FILE REFERENCE: 06087.0200.CPUS01  
;; CURRENT APPLICATION NUMBER: US/10/310,914A  
;; CURRENT FILING DATE: 2002-12-06  
;; NUMBER OF SEQ ID NOS: 1388402  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 1145229  
;; LENGTH: 18  
;; TYPE: RNA  
;; ORGANISM: Human  
US-10-310-914A-1145229

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 76.5%; Pred. No. 8.5e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 981 GCCCATCTGCTGCTGC 997  
Db 2 CGCCACCUGCUGGCTGC 18

RESULT 1108  
US-10-310-914A-1350814/c  
;; Sequence 1350814, Application US/10310914A  
;; Publication No. US2006003322A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bentwich, Isaac  
;; APPLICANT: Shiller, Kuzat  
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
;; FILE REFERENCE: 06087.0200.CPUS01  
;; CURRENT APPLICATION NUMBER: US/10/310,914A  
;; CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1350814  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1350814

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 8.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1346 CCCTGACCTGACCTCC 1362  
DB 17 CCCTGACCTGACCTCC 1

RESULT 1109  
US-10-665-951-1515  
Sequence 1515, Application US/10665951  
Publication No. US20040138163A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwigen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/131 (MHB02-742-F)  
CURRENT APPLICATION NUMBER: US/10/665,951  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 10/664,668  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: PCT/US 03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 10/287,949  
PRIOR FILING DATE: 2002-11-04  
PRIOR APPLICATION NUMBER: US 10/306,747  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: PCT/US 02/17674  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2455  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1515  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense  
US-10-665-951-1515

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGGCGCCAGCCACGAGA 155  
DB 2 AGGCGCCAGCCACGAGA 18

RESULT 1110

US-10-665-951-1762/c  
Sequence 1762, Application US/10665951  
Publication No. US20040138163A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwigen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/141 (MHB02-742-N)  
CURRENT APPLICATION NUMBER: US/10/758,155  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 10/664,668  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: PCT/US 03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 10/287,949  
PRIOR FILING DATE: 2002-11-04  
PRIOR APPLICATION NUMBER: US 10/306,747  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: PCT/US 02/17674  
PRIOR FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2455  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1762  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-665-951-1762

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGGCGCCAGCCACGAGA 155  
DB 18 AGGCGCCAGCCACGAGA 2

RESULT 1111  
US-10-758-155-1515  
Sequence 1515, Application US/10758155  
Publication No. US20050075304A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: McSwigen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/141 (MHB02-742-N)  
CURRENT APPLICATION NUMBER: US/10/758,155  
PRIOR FILING DATE: 2004-01-12  
PRIOR APPLICATION NUMBER: US 10/665,951  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US 10/664,668  
PRIOR FILING DATE: 2003-09-18



```

; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-758-155-1515

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      139 AGGGCCAGCCACAGGA 155
        |||||
Db       2 AGGCGCCAGCCACCGGA 18

```

```

RESULT 1112
US-10-758-155-1762/c
; Sequence 1762, Application US/10758155
; Publication No. US20050075304A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/141 (MBH02742-N)
; CURRENT APPLICATION NUMBER: US/10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751

```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-758-155-1762

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      139 AGGGCCAGCCACAGGA 155
        |||||
Db       18 AGGCGCCAGCCACCGGA 2

```

```

RESULT 1113
US-10-831-620-1515
; Sequence 1515, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/152 (MBH02-742-O)
; CURRENT APPLICATION NUMBER: US/10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/712,633
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-831-620-1515

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      139 AGGGCCAGCCACAGGA 155
        |||||
Db       2 AGGCGCCAGCCACCGGA 18

```

```
RESULT 1114
US-10-831-620-1762/C
; Sequence 1762, Application US/10831620
; Publication No. US20050148530A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Rayco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/152 (MBHB02-742-C)
; CURRENT APPLICATION NUMBER: US/10/831,620
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/758,155
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/712,633
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,951
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2751
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1762
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-831-620-1762
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGCGCCGACGACGAGA 155
DB      18 AGCGCCGACGACGCGA 2

RESULT 1115
US-10-923-330-216
; Sequence 216, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MBHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
```

```
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 216
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-923-330-216
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      463 AATACAGTGTGAACCT 479
DB      3 AAGCAGUGUGAACU 19

RESULT 1116
US-10-923-330-439/C
; Sequence 439, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MBHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 439
; LENGTH: 19
```

```

TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-330-439

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. NO. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

OY      463 AATACAGTGTGAACCTT 479
      |||||||
Db      17 AAGACAGTGTGAACCTT 1

RESULT 1117
US-10-844-076-1515
Sequence 1515, Application US/108444076
Publication No. US20050171039A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Belgelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: 400/159 (MBHB02-742-R)
CURRENT APPLICATION NUMBER: US/10/844,076
CURRENT FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: US 10/831,620
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/764,957
PRIOR FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/758,155
PRIOR FILING DATE: 2004-01-12
PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/712,633
PRIOR FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/670,011
PRIOR FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/665,951
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: US 10/664,668
PRIOR FILING DATE: 2003-09-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2755
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1515
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-844-076-1515

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. NO. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

OY      139 AGCGCCAGCCACAGGA 155
      |||||||
Db      2 AGCGCCAGCCACCGGA 18

RESULT 1118
US-10-844-076-1762/c
Sequence 1762, Application US/108444076

```

```

: Publication No. US20050171039A1
: GENERAL INFORMATION:
: APPLICANT: Sirna Therapeutics, Inc.
: APPLICANT: McSwiggen, James
: APPLICANT: Beigelman, Leonid
: APPLICANT: Pavco, Pamela
: TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
: TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
: FILE REFERENCE: 400/159 (MBRH02-742-R)
: CURRENT APPLICATION NUMBER: US/10/844,076
: CURRENT FILING DATE: 2004-05-11
: PRIOR APPLICATION NUMBER: US 10/831,620
: PRIOR FILING DATE: 2004-04-23
: PRIOR APPLICATION NUMBER: US 10/764,957
: PRIOR FILING DATE: 2004-01-26
: PRIOR APPLICATION NUMBER: US 10/757,803
: PRIOR FILING DATE: 2004-01-14
: PRIOR APPLICATION NUMBER: US 10/758,155
: PRIOR FILING DATE: 2004-01-12
: PRIOR APPLICATION NUMBER: US 10/720,448
: PRIOR FILING DATE: 2003-11-24
: PRIOR APPLICATION NUMBER: US 10/712,633
: PRIOR FILING DATE: 2003-11-13
: PRIOR APPLICATION NUMBER: US 10/693,059
: PRIOR FILING DATE: 2003-10-23
: PRIOR APPLICATION NUMBER: US 10/670,011
: PRIOR FILING DATE: 2003-09-23
: PRIOR APPLICATION NUMBER: US 10/665,951
: PRIOR FILING DATE: 2003-09-18
: PRIOR APPLICATION NUMBER: US 10/664,668
: PRIOR FILING DATE: 2003-09-18
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 2755
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 1762
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-844-076-1762

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCAGCCACACGA 155
      |||||
Db      18 AGGCGCAGCCACCGGA 2

RESULT 1119
US-10-923-182-62
: Sequence 62, Application US/10923182
: Publication No. US2005017666A1
: GENERAL INFORMATION:
: APPLICANT: Sirna Therapeutics, Inc.
: APPLICANT: James, McSwiggen
: APPLICANT: Ivan, Roberts
: TITLE OF INVENTION: RNA Interference Mediated Inhibition of GPR4 and AAI Gene
: TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
: FILE REFERENCE: 400/227 (MBRH04-423-A)
: CURRENT APPLICATION NUMBER: US/10/923,182
: CURRENT FILING DATE: 2004-08-20
: PRIOR APPLICATION NUMBER: US 60/570,086
: PRIOR FILING DATE: 2004-05-11
: PRIOR APPLICATION NUMBER: PCT/US04/16390
: PRIOR FILING DATE: 2004-05-24
: PRIOR APPLICATION NUMBER: US 10/826,966
: PRIOR FILING DATE: 2004-04-16
: PRIOR APPLICATION NUMBER: PCT/US04/13456
: PRIOR FILING DATE: 2004-04-30

```

```
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent version 3.3
; SEQ ID NO 62
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-923-182-62

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1110 CAACCCGATCATCTACT 1126
Db      3 CAACCCGACACACACU 19

RESULT 1120
; Sequence 149, Application US/10923182
; Publication No. US2005017666A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: James, McSwiggen
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of GPR4 and AA1 Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/227 (MEHB04-423-A)
; CURRENT APPLICATION NUMBER: US/10/923,182
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/570,086
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent version 3.3
; SEQ ID NO 149
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-182-149

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1110 CAACCCGATCATCTACT 1126
Db      17 CAACCCGATCATCTACT 1

RESULT 1121
US-10-962-898-1515
; Sequence 1515, Application US/10962898
; Publication No. US2005022206A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/236 (MEHB02-742-0)
; CURRENT APPLICATION NUMBER: US/10/962,898
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/944,644
; PRIOR FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: Patent version 3.3
; SEQ ID NO 1515
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-962-898-1515

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      139 AGGCGCCAGCCACGGA 155
Db      2 AGGCGCCAGCCACGGA 18

RESULT 1122
US-10-962-898-1762/C
; Sequence 1762, Application US/10962898
; Publication No. US2005022206A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: Richards, Ivan
```

APPLICANT: McSwigen, James  
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/236 (MBHB02-742-U)  
CURRENT FILING DATE: 2004-10-12  
PRIOR APPLICATION NUMBER: US 10/944,644  
PRIOR FILING DATE: 2004-09-16  
PRIOR APPLICATION NUMBER: US 10/844,076  
PRIOR FILING DATE: 2004-05-11  
PRIOR APPLICATION NUMBER: US 10/831,620  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 10/764,957  
PRIOR FILING DATE: 2004-01-26  
PRIOR APPLICATION NUMBER: US 10/670,011  
PRIOR FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: US 10/665,255  
PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/664,767  
PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 4252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1762  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-962-898-1762

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 139 AGGCGCCAGCCACGCA 155  
Db 18 AGGCGCCAGCCACGCA 2

RESULT 1123  
US-10-944-611-1515  
Sequence 1515, Application US/10944611  
Publication No. US20050233998A1  
GENERAL INFORMATION:  
APPLICANT: Sirta Therapeutics, Inc.  
APPLICANT: Jadhav, Vasant  
APPLICANT: Kossen, Karl  
APPLICANT: Zinnen, Shawn  
APPLICANT: Vaish, Narendra  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/235 (MBHB02-742-S)  
CURRENT FILING DATE: 2004-09-16  
PRIOR APPLICATION NUMBER: US 10/944,611  
PRIOR FILING DATE: 2004-09-16  
PRIOR APPLICATION NUMBER: US 10/844,076  
PRIOR FILING DATE: 2004-05-11  
PRIOR APPLICATION NUMBER: US 10/831,620  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 10/764,957  
PRIOR FILING DATE: 2004-01-26  
PRIOR APPLICATION NUMBER: US 10/670,011  
PRIOR FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: US 10/665,255

PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/664,767  
PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: PCT/US04/16390  
PRIOR FILING DATE: 2004-05-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 4252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1515  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r  
US-10-944-611-1515

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 139 AGGCGCCAGCCACGCA 155  
Db 2 AGGCGCCAGCCACGCA 18

RESULT 1124  
US-10-944-611-1762/c  
Sequence 1762, Application US/10944611  
Publication No. US20050233998A1  
GENERAL INFORMATION:  
APPLICANT: Sirta Therapeutics, Inc.  
APPLICANT: Jadhav, Vasant  
APPLICANT: Kossen, Karl  
APPLICANT: Zinnen, Shawn  
APPLICANT: Vaish, Narendra  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial  
TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: 400/235 (MBHB02-742-S)  
CURRENT FILING DATE: 2004-09-16  
PRIOR APPLICATION NUMBER: US 10/844,076  
PRIOR FILING DATE: 2004-05-11  
PRIOR APPLICATION NUMBER: US 10/831,620  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 10/764,957  
PRIOR FILING DATE: 2004-01-26  
PRIOR APPLICATION NUMBER: US 10/670,011  
PRIOR FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: US 10/665,255  
PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/664,767  
PRIOR FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: PCT/US04/16390  
PRIOR FILING DATE: 2004-05-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 4252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1762  
LENGTH: 19

```
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-944-611-1762

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      139 AGGCGCCAGCCACGGA 155
Db      18 AGCGCCAGCCACCGCA 2

RESULT 1125
US-10-206-693-35
; Sequence 35, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Nogo and Nogo Receptor Gene
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-206-693-35

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 1;

Qy      619 CCCCTCCAGCCCGGCT 635
Db      1 CCCCGCAGCCCGGCU 17

RESULT 1126
US-10-206-693-261/c
; Sequence 261, Application US/10206693
; Publication No. US20050261212A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Nogo and Nogo Receptor Gene
; FILE REFERENCE: 900/034 (MBHB02-732)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 261
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-693-261

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      619 CCCCTCCAGCCCGGCT 635
```

```
Db      19 CCCCCGACCCCGGCT 3

RESULT 1127
US-10-310-914A-288078/c
; Sequence 288078, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288078
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-288078

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      653 AAGTGGTCATCTGTGTC 669
Db      17 ACGTGGTCATCTGTGTC 1

RESULT 1128
US-10-310-914A-394088/c
; Sequence 394088, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-394088

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      1686 GAGCCAGCTTTCTCTCA 1702
Db      17 GGGCCAGCTTTCTCTCA 1

RESULT 1129
US-10-310-914A-410563/c
; Sequence 410563, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 410563
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-410563
```

CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 410563  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-410563

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 919 CACGAGCAAGCTCTGC 935  
DB 17 CACGAGCAAGCTCTGC 1

RESULT 1130  
US-10-310-914A-477720  
Sequence 477720, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 477720  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-477720

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 9e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1437 CACAGGCGCTTTGGCAG 1453  
DB 3 CACAGGCGCTTTGGCAG 19

RESULT 1131  
US-10-310-914A-522254  
Sequence 522254, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 522254  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-522254

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 9e+02;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GCTTACGCTTCTCTCC 1419  
||:||||:||||:|

DB 3 GCUCGACGCTTCTCTCC 19

RESULT 1132  
US-10-310-914A-522262  
Sequence 522262, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 522262  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-522262

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 9e+02;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GCTTACGCTTCTCTCC 1419  
DB 1 GCUCGACGCTTCTCTCC 17

RESULT 1133  
US-10-310-914A-629950/C  
Sequence 629950, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 629950  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-629950

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 AGTTACGCTTTCAAAA 78  
DB 19 AGTTACGCTTTCAATTA 3

RESULT 1134  
US-10-310-914A-742052  
Sequence 742052, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiller, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06

```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 742052
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-742052

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1296 GGGGGCCACAGAGAGG 1312
Db 3 GGGGGCCACAGAGAGG 19

RESULT 1135
US-10-310-914A-860138/c
; Sequence 860138, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 860138
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-860138

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 664 TGTGTCATCTGGGTCT 680
Db 18 TGTGTCATCTGGGTCT 2

RESULT 1136
US-10-310-914A-1181389
; Sequence 1181389, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1181389
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1181389

Query Match
Best Local Similarity 76.5%; Score 15.4; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 894 CCCCCGAGCTCTCTG 910
Db 1 CCCCCGAGCTCTCTG 17

; NUMBER OF SEQ ID NOS: 1280868/c
; Sequence 1280868, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1280868
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1280868

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 963 TGTGTCGTGTGACCT 979
Db 17 TGTGTCGTGTGACCT 1

RESULT 1138
US-10-310-914A-1309499
; Sequence 1309499, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1309499
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1309499

Query Match
Best Local Similarity 58.8%; Score 15.4; DB 1; Length 19;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 418 TTTCTGCTGAACCTGCC 434
Db 3 UUDCTGUGAACGUGGC 19

RESULT 1139
US-10-310-914A-1319661
; Sequence 1319661, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```



SOFTWARE: PatentIn version 3.3

SEQ ID NO 1319661

LENGTH: 19

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1319661

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 64.7%; Pred. No. 9e+02; 1;

Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GCTCAGCTTCTCTCC 1419

Db 1 GCUCACGCUCCUCC 17

RESULT 1140

US-10-310-914A-1375299/c

Sequence 1375299, Application US/10310914A

Publication No. US2006003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiller, Kuzel

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310.914A

PRIOR FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 1375299

LENGTH: 19

TYPE: RNA

ORGANISM: Human

US-10-310-914A-1375299

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; 1;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCCAGCCCGGCT 635

Db 17 CCCACACGCGCGGCT 1

RESULT 1141

US-11-083-784-2195

Sequence 2195, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 2195

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-2195

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 70.6%; Pred. No. 9e+02; 1;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 463 AATCAGTGGGAACTT 479

Db 3 AAGCAGUGGUGAACUU 19

RESULT 1142

US-11-083-784-19634/c

Sequence 19634, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 19634

LENGTH: 19

TYPE: RNA

ORGANISM: Homo sapiens

US-11-083-784-19634

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02; 1;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420

Db 17 CTTGAGCTTCTCTCCA 1

RESULT 1143

US-11-083-784-51038/c

Sequence 51038, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmoon, Inc.

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083.784

PRIOR FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714.333

PRIOR FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 51038

LENGTH: 19

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-51038

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1005 CATCTTCTTCTCTGC 1021
DB 17 CATCTTCTTCTCTGC 1

RESULT 1144
US-11-083-784-61485/c
; Sequence 61485, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 61485
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-61485

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 CTCACACTGGAGCTTGC 1546
DB 17 CTCACACTGGAGCTTGC 1

RESULT 1145
US-11-083-784-66269/c
; Sequence 66269, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 66269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-66269

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1067 TCTACCTGGCCATCATG 1083
DB 19 TCTTCTGGCCATCATG 3

RESULT 1146
US-11-083-784-66270/c
; Sequence 66270, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 66270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-66270

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1067 TCTACCTGGCCATCATG 1083
DB 17 TCTTCTGGCCATCATG 1

RESULT 1147
US-11-083-784-119668/c
; Sequence 119668, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 119668  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-119668

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

OY 1358 CCTCAACTGCTCTTCA 1374  
Db 18 CCTCAACTGCTCTTCA 2

RESULT 1148  
US-11-083-784-132395/c  
; Sequence 132395, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 132395  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-132395

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

OY 1005 CATCTTCCTCCTGC 1021  
Db 17 CATCTTCCTCCTGC 1

RESULT 1149  
US-11-083-784-143402/c  
; Sequence 143402, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333

;; PRIOR FILING DATE: 2003-11-14  
;; PRIOR APPLICATION NUMBER: 60/502,050  
;; PRIOR FILING DATE: 2003-09-10  
;; PRIOR APPLICATION NUMBER: 60/426,137  
;; PRIOR FILING DATE: 2002-11-14  
;; NUMBER OF SEQ ID NOS: 1591911  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 143402  
;; LENGTH: 19  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-11-083-784-143402

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

OY 1446 TTGGCAGTGCGAGCCC 1462  
Db 17 TTGGCAGTGCGAGCCC 1

RESULT 1150  
US-11-083-784-202084  
; Sequence 202084, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 202084  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-202084

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 12; Conservative 4; Mismatches 1;

OY 1033 CCGATCTTAAGTGA 1049  
Db 1 CCGAUCUCUACUGAA 17

RESULT 1151  
US-11-083-784-202116  
; Sequence 202116, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US

```

CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 202116
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-202116

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY      1033 CCAGATCTTACTCTGAA 1049
      |||||:|:|:|:|:|:|
Db      3 CCAGATCTTACTCTGAA 19

RESULT 1152
US-11-083-784-202174
Sequence 202174, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134990US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 202174
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-202174

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY      1033 CCAGATCTTACTCTGAA 1049
      |||||:|:|:|:|:|:|
Db      1 CCAGATCTTACTCTGAA 17

RESULT 1153
US-11-083-784-202197
Sequence 202197, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William

```

```

TITLE OF INVENTION: Functional and Hyperfunctional siRNA
APPLICANT: Scaringe, Stephen
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 202197
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-202197

Query Match      0.9%;   Score 15.4;   DB 1;   Length 19;
Best Local Similarity 70.6%;   Pred. No. 9e+02;   1;   Indels      0;   Gaps      0;
Matches 12;   Conservative 4;   Mismatches      1;

QY      1033   CCAGATCTCTACTGAA 1049
Db      3      CCAGATCUCUAUCUGAA 19
||||:|:|:|:|

RESULT 1154
US-11-083-784-232135/c
; Sequence 232135, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-232135

Query Match      0.9%;   Score 15.4;   DB 1;   Length 19;
Best Local Similarity 94.1%;   Pred. No. 9e+02;   1;   Indels      0;   Gaps      0;
Matches 16;   Conservative 0;   Mismatches      1;

QY      1024   TACATCAACCCAGATCT 1040
Db      17      TACATCAACCCAAATCT 1
|||||:|:|:|:|

RESULT 1155
US-11-083-784-232235/c
; Sequence 232235, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

```



```
US-11-083-784-360639
; Sequence 360639, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 360639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-360639
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1;
```

```
QY      1350 GGACCTGACCTCTCACT 1366
          |||||:|||||:
Db       1  GGACCTGGCTCCACU 17
```

```
RESULT 1160
US-11-083-784-368528
; Sequence 368528, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 368528
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-368528
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1;
```

```
QY      1742 GCATGCCAGTCTCAT 1758
          |||||:|||||:
Db       2  GCAAGCGAGUGCUCAU 18
```

```
RESULT 1161
US-11-083-784-371445/C
; Sequence 371445, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 371445
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-371445
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

```
QY      651 CAAAGTGTCTCTCTG 667
          |||||:|||||:
Db       18  CAAAGTGGCCATCTGT 2
```

```
RESULT 1162
US-11-083-784-421451/C
; Sequence 421451, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 421451
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-421451
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;
```

OY 242 TCTCCCAACATCTCC 258  
|||  
Db 17 TCTCCCAATATCTCC 1

RESULT 1163  
US-11-083-784-425085  
; Sequence 425085, Application US/11083784  
; Publication NO. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 425085  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-425085

Query Match 0.9%, Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1307 AGGAGAGCCGAGGAC 1323  
|||  
Db 1 AGGAGAGCCGAGGAC 17

RESULT 1164  
US-11-083-784-460346/c  
; Sequence 460346, Application US/11083784  
; Publication NO. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 460346  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-460346

Query Match 0.9%, Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 651 CAAAGTGATCTGTG 667  
|||  
Db 18 CAAAGAGTATCTGTG 2

RESULT 1165  
US-11-083-784-460400/c  
; Sequence 460400, Application US/11083784  
; Publication NO. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 460400  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-460400

Query Match 0.9%, Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 651 CAAAGTGATCTGTG 667  
|||  
Db 18 CAAAGAGTATCTGTG 2

RESULT 1166  
US-11-083-784-501423  
; Sequence 501423, Application US/11083784  
; Publication NO. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 501423  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-11-083-784-501423

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 70.6%; Pred. No. 9e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 463 AATACAGTGTGACCTT 479  
DB 3 AAGACAGUGUGAACCU 19

RESULT 1167

US-11-083-784-578794/C  
; Sequence 578794, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 578794  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-578794

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 TTCTGGAAGTGACCTT 1737  
DB 19 TTCTGGAAGTGACCTT 3

RESULT 1168  
US-11-083-784-671090/C  
; Sequence 671090, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 671090

; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-671090

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 17 CTTGAGCTTCTCTCCA 1

RESULT 1169  
US-11-083-784-674587  
; Sequence 674587, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 674587  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-674587

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 9e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1269 CTTGAGACCACTCT 1285  
DB 1 CCAGAGACCACTCAV 17

RESULT 1170  
US-11-083-784-688433/C  
; Sequence 688433, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14



```
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 688433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-688433
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      404 CAGTACGACTATT 420
Db      18 CAGTACGACTATT 2
```

```
RESULT 1171
US-11-083-784-704511
; Sequence 704511, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704511
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-704511
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 9e+02;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      578 TGACGCTGTGCGCTTT 594
Db      1 TGACGAGUGGCGCCUU 17
```

```
RESULT 1172
US-11-083-784-704520
; Sequence 704520, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 704520
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-704520
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 9e+02;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      578 TGACGCTGTGCGCTTT 594
Db      3 TGACGAGUGGCGCCUU 19
```

```
RESULT 1173
US-11-083-784-751946/c
; Sequence 751946, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 751946
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-751946
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1659 TTTGCTGAGCTGTAA 1675
Db      17 TTTGCTGAGCTGTAA 1
```

```
RESULT 1174
US-11-083-784-820807/c
; Sequence 820807, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
```

```
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 820807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-820807

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 TTCTGGAAGTGAAGCTTT 1737
Db 19 TTCTGGAAGGGAAGCTTT 3

RESULT 1175
US-11-083-784-896406/c
; Sequence 896406, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 896406
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-896406

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 261 TAACACTTCGGAACCA 277
Db 19 TAACACTTCGGAACCA 3

RESULT 1176
US-11-083-784-911965
; Sequence 911965, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 911965
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-911965

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1643 AACCAATCACTGAAGT 1659
Db 3 AACCAATCACTGAAGT 19

RESULT 1177
US-11-083-784-917716/c
; Sequence 917716, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 917716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-917716

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 653 AAGTGTATCTGTGTC 669
Db 18 AAGTGTATCTGTGTC 2

RESULT 1178
US-11-083-784-926899/c
; Sequence 926899, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 926899  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-926899

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 AGAGCTCAGCTTCTCC 1416  
Db 18 AGAGTTCAGCTCTCC 2

RESULT 1179  
US-11-083-784-976398/C  
Sequence 976398, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18/714,333  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 976398  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-976398

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 998 CTTCCACATCTTCTTC 1014  
Db 18 CTTCTCATCTCTCTC 2

RESULT 1180  
US-11-083-784-1028300/C  
Sequence 1028300, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.

APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1028300  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1028300

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 241 CTCTCCCAACATCTC 257  
Db 18 CTCTCCCAACATCTC 2

RESULT 1181  
US-11-083-784-1077507/C  
Sequence 1077507, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1077507  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1077507

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 CATTCACCTTGAGTC 1591  
Db 19 CATTCACATTCAGTC 3

RESULT 1182  
US-11-083-784-1098844  
Sequence 1098844, Application US/11083784

```

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098844
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1098844

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY      1702 AAGAGCCCAATGATTC 1718
DB      3 AAGAGCCCAATGATTC 19

```

```

RESULT 1183
US-11-083-784-1245691/c
; Sequence 1245691, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1245691
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1245691

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      652 AAGGTGCTATCTGCT 668
DB      17 AAGGTGCTATCTGCT 1

```

```

RESULT 1184
US-11-083-784-1277052/c
; Sequence 1277052, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277052
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1277052

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      802 ATCTGTGTGACTGTGCT 818
DB      19 ATCTGTGTGACTGTCT 3

```

```

RESULT 1185
US-11-083-784-1277082/c
; Sequence 1277082, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1277082

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      801 CATGTGTGACTGTGC 817

```

Db 17 CATCTGTGTGACTGTCC 1

RESULT 1186

US-11-083-1239074  
; Sequence 1239074, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1239074  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1239074

Query Match

Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1306 GAGAGAGCCAGGCA 1322

Db 2 GAGAGAGCCAGGCA 18

RESULT 1187

US-11-083-784-1302380  
; Sequence 1302380, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1302380  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1302380

Query Match

Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 9e+02;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 544 CCCATGCCGCTGTCTT 560  
Db 2 CCCAUGCCTGCTGCTU 18

RESULT 1188

US-11-083-784-1335689/c  
; Sequence 1335689, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1335689  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1335689

Query Match

Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420

Db 17 CTGACGTTCTCTCCA 1

RESULT 1189

US-11-083-784-1362687  
; Sequence 1362687, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1362687  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-1362687

Query Match

Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 9e+02;  
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;



SEQ ID NO 1464506  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1464506

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

QY 1529 CCTCAGCTGGGACTTG 1545  
DB 17 CCACACCTGGGACTTG 1

RESULT 1194  
US-11-083-784-1474304/C  
Sequence 1474304, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1474304  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1474304

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

QY 418 TTCTGGTGAACCTGGC 434  
DB 19 TTCTGGTGAACCTGGC 3

RESULT 1195  
US-11-083-784-1485805/C  
Sequence 1485805, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1485805  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1485805

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1;

QY 1404 CTTGAGCTTCTCTCCA 1420  
DB 17 CTTGAGCTTCTCTCCA 1

RESULT 1196  
US-11-083-784-1498825  
Sequence 1498825, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1498825  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-1498825

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 11; Conservative 5; Mismatches 1;

QY 1651 CACTGAACTTGTCTGAG 1667  
DB 2 CACTGAACTTGTCTGAG 18

RESULT 1197  
US-11-083-784-1498858  
Sequence 1498858, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1498858
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1498858

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1;

Qy      1651 CACTGAACCTTGTGAG 1667
Db      1 CACUGAACUUGAUGAG 17

RESULT 1198
US-11-083-784-1515526/c
; Sequence 1515526, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515526
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1515526

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      1279 ACCATCTCCACAGTGT 1295
Db      19 ACCATCTCCACAGTGT 3

RESULT 1199
US-11-083-784-1515845/c
; Sequence 1515845, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
```

```
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515845
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1515845

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

Qy      1445 CTTGGCAGGTGCAGCC 1461
Db      17 CTTGGCAGGTGCAGCC 1

RESULT 1200
US-11-101-244-2195
; Sequence 2195, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 2195
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-2195

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 1;

Qy      463 AATACAGTGTGTAATT 479
Db      3 AAGACAGTGTGTAACU 19

RESULT 1201
US-11-101-244-19634/c
; Sequence 19634, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```



```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1591911
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-19634
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1404 CTTGAGCTTCTCTCCA 1420
Db      17 CTTGAGCTTCTCTCCA 1
```

```
RESULT 1202
US-11-101-244-51038/C
; Sequence 51038, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 51038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-51038
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1005 CATCTTCTCTCTCTGC 1021
Db      17 CATCTTCTCTCTCTGC 1
```

```
RESULT 1203
US-11-101-244-61485/C
; Sequence 61485, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
```

```
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 61485
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-61485
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1530 CTCAGACTGGGACTTGC 1546
Db      17 CTCAGACTGGGACTTGC 1
```

```
RESULT 1204
US-11-101-244-66269/C
; Sequence 66269, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 66269
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-66269
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1067 TCTACCTGGCCATCATG 1083
Db      19 TCTTCTGGCCATCATG 3
```

```
RESULT 1205
US-11-101-244-66270/C
; Sequence 66270, Application US/11/101,244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 66270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-66270
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1067 TCTACCTGGCCATCATG 1083
Db      17  TCTTCTGCGCATCATG 1
```

```
RESULT 1206
US-11-101-244-119668/c
; Sequence 119668, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 119668
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-119668
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1358 CCTCCAGCTGCTCTCA 1374
Db      18  CCTTCACTGCTCTTCA 2
```

```
RESULT 1207
US-11-101-244-132395/c
; Sequence 132395, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

```
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 132395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-132395
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1005 CATCTTCTCTCTCTGTC 1021
Db      17  CATCTTCTCTCTCTGTC 1
```

```
RESULT 1208
US-11-101-244-143402/c
; Sequence 143402, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 143402
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-143402
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1446 TTGGCAGCTGCAGCCC 1462
Db      17  TTGGCAGCTGCAGCCC 1
```

```
RESULT 1209
US-11-101-244-202084
; Sequence 202084, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```

: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 151911
: SOFTWARE: Propletary
: SEQ ID NO 202084
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
: US-11-244-202084

```

Query Match	0.9%	Score 15.4	DB 1	Length 19
Best Local Similarity	70.6%	Pred. No. 9e+02		
Matches 12	Conservative 4	Mismatches 1	Indels 0	Gaps 0

```
QY      1033 CCAGATCTCTACCTGAA 1049
          |||||:|:|:|:|
Db      1 CCAGAUUCUACUUGAA 17
```

```

RESULT 1210
US-11-101-244-202116
? Sequence 202116, Application US/11101244
? Publication No. US20050246794A1
? GENERAL INFORMATION:
? APPLICANT: Dharmacon, Inc.
? APPLICANT: Khvorova, Anastasia
? APPLICANT: Reynolds, Angela
? APPLICANT: Leake, Devin
? APPLICANT: Marshall, William
? APPLICANT: Scaringe, Stephen
? TITLE OF INVENTION: Functional and Hyperfunctional siRNA
? FILE REFERENCE: 13493US
? CURRENT APPLICATION NUMBER: US/11/101,244
? CURRENT FILING DATE: 2005-04-07
? PRIOR APPLICATION NUMBER: 60/502,050
? PRIOR FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: 60/426,137
? PRIOR FILING DATE: 2002-11-14
? NUMBER OF SEQ ID NOS: 1591911
? SOFTWARE: Proprietary
? SEQ ID NO 202116
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Homo sapiens
? US-11-101-244-202116

```

Query Match	0.9%	Score 15.4;	DB 1;	Length 19;
Best Local Similarity	70.6%	Pred. No. 9e+02;		
Matches 12;	Conservative 4;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1033	CCAGATCTTACTGAA	1049
		: : : :	
Db	3	CCAGATCTTACTGAA	19

RESULT 1211  
US-11-101-244-202174  
Sequence 202174, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khavrova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leeke, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaring, Stephen  
TITLE OR INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137

```

? PRIOR FILING DATE: 2002-11-14
? NUMBER OF SEQ ID NOS: 15919111
? SOFTWARE: Proprietary
? SEQ ID NO 202174
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Homo sapiens
US-11-101-244-202174

```

```
Query Match      0.9%; Score 15.4; DB 1; length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1033 CCAGATCTTACCTGAA 1049
          |||||:|:|:|:|:|
Db       1 CCAGAUUCUACUTGAA 17
```

```

RESULT 1212
US-11-101-244-202197
Sequence 202197, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, David
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 11499US
CURRENT APPLICATION NUMBER: US/11/101, 244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502, 050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426, 137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 202197
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-202197

```

Query Match	0.9%	Score 15.4;	DB 1;	Length 19;
Best Local Similarity	70.6%	Pred. No. 9e+02;		
Matches 12;	Conservative 4;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1033 CCAGATCTTACCTGAA 1049
          |||||:::|:|:|
Db       3  CCAGAUUCUACUUGAA 19
```

RESULT 1213  
US-11-101-244-232135/c  
Sequence 232135, Application US/11101244  
Publication No. US2005024679A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorovova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 114950US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14

```

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232135
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-232135

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1024 TACATCAACCCAGATCT 1040
DB 17 TACATCAACCCAAATCT 1

RESULT 1214
US-11-101-244-232235/c
; Sequence 232235, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 232235
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-232235

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1024 TACATCAACCCAGATCT 1040
DB 17 TACATCAACCCAAATCT 1

RESULT 1215
US-11-101-244-237477/c
; Sequence 237477, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

```

```

; SOFTWARE: Proprietary
; SEQ ID NO 237477
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-237477

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1404 CTTGACGCTCTCTCCCA 1420
DB 17 CTTGACGCTCTCTCCA 1

RESULT 1216
US-11-101-244-262644
; Sequence 262644, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 262644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-262644

Query Match
Best Local Similarity 76.5%; Score 15.4; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 313 TGGGACGCTGCTTACAC 329
DB 2 UGGGAGAGCTGCGTACAC 18

RESULT 1217
US-11-101-244-304519
; Sequence 304519, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

```

```
; SEQ ID NO 304519
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-304519
```

```
Query Match          0.9%: Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      993 GCTGCTTCATCATCT 1009
Db      3 GTCGCCCTCCCAUVCU 19
```

```
RESULT 1218
US-11-101-244-360639
; Sequence 360639, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 360639
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-360639
```

```
Query Match          0.9%: Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1350 GGAAGTGTCTCTCACT 1366
Db      1 GGACCTGGCCCTCCACTU 17
```

```
RESULT 1219
US-11-101-244-368528
; Sequence 368528, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 368528
```

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-368528
```

```
Query Match          0.9%: Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 9e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1742 GCATGCGAGTCTCAT 1758
Db      2 GCAAGCGAGGCUCAU 18
```

```
RESULT 1220
US-11-101-244-371445/C
; Sequence 371445, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 371445
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-371445
```

```
Query Match          0.9%: Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      651 CAAAGTGTCTCTGTG 667
Db      18 CAAAGTGTCTCTGTG 2
```

```
RESULT 1221
US-11-101-244-421451/C
; Sequence 421451, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 421451
; LENGTH: 19
```

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-421451

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 242 TCTCCCAACATCTCC 258  
Db 17 TCTCCCAATCTCC 1

RESULT 1222  
US-11-101-244-425085  
; Sequence 425085, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 425085  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-425085

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1307 AGGAGGACCGAGGAC 1323  
Db 1 AGGAGGACCGAGGAC 17

RESULT 1223  
US-11-101-244-460346/C  
; Sequence 460346, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 460346  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

; ORGANISM: Homo sapiens  
US-11-101-244-460346

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 651 CAAAGTGTCTGTGTG 667  
Db 18 CAAAGTGTCTGTGTG 2

RESULT 1224  
US-11-101-244-460400/C  
; Sequence 460400, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 460400  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-460400

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 651 CAAAGTGTCTGTGTG 667  
Db 18 CAAAGTGTCTGTGTG 2

RESULT 1225  
US-11-101-244-501423  
; Sequence 501423, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 501423  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens



Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 404 CAGTGACGAACCTATTTT 420  
Db 18 CAGTGATGAACCTATTTT 2

## RESULT 1230

US-11-101-244-704511  
; Sequence 704511, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 704511  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-704511

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 58.8%; Pred. No. 9e+02;  
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 578 TGACGGCTGTGCGCTTT 594  
Db 1 TGACGGAGUGGCGCTTU 17

## RESULT 1231

US-11-101-244-704520  
; Sequence 704520, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 704520  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-704520

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 58.8%; Pred. No. 9e+02;  
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 578 TGACGGCTGTGCGCTTT 594  
Db 3 TGACGGAGUGGCGCTTU 19

## RESULT 1232

US-11-101-244-751946/c  
; Sequence 751946, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 751946  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-751946

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1659 TTTCCTAGCCTGTAA 1675  
Db 17 TTTCCTAGCCTGTAA 1

## RESULT 1233

US-11-101-244-820807/c  
; Sequence 820807, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 820807  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-820807

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;



Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1721 TTCTCGAAGTGACTTT 1737  
Db 19 TTCTCGAAGGACTTT 3

RESULT 1234  
US-11-101-244-896406/c  
; Sequence 896406, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 896406  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-896406  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 261 TAACACTCGGACCCA 277  
Db 19 TAACACTCGGACCCA 3

RESULT 1235  
US-11-101-244-911965  
; Sequence 911965, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 911965  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-911965

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 9e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1643 AACCAATCACTGACT 1659  
Db 3 AACCAAUCAACUGAAAU 19

RESULT 1236  
US-11-101-244-917716/c  
; Sequence 917716, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 917716  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-917716  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 653 AAGTGTCATCTGTGTC 669  
Db 18 AAGTGTCATCTGTGTC 2

RESULT 1237  
US-11-101-244-926899/c  
; Sequence 926899, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 926899  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-926899

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1400 AGAGCTTCAGCTTCTCC 1416  
 DB 18 AGAGGTTCACTTCTCC 2

RESULT 1238  
 US-11-101-244-976398/c  
 ; Sequence 976398, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 134990S  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 976398  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-976398

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 998 CCTTCCACATCTTCTTC 1014  
 DB 18 CCTTCCATCTCTCTTC 2

RESULT 1239  
 US-11-101-244-1028300/c  
 ; Sequence 1028300, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 134990S  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1028300  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-1028300

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 241 CTCTCCCAACATCTC 257

DB 18 CTCTCCCAACATCTC 2

RESULT 1240  
 US-11-101-244-1077507/c  
 ; Sequence 1077507, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 134990S  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1077507  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-1077507

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1575 CATTCCATCTTGATC 1591  
 DB 19 CATTCCATCTTGATC 3

RESULT 1241  
 US-11-101-244-1098844  
 ; Sequence 1098844, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 134990S  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1098844  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-101-244-1098844

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 76.5%; Pred. No. 9e+02;  
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1702 AAGAGCCCATGATCTC 1718

Db 3 AAGAGCCCAUUCUUC 19

```
RESULT 1242
US-11-101-244-1245691/c
; Sequence 1245691, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1245691
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1245691
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 652 AAAGTGTGATCTGTGT 668
Db 17 AAAGTGTGATCTGTGT 1

RESULT 1243
US-11-101-244-1277052/c
; Sequence 1277052, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277052
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1277052
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 1244
US-11-101-244-1277082/c
; Sequence 1277082, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1277082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1277082
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 801 CATCTGTGACTGTGC 817
Db 17 CATCTGTGACTGTGC 1

RESULT 1245
US-11-101-244-1299074
; Sequence 1299074, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OR INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1299074
```

```
Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 1246

```

US-11-101-244-1302380
/ Sequence 1302380, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1302380
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1302380

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1;

```

```

QY      544 CCATCGCCGCTGTCTT 560
      |||:|||||:|:|:|
DB      2 CCATCGCCGCTGTCTT 18

```

```

RESULT 1247
US-11-101-244-1335689/c
/ Sequence 1335689, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1335689
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1335689

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

```

```

QY      1404 CTTGAGTTCTCTTCCA 1420
      |||:|||||:|:|:|
DB      17 CTTGAGTTCTCTTCCA 1

```

RESULT 1248

```

US-11-101-244-1362687
/ Sequence 1362687, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1362687
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1362687

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 1;

```

```

QY      1029 CAACCCGATCTCTACC 1045
      |||:|||||:|:|:|
DB      1 CAACCCGATCTCTACC 17

```

```

RESULT 1249
US-11-101-244-1374698/c
/ Sequence 1374698, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1374698
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1374698

```

```

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1;

```

```

QY      999 CTTCCACATCTTCTTCC 1015
      |||:|||||:|:|:|
DB      17 CTTCCACATCTTCTTCC 1

```

RESULT 1250

```

US-11-101-244-1410088/c
; Sequence 1410088, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1410088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1410088

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1402 AGCTTCAGCTTCCTC 1418
Db      17 AGCTTCGCTTCCTC 1

```

```

RESULT 1251
US-11-101-244-1450085
; Sequence 1450085, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1450085
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1450085

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1495 GGAATTCCTTCATCT 1511
Db      1 GGAATGCTTCUACAUCU 17

```

```

RESULT 1252
US-11-101-244-1464506/c

```

```

; Sequence 1464506, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1464506
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1464506

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1529 CCTCAGCTGGAGCTTG 1545
Db      17 CCACACACTGGAGCTTG 1

```

```

RESULT 1253
US-11-101-244-1474304/c
; Sequence 1474304, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1474304
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1474304

```

```

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      418 TTTCGTGAACCTGGC 434
Db      19 TTTCGTGAACCTGGC 3

```

```

RESULT 1254
US-11-101-244-1485805/c
; Sequence 1485805, Application US/11101244

```

```
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07,050
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1485805
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1485805

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1404 CTTGAGCTTCTCCTCCA 1420
DB      17 CTTGAGCTTCTCCTCCA 1

RESULT 1255
US-11-101-244-1498825
/ Sequence 1498825, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1498825
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1498825

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1651 CACTGAACCTTGTGCTGAG 1667
DB      2 CACUGAACUUGAUGAG 18

RESULT 1256
US-11-101-244-1498858
/ Sequence 1498858, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1498858
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1498858

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1651 CACTGAACCTTGTGCTGAG 1667
DB      1 CACUGAACUUGAUGAG 17

RESULT 1257
US-11-101-244-1515526/c
/ Sequence 1515526, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1515526
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1515526

Query Match      0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02; 1; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1279 ACCATCTCCACAGTGT 1295
DB      19 ACCATCTCCACAGTGT 3

RESULT 1258
US-11-101-244-1515845/c
/ Sequence 1515845, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

```
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorovaya, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leahe, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 1515845
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-1515845

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1445 CTTTGCAGGTGCAGCC 1461
Db      17  CGTTGGCAGGTGCAGCC 1

RESULT 1259
US-11-058-582-229
;; Sequence 229, Application US/11058582
;; Publication No. US20050260620A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: McSwigen, James
;; APPLICANT: Christiano, Angela
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Retinoblastoma (Rb1) Gene
;; FILE REFERENCE: 400/250 (MBHB 05-059-A)
;; CURRENT APPLICATION NUMBER: US/11/058,582
;; CURRENT FILING DATE: 2005-02-15
;; PRIOR APPLICATION NUMBER: US 11/039,680
;; PRIOR FILING DATE: 2005-01-18
;; PRIOR APPLICATION NUMBER: US 10/923,536
;; PRIOR FILING DATE: 2004-08-20
;; PRIOR APPLICATION NUMBER: PCT/US04/16390
;; PRIOR FILING DATE: 2004-05-24
;; PRIOR APPLICATION NUMBER: US 10/826,966
;; PRIOR FILING DATE: 2004-04-16
;; PRIOR APPLICATION NUMBER: US 10/757,803
;; PRIOR FILING DATE: 2004-01-14
;; PRIOR APPLICATION NUMBER: US 10/720,448
;; PRIOR FILING DATE: 2003-11-24
;; PRIOR APPLICATION NUMBER: US 10/693,059
;; PRIOR FILING DATE: 2003-10-23
;; PRIOR APPLICATION NUMBER: US 10/444,853
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT/US03/05346
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT/US03/05028
;; PRIOR FILING DATE: 2003-02-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 650
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 229
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-11-058-582-229
```

```
US-11-058-582-229

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 9e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy      1550 AAGGTCAGTATGGGTT 1566
Db      3  AAGGGUCAUUAGGGUU 19

RESULT 1260
US-11-058-582-492/C
;; Sequence 492, Application US/11058582
;; Publication No. US20050260620A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: McSwigen, James
;; APPLICANT: Christiano, Angela
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Retinoblastoma (Rb1) Gene
;; FILE REFERENCE: 400/250 (MBHB 05-059-A)
;; CURRENT APPLICATION NUMBER: US/11/058,582
;; CURRENT FILING DATE: 2005-02-15
;; PRIOR APPLICATION NUMBER: US 11/039,680
;; PRIOR FILING DATE: 2005-01-18
;; PRIOR APPLICATION NUMBER: US 10/923,536
;; PRIOR FILING DATE: 2004-08-20
;; PRIOR APPLICATION NUMBER: PCT/US04/16390
;; PRIOR FILING DATE: 2004-05-24
;; PRIOR APPLICATION NUMBER: US 10/826,966
;; PRIOR FILING DATE: 2004-04-16
;; PRIOR APPLICATION NUMBER: US 10/757,803
;; PRIOR FILING DATE: 2004-01-14
;; PRIOR APPLICATION NUMBER: US 10/720,448
;; PRIOR FILING DATE: 2003-11-24
;; PRIOR APPLICATION NUMBER: US 10/693,059
;; PRIOR FILING DATE: 2003-10-23
;; PRIOR APPLICATION NUMBER: US 10/444,853
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: PCT/US03/05346
;; PRIOR FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: PCT/US03/05028
;; PRIOR FILING DATE: 2003-02-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 650
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 492
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-11-058-582-492

Query Match          0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1550 AAGGTCAGTATGGGTT 1566
Db      17  AAGGTCATTTATGGGTT 1

RESULT 1261
US-09-866-108-6966
;; Sequence 6966, Application US/09866108
;; Patent No. US20020048800A1
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
```

```
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6966
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6966

Query Match      0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      28 CAGTGCATCCAGAG 42
      |||
DB      3 CAGTGCATCCAGAG 17
```

RESULT 1262

```
US-09-866-108-6967
; Sequence 6967, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

```
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6967
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6967

Query Match      0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      28 CAGTGCATCCAGAG 42
      |||
DB      2 CAGTGCATCCAGAG 16
```

RESULT 1263

```
US-09-866-108-6968
; Sequence 6968, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
```



;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 60/266,860  
;; PRIOR FILING DATE: 2001-02-05  
;; NUMBER OF SEQ ID NOS: 15752  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; SEQ ID NO 6968  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108-6968

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CAGTGCATCCAGAG 42  
Db 1 CAGTGCATCCAGAG 15

RESULT 1264  
US-09-780-164-702  
;; Sequence 702, Application US/09780164  
;; Publication No. US20030092646A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: Meswigen, Jim  
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20  
;; FILE REFERENCE: 400/010  
;; CURRENT APPLICATION NUMBER: US/09/780,164  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 60/185,516  
;; PRIOR FILING DATE: 2000-02-28  
;; NUMBER OF SEQ ID NOS: 2603  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 702  
;; LENGTH: 17  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-09-780-164-702

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 60.0%; Pred. No. 8.5e+02;  
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 802 ATGTGTGACTGTG 816  
Db 1 AUCUGUGACUGUG 15

RESULT 1265  
US-10-723-361-6966  
;; Sequence 6966, Application US/10723361  
;; Publication No. US20040137589A1  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharon G.

;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
;; FILE REFERENCE: PB0105  
;; CURRENT APPLICATION NUMBER: US/10/723,361  
;; PRIOR FILING DATE: 2003-11-26  
;; PRIOR APPLICATION NUMBER: US 09/866,108  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263,6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; SEQ ID NO 6966  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-723-361-6966

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CAGTGCATCCAGAG 42  
Db 3 CAGTGCATCCAGAG 17

RESULT 1266  
US-10-723-361-6967  
;; Sequence 6967, Application US/10723361  
;; Publication No. US20040137589A1  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharon G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
;; FILE REFERENCE: PB0105  
;; CURRENT APPLICATION NUMBER: US/10/723,361  
;; PRIOR FILING DATE: 2003-11-26  
;; PRIOR APPLICATION NUMBER: US 09/866,108  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263,6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 15755  
 SOFTWARE: Aecomica Sequence Listing Engine  
 SEQ ID NO 6967  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-723-361-6967

Query Match 0.8%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
 DB 2 CAGTGCATCCAGAAG 16

RESULT 1267

US-10-723-361-6968  
 Sequence 6968, Application US/107233361  
 Publication No. US20040137589A1

GENERAL INFORMATION:  
 APPLICANT: GU, Yizhong  
 APPLICANT: JI, Yonggang  
 APPLICANT: PENN, Sharon G.  
 APPLICANT: HANZEL, David K.  
 APPLICANT: RANK, David R.  
 APPLICANT: CHEN, Wensheng  
 APPLICANT: SHANNON, Mark  
 TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
 FILE REFERENCE: PB0105  
 CURRENT FILING DATE: 2003-11-26  
 PRIOR APPLICATION NUMBER: US/10/723,361  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 09/866,108  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 15755  
 SOFTWARE: Aecomica Sequence Listing Engine  
 SEQ ID NO 6968  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-723-361-6968

Query Match 0.8%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
 DB 1 CAGTGCATCCAGAAG 15

RESULT 1268

US-10-241-313-5  
 Sequence 5, Application US/10241313  
 Publication No. US20030118506A1

GENERAL INFORMATION:  
 APPLICANT: O'Malley, Karen L.  
 APPLICANT: Todd, Richard D.  
 TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor  
 FILE REFERENCE: WU 102 CON DIV(2)  
 CURRENT APPLICATION NUMBER: US/10/241,313  
 CURRENT FILING DATE: 2002-09-11  
 PRIOR APPLICATION NUMBER: US 08/475,742  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: US 08/261,293  
 PRIOR FILING DATE: 1994-06-16  
 PRIOR APPLICATION NUMBER: US 08/014,013  
 PRIOR FILING DATE: 1993-01-28  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: primer- TM  
 PUBLICATION INFORMATION: VI/VII primer set ord-403  
 TITLE: The rat dopamine D4 receptor: sequence, gene structure  
 TITLE: and demonstration of expression in the cardiovascular  
 TITLE: system  
 JOURNAL: New Biol.  
 VOLUME: 4  
 PAGES: 1-9  
 DATE: 1992  
 US-10-241-313-5

Query Match 0.8%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TGCTGCTGCCCTTC 1002  
 DB 1 TGCTGCTGCCCTTC 15

RESULT 1269

US-10-854-018-3/c  
 Sequence 3, Application US/10854018  
 Publication No. US20050014246A1

GENERAL INFORMATION:  
 APPLICANT: Hitachi, Ltd.  
 TITLE OF INVENTION: Chemical reaction apparatus  
 FILE REFERENCE: H0300729  
 CURRENT APPLICATION NUMBER: US/10/854,018  
 CURRENT FILING DATE: 2004-05-26  
 PRIOR APPLICATION NUMBER: JP 2003-196178  
 PRIOR FILING DATE: 2003-07-14  
 NUMBER OF SEQ ID NOS: 20  
 SEQ ID NO 3  
 LENGTH: 18  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-854-018-3

Query Match 0.8%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTCTGGGCTTC 1158  
Db 17 TTCGCTCTGGGCTTC 3

RESULT 1270

US-10-854-018-13  
Sequence 13, Application US/10854018  
Publication No. US20050014246A1  
GENERAL INFORMATION:  
APPLICANT: Hitachi, Ltd.  
TITLE OF INVENTION: Chemical reaction apparatus  
FILE REFERENCE: H0300729  
CURRENT APPLICATION NUMBER: US/10/854, 018  
CURRENT FILING DATE: 2004-05-26  
PRIOR APPLICATION NUMBER: JP 2003-196178  
PRIOR FILING DATE: 2003-07-14  
NUMBER OF SEQ ID NOS: 20  
SEQ ID NO 13  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-854-018-13

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTCTGGGCTTC 1158  
Db 2 TTCGCTCTGGGCTTC 16

RESULT 1271

US-10-310-914A-449129/C  
Sequence 449129, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 449129  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-449129

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1325 GCCCCAGGCCACAC 1339  
Db 18 GCCCCAGGCCACAC 4

RESULT 1272

US-10-310-914A-767846/C  
Sequence 767846, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 767846  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-767846

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 TCTTCTCTGCGCCT 1024  
Db 18 TCTTCTCTGCGCCT 4

RESULT 1273

US-10-310-914A-1113869  
Sequence 1113869, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1113869  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1113869

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 80.0%; Pred. No. 9.1e+02;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 249 AAACATCTCCACTAA 263  
Db 4 AAACATCTCCACTAA 18

RESULT 1274

US-10-310-914A-1357464/C  
Sequence 1357464, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310, 914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1357464  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1357464

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTCGCTTCTCCTC 1418  
Db 15 CTCGCTTCTCCTC 1

## RESULT 1275

US-11-044-498-3/c  
; Sequence 3, Application US/11044498  
; Publication No. US20060083667A1  
; GENERAL INFORMATION: Software Engineering Co., Ltd.  
; APPLICANT: Hitachi Chemical Reaction Apparatus  
; TITLE OF INVENTION: PH-2343  
; FILE REFERENCE: PH-2343  
; CURRENT APPLICATION NUMBER: US/11/044,498  
; CURRENT FILING DATE: 2005-01-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized DNA  
US-11-044-498-3

Query Match 0.8%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCGCTCTGGGCTTC 1158  
Db 17 TTCGCTCTGGGCTTC 3

## RESULT 1276

US-09-067-638B-50/c  
; Sequence 50, Application US/09067638B  
; Patent No. US2002028923A1  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowsett  
; APPLICANT: Brenda F. Baker  
; APPLICANT: John McNeil  
; APPLICANT: Susan M. Freier  
; APPLICANT: Henry M. Sasnor  
; APPLICANT: Douglas G. Brooks  
; APPLICANT: Cara Ohashi  
; APPLICANT: Jacqueline R. Wyatt  
; APPLICANT: Alexander Borchers  
; APPLICANT: Timothy A. Vickers  
; TITLE OF INVENTION: Identification of Genetic  
; TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and  
; TITLE OF INVENTION: Generation of Oligonucleotides for Gene  
; TITLE OF INVENTION: Modulation  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOODCOCK WASHURN KURTZ  
; ADDRESSEE: MACKIEWICZ & NORIS LLP  
; STREET: 1 LIBERTY PLACE 46TH FLOOR  
; CITY: PHILADELPHIA  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-Windows NT  
; SOFTWARE: WORD PERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,638B  
; FILING DATE: 28-APR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/081,483  
; FILING DATE: 13-APR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: John W. Caldwell  
; REGISTRATION NUMBER: 28,937  
; REFERENCE/DOCKET NUMBER: ISIS-2960  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-067-638B-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423  
Db 18 TCAGCTTCTCTCCATG 1

## RESULT 1277

US-10-116-325-50/c  
; Sequence 50, Application US/10116325  
; Publication No. US2003011379A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowsett, Lex M.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: McNeil, John  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Sasnor, Henry M.  
; APPLICANT: Brooks, Douglas G.  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Borchers, Alexander  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides  
; TITLE OF INVENTION: Generation of Oligonucleotides for Gene Modulation  
; FILE REFERENCE: ISIS5026  
; CURRENT APPLICATION NUMBER: US/10/116,325  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/067,638  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/081,483  
; PRIOR FILING DATE: 1998-04-13  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 50  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US2003011379A1e1 Sequence  
US-10-116-325-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423  
Db 18 TCAGCTTCTCTCCATG 1

RESULT 1278  
US-10-388-263-50/c  
; Sequence 50, Application US/10388263  
; Publication No. US2003028597A1

```

; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooke, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-50

```

```

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1406 TCAGCTTCTCTCCAAAG 1423
Db      18 TCGGCTTCTTCTCCAAAG 1

```

```

RESULT 1279
US-10-016-248-66
; Sequence 66, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsebrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide primer
US-10-016-248-66

```

```

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;

```

```

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      315 GGCAGCTGCTTACACGGT 332
Db      1 GGCAGCGCCCTTACACGGT 18

```

```

RESULT 1280
US-10-698-689-50/c
; Sequence 50, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-698-689-50

```

```

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1406 TCAGCTTCTCTCCAAAG 1423
Db      18 TCGGCTTCTTCTCCAAAG 1

```

```

RESULT 1281
US-10-698-689-214
; Sequence 214, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214

```

LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-698-689-214

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423  
DB 1 TCAGCTTCTCTCCATG 18

RESULT 1282  
US-10-830-475-50/c  
Sequence 50, Application US/10930475  
Publication No. US2004019781A1  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowseert  
Brenda F. Baker  
John McNeill  
Susan M. Freier  
Henri M. Saemor  
Douglas G. Brooks  
Cara Ohashi  
Jacqueline R. Wyatt  
Alexander Borchers  
Timothy A. Vickers  
TITLE OF INVENTION: Identification of Genetic  
Targets for Modulation By Oligonucleotides and  
Modulation  
Generation of Oligonucleotides for Gene  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOODCOCK WASHBURN KURTZ  
STREET: 1 LIBERTY PLACE 46TH FLOOR  
CITY: PHILADELPHIA  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
COMPUTER: IBM  
OPERATING SYSTEM: PC-Windows NT  
SOFTWARE: WORD PERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/830,475  
FILING DATE: 21-Apr-2004  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,638B  
FILING DATE: 28-APR-1998  
APPLICATION NUMBER: 60/081,483  
FILING DATE: 13-APR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Caldwell  
REGISTRATION NUMBER: 28,937  
REFERENCE/DOCKET NUMBER: ISIS-2960  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-10-830-475-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423  
DB 18 TCAGCTTCTCTCCATG 1

RESULT 1283  
US-10-649-467-50/c  
Sequence 50, Application US/10649467  
Publication No. US20050033524A1  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowseert  
Brenda F. Baker  
John McNeill  
Susan M. Freier  
Henri M. Saemor  
Douglas G. Brooks  
Cara Ohashi  
Jacqueline R. Wyatt  
Alexander Borchers  
Timothy A. Vickers  
TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides  
FILE REFERENCE: ISIS085-100 (ISIS2960US.C2)  
CURRENT APPLICATION NUMBER: US/10/649,467  
CURRENT FILING DATE: 2003-08-27  
PRIOR APPLICATION NUMBER: 09/067,636  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/081,483  
PRIOR FILING DATE: 1998-04-13  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound  
US-10-649-467-50

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423  
DB 18 TCAGCTTCTCTCCATG 1

RESULT 1284  
US-10-934-798-89/c  
Sequence 89, Application US/10934798  
Publication No. US20050142581A1  
GENERAL INFORMATION:  
APPLICANT: Richard H. Griffey  
David J. Becker  
C. Frank Bennett  
Donna T. Ward  
Susan M. Freier  
TITLE OF INVENTION: MICRORNA AS LIGANDS AND TARGET MOLECULES  
FILE REFERENCE: CORE0020US  
CURRENT APPLICATION NUMBER: US/10/934,798  
CURRENT FILING DATE: 2004-09-03  
PRIOR APPLICATION NUMBER: 60/500,824  
PRIOR FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: 60/500,730  
PRIOR FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: 60/504,495  
PRIOR FILING DATE: 2003-09-17

```

; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-934-798-89

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1406 TCAGCTTCTCTCCCATG 1423
Db      18 TCGGCTTCTCTCCCATG 1

RESULT 1285
US-10-934-798-208/c
; Sequence 208, Application US/10934798
; Publication No. US20050142581A1
; GENERAL INFORMATION:
; APPLICANT: Richard H. Giffey
; APPLICANT: C. Frank Bennett
; APPLICANT: David J. Ecker
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: MICRORNA AS LIGANDS AND TARGET MOLECULES
; FILE REFERENCE: CORE0020US
; CURRENT APPLICATION NUMBER: US/10/934,798
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/500,824
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/500,730
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/504,495
; PRIOR FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-934-798-208

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1406 TCAGCTTCTCTCCCATG 1423
Db      18 TCGGCTTCTCTCCCATG 1

RESULT 1286
US-10-310-914A-77047
; Sequence 77047, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77047
```

```

; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-77047

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      930 CTGTGCCAAGGCCAAGT 947
Db      1 CACUGCCAAAGGCCAAGU 18

RESULT 1287
US-10-310-914A-83639
; Sequence 83639, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83639
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-83639

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1326 CCCCAAGGCCACACCTTC 1343
Db      1 CCUCAAGGCCACCCCTTC 18

RESULT 1288
US-10-310-914A-101443
; Sequence 101443, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101443
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-101443

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1511 TGGAACCATCAGAAACAC 1528
Db      1 UGGAACCAAAAGAAACAC 18

RESULT 1289
```

```

US-10-310-914A-213729
; Sequence 213729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213729
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-213729

```

```

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 984 CATCTGCTGCTGCCCTT 1001
Db 1 CACTCGCUGACUGCAGCUU 18

```

```

RESULT 1290
US-10-310-914A-309009/c
; Sequence 309009, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 309009
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-309009

```

```

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 13 CCGGGGCGAGCGGCGAG 30
Db 18 CCGGGGCGAGCGGCGAG 1

```

```

RESULT 1291
US-10-310-914A-336351
; Sequence 336351, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 336351
; LENGTH: 18

```

```

; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-336351

```

```

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1284 CTCACAGTGTGGGGGC 1301
Db 1 CUCCCGACUGUGGGGCGC 18

```

```

RESULT 1292
US-10-310-914A-427752/c
; Sequence 427752, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 427752
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-427752

```

```

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1001 TCCACATCTTCTTCTCC 1018
Db 18 TCCCTCTCTTCTTCTCC 1

```

```

RESULT 1293
US-10-310-914A-465296
; Sequence 465296, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465296
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465296

```

```

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1001 TCCACATCTTCTTCTCC 1018
Db 1 UCCUCUCUCUCUCUCUC 18

```

```

RESULT 1294
US-10-310-914A-472856/c

```



```

; Sequence 472856, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 472856
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-472856

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 732 GCCCAGCAGACTCGTGTG 749
Db 18 GCCCAGCAGACGCTGGG 1

RESULT 1295
US-10-310-914A-519019
; Sequence 519019, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519019
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-519019

Query Match
Best Local Similarity 83.3%; Score 14.8; DB 1; Length 18;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 128 CCTGAGCCCCGAGCGCC 145
Db 1 CCTGAGUGCCAGCGCC 18

RESULT 1296
US-10-310-914A-519948/C
; Sequence 519948, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519948
; LENGTH: 18
; TYPE: RNA

; ORGANISM: Human
US-10-310-914A-519948

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 694 GCCTCCCCCAGGCTGAC 711
Db 18 GCCATCCCCCAGGCTCC 1

RESULT 1297
US-10-310-914A-519969
; Sequence 519969, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519969
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-519969

Query Match
Best Local Similarity 72.2%; Score 14.8; DB 1; Length 18;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1283 TCCTCAGAGTGGGCGGG 1300
Db 1 UCUCACGGGGGUGGGGG 18

RESULT 1298
US-10-310-914A-585840/C
; Sequence 585840, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 585840
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-585840

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 GAGCCCGAGCGCCAGCC 149
Db 18 GAGCCTCAGGCCCGCAGCC 1

RESULT 1299
US-10-310-914A-601989/C
; Sequence 601989, Application US/10310914A
```

```
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Knuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 601989
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-601989

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1168 TTCCGCTGCTGCCCCCTTC 1185
Db      18  TTCCGAGATTCCCTTC 1

RESULT 1300
US-10-310-914A-645930/c
/ Sequence 645930, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Knuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 645930
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-645930

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      685 CTCTGCTGCTGCCCCCTTC 702
Db      18  CTCTGCTGCTGCCCCCTTC 1

RESULT 1301
US-10-310-914A-696092/c
/ Sequence 696092, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Knuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 696092
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human

US-10-310-914A-696092

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      984 CATCTGCTGCTGCCCCCTT 1001
Db      18  CATATCAGGCTTCCTTC 1

RESULT 1302
US-10-310-914A-707873/c
/ Sequence 707873, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Knuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 707873
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-707873

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1592 AAAAATCTCAATCTTC 1609
Db      18  AAAAAGTCTAATCTTC 1

RESULT 1303
US-10-310-914A-768979
/ Sequence 768979, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Knuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 768979
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-768979

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCCACATCTTCTCTCC 1018
Db      1  UCCUCUCUCUCUCUC 18

RESULT 1304
US-10-310-914A-795204/c
/ Sequence 795204, Application US/10310914A
/ Publication No. US20060003322A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 795204
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-795204

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      623 TCCAGCCCCGGCTGCTCAG 640
Db      18 TCCATCCCCGGCAGCTCAG 1

RESULT 1305
US-10-310-914A-809520
; Sequence 809520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 809520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-809520

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 9.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1638 ACTCAACCAATGACATG 1655
Db      1 ACUCAUCCCAAUACACUG 18

RESULT 1306
US-10-310-914A-847106/c
; Sequence 847106, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 847106
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-847106

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1243 CAGGACAGTGTGTACAA 1260
Db      1 CAGGACAGUAAUACAA 18

RESULT 1309
US-10-310-914A-923895/c
; Sequence 923895, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 874025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-874025

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1007 TCTTCTCTCTCTGCGCCT 1024
Db      1 UCUGCUUCUCCUCCUCCU 18

RESULT 1308
US-10-310-914A-885132
; Sequence 885132, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 885132
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-885132

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1615 CTTGACACCTCATGCT 1632
Db      18 CTGTGCACCTCTCTGCT 1

RESULT 1307
US-10-310-914A-874025
; Sequence 874025, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 874025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-874025

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1615 CTTGACACCTCATGCT 1632
Db      18 CTGTGCACCTCTCTGCT 1
```

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 923895
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-923895

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 GCGGGCAGCGCGCGCATG 32
Db      18 GCGGGCAGCGCGCGCGGAG 1

RESULT 1310
US-10-310-914A-937032/c
; Sequence 937032, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 937032
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-937032

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      685 CTCCTGCTGGCCTTCC 702
Db      18 CCCGAGCTGGCCTTCCC 1

RESULT 1311
US-10-310-914A-946378/c
; Sequence 946378, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 946378
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-946378
```

```

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1165 GCCTCCGGTGCTGCC 1182
Db      18 GCCTCCGAGCTGCC 1

RESULT 1312
US-10-310-914A-965107/c
; Sequence 965107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 965107
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-965107

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      998 CCTTCCACATCTTCTCC 1015
Db      18 CCTTCCACATCTTCTCC 1

RESULT 1313
US-10-310-914A-971333
; Sequence 971333, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 971333
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-971333

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1001 TCACATCTTCTCTCC 1018
Db      1 UCCUCUCUCUCUCUC 18

RESULT 1314
US-10-310-914A-981336/c
; Sequence 981336, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

APPLICANT: Shiler, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 981336  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-981336

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1308 GGAGAGCCAGAGCGG 1325  
Db 18 GGAGAGCCAGCGCGG 1

RESULT 1315  
US-10-310-914A-984119  
Sequence 984119, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 984119  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-984119

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 61.1%; Pred. No. 9.4e+02;  
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 676 GTCCTGGCTCTGCTG 693  
Db 1 GGCCTUGGCUCUCUCUG 18

RESULT 1316  
US-10-310-914A-990023/c  
Sequence 990023, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 990023  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-990023

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1729 AGTGACTTTGGCTGCATG 1746  
Db 18 AGTGATTTTGGCTGCATG 1

RESULT 1317  
US-10-310-914A-999624  
Sequence 999624, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 999624  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-999624

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 72.2%; Pred. No. 9.4e+02;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1455 TGACGCCCCCAGTGCCTT 1472  
Db 1 UGCAGCCCCCUCUGCCCU 18

RESULT 1318  
US-10-310-914A-1004988/c  
Sequence 1004988, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kuzat  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1004988  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-1004988

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 CTTCACCCCTCCCTGCTG 116  
Db 18 CTGCTCCCTCCCTGCTG 1

RESULT 1319  
US-10-310-914A-1093902/c  
Sequence 1093902, Application US/10310914A  
Publication No. US2006003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shiler, Kuzat

```

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1093902
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1093902

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      156 CTCTGCTGCAGAGCGGGG 173
Db      18 CTGTGCTGCAGAGCGGGG 1

RESULT 1320
US-10-310-914A-1169386
; Sequence 1169386, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1169386
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1169386

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 9.4e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      525 CAAGTCCACCAACTTCTT 542
Db      1 CAGAATCCACCAATUDCU 18

RESULT 1321
US-10-310-914A-1219917
; Sequence 1219917, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1219917
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1219917

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 9.4e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      1436 CCACAGGCGCTTGGCAG 1453
Db      1 CCUCAGGGCCUCUGGCAG 18

RESULT 1323
US-10-310-914A-1249080/c
; Sequence 1249080, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1249080
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1249080

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      134 GCCCCAGGCGCCGAGCCAC 151
Db      18 GCCCCAGGCGCCGAGCCAC 1

RESULT 1324
US-10-310-914A-1255023/c
; Sequence 1255023, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      1145 TCCGCTGTGGGCTTCAAGC 1162
Db      1 UCCCTUCGGGCTTCCAGC 18

RESULT 1322
US-10-310-914A-1234776
; Sequence 1234776, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1234776
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1234776

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 9.4e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      1436 CCACAGGCGCTTGGCAG 1453
Db      1 CCUCAGGGCCUCUGGCAG 18

RESULT 1323
US-10-310-914A-1249080/c
; Sequence 1249080, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1249080
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1249080

Query Match          0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      134 GCCCCAGGCGCCGAGCCAC 151
Db      18 GCCCCAGGCGCCGAGCCAC 1

RESULT 1324
US-10-310-914A-1255023/c
; Sequence 1255023, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
```

```

; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1255023
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1255023

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      685 CTCCTGCTGGCCTTCCCC 702
Db      18 CTCCTGCTGGCCTTCCCC 1

RESULT 1325
US-10-310-914A-1329744/c
; Sequence 1329744, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1329744
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1329744

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      685 CTCCTGCTGGCCTTCCCC 702
Db      18 CTCCTGCTGGCCTTCCCC 1

RESULT 1326
US-10-310-914A-1337516/c
; Sequence 1337516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1337516
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1337516

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1181 CCTTCATCAGCGCGCGC 1198
Db      18 CTTTCAGCAGCGCAGCGC 1

RESULT 1327
US-10-310-914A-1366802/c
; Sequence 1366802, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1366802
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1366802

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      366 AGTGATGTGATGATCTT 383
Db      18 AGTGATGTGATGATCTT 1

RESULT 1328
US-10-310-914A-1383827/c
; Sequence 1383827, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1383827
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1383827

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1434 GGCACAGGCGCTTTGGC 1451
Db      18 GGCACAGGCGCATCTGGC 1

RESULT 1329
US-11-069-908-3801/c
; Sequence 3801, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MURRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; TITLE OF INVENTION: CONDITIONS

```

```
FILE REFERENCE: 029011-0402
CURRENT APPLICATION NUMBER: US/11/069,908
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 60/547,823
PRIOR FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 7098
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3801
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-3801

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1292 TGGTGGGGGCCACGAGG 1309
DB 18 TGGTGGAGGCGCTCGAGG 1

RESULT 1330
US-11-226-882A-50/c
Sequence 50, Application US/11226882A
Publication No. US20060069518A1
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
APPLICANT: Brenda F. Baker
APPLICANT: John McNeil
APPLICANT: Susan M. Freier
APPLICANT: Henri M. Sasmor
APPLICANT: Douglas G. Brooks
APPLICANT: Cara Ohashi
APPLICANT: Jacqueline R. Wyatt
APPLICANT: Alexander Borchers
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides
FILE REFERENCE: ISIS0085-104 (ISIS2960US C4)
CURRENT APPLICATION NUMBER: US/11/226,882A
CURRENT FILING DATE: 2005-09-14
PRIOR APPLICATION NUMBER: 09/067,638
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/081,483
PRIOR FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound
US-11-226-882A-50

Query Match
Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCTCCATG 1423
DB 18 TCGGCTTCTCTCCATG 1

RESULT 1331
US-10-310-914A-467163
Sequence 467163, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
```

```
APPLICANT: Shiler, Kuvatz
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 467163
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-467163

Query Match
Best Local Similarity 0.8%; Score 14.6; DB 1; Length 22;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 893 TCCCGGGAGCTCTGACC 913
DB 1 UCCCGGGAGACUCCUGGCC 21

RESULT 1332
US-10-310-914A-467164
Sequence 467164, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuvatz
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 467164
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-467164

Query Match
Best Local Similarity 0.8%; Score 14.6; DB 1; Length 22;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 893 TCCCGGGAGCTCTGACC 913
DB 1 UCCCGGGAGACUCCUGGCC 21

RESULT 1333
US-09-930-503-14/c
Sequence 14, Application US/09930503
Publication No. US20030060438A1
GENERAL INFORMATION:
APPLICANT: HENRY, JAMES
APPLICANT: CAHILL, CATHERINE
APPLICANT: YASHPIL, KIRAN
TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
FILE REFERENCE: 39245-173913
CURRENT APPLICATION NUMBER: US/09/930,503
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/226,086
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
```



```
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-930-503-14

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CGAATGATACGTC 222
DB 16 CAAATGATACGTC 1

RESULT 1334
US-10-712-672-1732
; Sequence 1732, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1732
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-712-672-1732

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 16;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 464 ATACAGTGTGAACCT 479
DB 1 AGACAGUGUGAACU 16

RESULT 1335
US-09-864-785-1566
; Sequence 1566, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1566
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; US-09-864-785-1566
```

```
Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 GCGCCAGCGCCGCGC 149
DB 2 GCGCCAGCGCCGCGC 17

RESULT 1336
US-09-930-503-13/c
; Sequence 13, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-930-503-13

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CGAATGATACGTC 222
DB 16 CAAATGATACGTC 1

RESULT 1337
US-09-780-533A-920
; Sequence 920, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatz, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowitra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00-878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 920
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-920

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCGCTCCAGCCCGCGC 634
DB 1 CCGCTCCAGCCCGCGC 634
```

```
Db          2 CCCCCCAGCCCCGC 17

RESULT 1338
US-09-848-754A-3108/c
; Sequence 3108, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3108
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3108

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1694 TTTTCCTCAAGAGCC 1709
Db          17 TTTTCCTCCAGAGCC 2

RESULT 1339
US-09-930-423-1361/c
; Sequence 1361, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1361

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1275 GACCACCATCTCCACA 1290
Db          17 GTCACCATCTCCACA 2

RESULT 1340
US-09-780-164-769
; Sequence 769, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516

; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 769
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-769

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 9.5e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY          799 CACATCTGTGTACTG 814
Db          2 CCCAUCUGUGACUG 17

RESULT 1341
US-09-745-237A-1361/c
; Sequence 1361, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1361

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1275 GACCACCATCTCCACA 1290
Db          17 GTCACCATCTCCACA 2

RESULT 1342
US-10-238-700-1302/c
; Sequence 1302, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level;
; FILE REFERENCE: 400/057 (MHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-1302

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 834 CCTGCTGTGATGGC 849  
Db 17 CCTGCTGTGATGGC 2

RESULT 1343  
US-10-712-672-342  
; Sequence 342, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowitra, Bharat  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 342  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-712-672-342

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 9.5e+02;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1687 GACCAGCTTTCCCA 1702  
Db 1 GGCCAGCUUCCUCA 16

RESULT 1344  
US-10-724-270-1302/C  
; Sequence 1302, Application US/10724270  
; Publication No. US20050080031A1  
; GENERAL INFORMATION:  
; APPLICANT: McSwigen, James  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/046-US (MBH02-326-A)  
; CURRENT APPLICATION NUMBER: US/10/724,270  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: PCT/US02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/296,249  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/294,140  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 10/238,700  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: US 10/163,552  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 10/157,580  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16  
; Remaining Prior Application data removed - See File Wrapper or PAM.  
; NUMBER OF SEQ ID NOS: 6810  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1302  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-724-270-1302

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 9.5e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 834 CCTGCTGTGATGGC 849  
Db 17 CCTGCTGTGATGGC 2

RESULT 1345  
US-09-930-503-12/C  
; Sequence 12, Application US/0930503  
; Publication No. US20030060438A1  
; GENERAL INFORMATION:  
; APPLICANT: HENRY, JAMES  
; APPLICANT: CAHILL, CATHERINE  
; APPLICANT: VASHEPL, KIRAN  
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND  
; FILE REFERENCE: 39245-173913  
; CURRENT APPLICATION NUMBER: US/09/930,503  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/226,086  
; PRIOR FILING DATE: 2000-08-18  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-930-503-12

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CGAATGATTAAGTC 222  
Db 16 CGAATGATTAAGTC 1

RESULT 1346  
US-09-774-381-11  
; Sequence 11, Application US/09774381  
; Publication No. US20030082677A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Pan, Yang  
; APPLICANT: Geating, David P.  
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES  
; FILE REFERENCE: MNI-107CP2  
; CURRENT APPLICATION NUMBER: US/09/774,381  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 08/941,354  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 09/010,674  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 60/061,149  
; PRIOR FILING DATE: 1997-10-06

```

; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-774-381-11

```

```

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1450 GCAGTGCAGCCCCCA 1465
Db      2 GCAGTGCAGCCCA 17

```

```

RESULT 1347
US-10-133-779-42/c
; Sequence 42, Application US/10133779
; Publication No. US20030165884A1
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonal, Richard
; APPLICANT: StemCyt, Inc.
; TITLE OF INVENTION: High Throughput Methods of HLA Typing
; FILE REFERENCE: 020035-000210US
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/10/133,779
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/172,768
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-779-42

```

```

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      438 GCGGAGGCTTCATG 453
Db      18 GCGGAGGCTTCATG 3

```

```

RESULT 1348
US-10-349-143-10970
; Sequence 10970, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CEP1
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10970
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-23427 for SEQ 3105, in compleme
US-10-349-143-10970

```

```

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1404 CTTGAGCTTCTCTCC 1419
Db      2 CTTGATCTTCTCTCC 17

```

```

RESULT 1349
US-10-138-674-3013/c
; Sequence 3013, Application US/10138674
; Publication No. US2004007565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3013

```

```

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      662 TCTGTGATCTGGAT 677
Db      18 TCTGTGATCTGAGT 3

```

```

RESULT 1350
US-10-287-949A-3013/c
; Sequence 3013, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.

```

```

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3013

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          662 TCTGTGTCATCTGGGT 677
Db          18 TCTGTGTCATCTGAGT 3

RESULT 1351
US-10-702-817-9
; Sequence 9, Application US/10702817
; Publication No. US20040147471A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1 EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10/702,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106,038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-9

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          105 CCTCTCTGTCGCTTT 120
Db          3 CCTCTCTCTGCTTT 18

RESULT 1352
US-10-509-009-22/c
; Sequence 22, Application US/10509009
; Publication No. US20050202430A1
; GENERAL INFORMATION:
; APPLICANT: Chiquet-Ehrismann, Ruth
; APPLICANT: Scherberich, Arnaud
; TITLE OF INVENTION: TENASCIN-W COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: 1/32411A/USN/FWI
; CURRENT APPLICATION NUMBER: US/10/509,009
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/BP03/03150
```

```

; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: GB0207224.7
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)...(18)
; OTHER INFORMATION: htnw6
US-10-509-009-22

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1276 ACCACCATCTCCACAG 1291
Db          16 ACCACCTCTCCACAG 1

RESULT 1353
US-10-951-303-3013/c
; Sequence 3013, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-951-303-3013

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          662 TCTGTGTCATCTGGGT 677
Db          18 TCTGTGTCATCTGAGT 3

RESULT 1354
US-10-750-185-14622
; Sequence 14622, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
```

APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT FILING DATE: 2003-12-31  
PRIORITY APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14622  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Forward Primer  
US-10-750-185-14622

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 720 CACAGAGACCATGCCAG 737  
|||||:|  
DB 1 CACAGAGCAGTGCACG 18

RESULT 1355  
US-10-750-623-14622  
Sequence 14622, Application US/10750623  
Publication No. US2005028753A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT FILING DATE: 2003-12-31  
PRIORITY APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14622  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Forward Primer  
US-10-750-623-14622

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 720 CACAGAGACCATGCCAG 737  
|||||:|  
DB 1 CACAGAGCAGTGCACG 18

RESULT 1356  
US-10-310-914A-72534  
Sequence 72534, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kvuza  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310,914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 72534  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-72534

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 151 CAGGACTGCTGCAG 166  
|||||:|  
DB 2 CAGGCCUCUGCUCAG 17

RESULT 1357  
US-10-310-914A-183276/C  
Sequence 183276, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kvuza  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 183276  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-183276

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 826 TTCCTCCCTGCTGG 841  
|||||:|  
DB 18 TTCCTCAGCTGCTGG 3

RESULT 1358  
US-10-310-914A-199415  
Sequence 199415, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Isaac  
APPLICANT: Shlier, Kvuza  
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
FILE REFERENCE: 06087.0200.CPUS01  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 199415  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-199415

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1263 CAGCCGCTGAGACC 1278  
Db 1 CAGCCGCTGAGACC 16

RESULT 1359  
US-10-310-914A-249340/c  
; Sequence 249340, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 249340  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-249340

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 687 CTTGCTGCTTCC 702  
Db 16 CTTGCTGCTTCC 1

RESULT 1360  
US-10-310-914A-417734  
; Sequence 417734, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 417734  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-417734

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 56.2%; Pred. No. 1e+03;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1008 CTTCTCTCTCTGCC 1023  
Db 1 CTTCTCTCTCTGCC 16

RESULT 1361  
US-10-310-914A-424159/c  
; Sequence 424159, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 424159  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-424159

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 424159  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-424159

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 817 CTGATCTACTTCTCC 832  
Db 17 CTGATCTACTTCTCC 2

RESULT 1362  
US-10-310-914A-436206/c  
; Sequence 436206, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 436206  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-436206

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 999 CTTCCACATCTTCTC 1014  
Db 17 CTTCCACATCTTCTC 2

RESULT 1363  
US-10-310-914A-436231/c  
; Sequence 436231, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 436231  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-436231

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY      999  CTTCCACATCTCTC 1014
           ||||| ||||| |||||
Db       18  CTTCCCATCTTCTC 3
           ||||| ||||| |||||

RESULT 1364
US-10-310-914A-441528/c
; Sequence 441528, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 441528
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-441528

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      895  CCGGCGACCTCCTCG 910
           ||||| ||||| |||||
Db       18  CCGGAGAGCTCCTCG 3
           ||||| ||||| |||||

RESULT 1365
US-10-310-914A-448431
; Sequence 448431, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 448431
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-448431

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      15  GCGGCGAGCGCGGCGAG 30
           ||||| ||||| |||||
Db       3   GCGGCGAGCGCGGCGG 18
           ||||| ||||| |||||

RESULT 1366
US-10-310-914A-572242/c
; Sequence 572242, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
```

```
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572242
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-572242

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      835  CTGCTGTGATTGGCT 850
           ||||| ||||| |||||
Db       18  CTGCTGTGTTTGGCT 3
           ||||| ||||| |||||

RESULT 1367
US-10-310-914A-581385
; Sequence 581385, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 581385
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-581385

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      727  ACCATGCCAGCAGAG 742
           ||||| ||||| |||||
Db       2   ACCAGGCCAGCAGAG 17
           ||||| ||||| |||||

RESULT 1368
US-10-310-914A-629984
; Sequence 629984, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 629984
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-629984

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1306 GAGGAGGAGCCAGAGC 1321
```





Db 3 CGCCGCTGCTTCGCC 18

RESULT 1374

```

US-10-310-914A-816050/c
: Sequence 816050, Application US/10310914A
: Publication No. US20060000322A1
: GENERAL INFORMATION:
: APPLICANT: Benrwich, Isaac
: APPLICANT: Shlier, Krystal
: TITLE OF INVENTION: Bioinformatically de-
: TITLE OF INVENTION: uses thereof
: FILE REFERENCE: 06087.0200 .CPUS01
: CURRENT APPLICATION NUMBER: US/10/310,914A
: CURRENT FILING DATE: 2002-12-06
: NUMBER OF SEQ ID NOS: 1388402
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 816050
: LENGTH: 18
: TYPE: RNA
: ORGANISM: Human
US-10-310-914A-816050

```

Query Match	0.8%;	Score 14.4;	DB 1;	length 18;
Best Local Similarity	93.8%;	Pred. No. 1e+03;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	667	GTCATCTGGGTCCTGG	682
Db	17	GTCATTGGGTCCTGG	2

RESULT 1375

```

US-10-310-914A-816837
/ Sequence 816837, Application US/10310914A
/ Publication NO. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Krzyzaczek
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087.0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 138402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 816837
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-816837

```

Query Match	0.8%;	Score 14.4;	DB 1;	Length 18;
Best Local Similarity	75.0%;	Pred. No. 1e+03;		
Matches 12;	Conservative	3;	Mismatches 1;	Indels 0;
				Gaps 0

```
QY      687  CCTGCTGACCTTCCCC  702
          ||::|||::|||
Db      1  CUGGCUAGGCTUGCCCC  16
```

**RESULT 1376**

```

US-10-310-914A-824133/c
; Sequence 824133, Application US/10310914A
; Publication NO. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06

```

```

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 824133
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-824133

```

Query Match	0.8%;	Score 14.4;	DB 1;	Length 18;
Best Local Similarity	93.8%;	Pred. No. 1e+03;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1283	TCTCCACAGTGGTGGC	1298
Db	16	TCTCCAGACTGGTGGC	1

RESULT 1377

```

US-10-310-914A-82413/C
/ Sequence 824134, Application US/10310914A
/ Publication No. US2006000322A1
/ GENERAL INFORMATION:
/ APPLICANT: Benrich, Isaac
/ APPLICANT: Shlier, Krusz
/ TITLE OF INVENTION: Bioinformatically deter
/ TITLE OF INVENTION: uses thereof
/ FILE REFERENCE: 06087.0200 .CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310, 914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 824134
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
/ US-10-310-914A-824134

```

Query Match	0.8%;	Score 14.4;	DB 1;	Length 18;
Best Local Similarity	93.8%;	Pred. No. 1e+03;		
Matches 15;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0.

QY	1283	TCTCCACAGTGTGG	1298
Db	16	TCTCCAGAGTGTGG	1

## RESULT 1378

```

US-10-310-914A-872243
/ Sequence 872243, Application US/10310914A
/ Publication No. US2006000322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kiyazaki
/ TITLE OF INVENTION: Bioinformatically detected
/ TITLE OF INVENTION: Bioinformatically detected
/ FILE REFERENCE: 06087, 0200, CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310, 914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 872243
/ LENGTH: 18
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-872243

```

Query Match	0.8%;	Score 14.4;	DB 1;	length 18;
Best Local Similarity	81.2%;	Pred. No. 1e+03;		
Matches 13; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0

QY 287 TGCACCGCCTGGCA 302  
: ||| ||||| : |||  
Db 3 UGCACCGCAGCCUGCA 18

```
RESULT 1379
US-10-310-914A-879849/c
; Sequence 879849, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 879849
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-879849

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1421 ATGTCCTCTCTCAGGC 1436
DB 17 ATGTCCTCTCTCAGGC 2

RESULT 1380
US-10-310-914A-902588/c
; Sequence 902588, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 902588
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-902588

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1148 GTCGCGCTTCAACA 1163
DB 16 GTTGGGCTTCAACA 1

RESULT 1381
US-10-310-914A-915824/c
; Sequence 915824, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 915824
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-915824

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1710 AATGATTCATTCT 1725
DB 17 AAGCATTCATTCT 2

RESULT 1382
US-10-310-914A-951224
; Sequence 951224, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 951224
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-951224

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1430 CCTAGCCACAGGCC 1445
DB 2 CCAAGCCACAGGCC 17

RESULT 1383
US-10-310-914A-969334/c
; Sequence 969334, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969334
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969334

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCAGCCCGGC 634
DB 17 CCTCTCAGCCCGGC 2
```

```

RESULT 1384
US-10-310-914A-1095570
Sequence 1095570, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1095570
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1095570

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 62.5%; Pred.No.1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      676 GTCCGTGCTCCTCGC 691
DB      1 GUCCTGCCTCCUCCUGC 16
|||:|||:|||:|||

RESULT 1385
US-10-310-914A-1127203/c
Sequence 1127203, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1127203
LENGTH: 18
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1127203

Query Match          0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred.No.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      990 CTGGCTGCCCTTCCAC 1005
DB      17 CTGGCTGCCCTCCACC 2
|||||
CTGGCTGCCCTCCACC 2

RESULT 1386
US-10-310-914A-1197826/c
Sequence 1197826, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: PatentIn version 3.3

```

```

; SEQ ID NO 1197826
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1197826

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 CCATGCCACGACGACT 743
Db 16 CCATGCCACGACGACT 1

RESULT 1387
US-10-310-914A-1202881/c
; Sequence 1202881, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1202881
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1202881

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1306 GAGGAGAGCCGACGAG 1321
Db 18 GAGGAGAGCCGACGAG 3

RESULT 1388
US-10-310-914A-1218505
; Sequence 1218505, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kivuzat
; TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1218505
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1218505

Query Match
Best Local Similarity 81.2%; Score 14.4; DB 1; Length 18;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1455 TGCAGCCCCCAGCTGCC 1470
Db 3 UCCAGCCCCCAGCTGCC 18

```

```
RESULT 1389
US-10-310-914A-123356
; Sequence 123356, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123356
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-123356

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 GAGCCCGAGGCCGAC 147
Db 2 GAGCCCGAGGCCGAC 17

RESULT 1390
US-10-310-914A-124978
; Sequence 124978, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124978
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-124978

Query Match
Best Local Similarity 87.5%; Score 14.4; DB 1; Length 18;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 628 CCCCGCTGTGAGCCA 643
Db 1 CCCCGCTGTGAGCCA 16

RESULT 1391
US-10-310-914A-1252017/c
; Sequence 1252017, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1252017

; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1252017

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1266 CCGCTGAGAGCACAC 1281
Db 18 CCGCTGAGAGCACAC 3

RESULT 1392
US-10-310-914A-1376270
; Sequence 1376270, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1376270
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1376270

Query Match
Best Local Similarity 87.5%; Score 14.4; DB 1; Length 18;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCAGCCCGGC 634
Db 1 CCCCTCAGCCCGGC 16

RESULT 1393
US-11-090-617-509
; Sequence 509, Application US/11090617
; Publication No. US20060024692A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Daigo, Yataro
; TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
; FILE REFERENCE: 082368-003500US
; CURRENT FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP04/04075
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/JP03/12072
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US 60/555,757
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/466,100
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/451,374
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,673
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 706
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 509
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
```

```
FEATURE:
; OTHER INFORMATION: Artificially synthesized S-oligonucleotide sequence for antisense
; OTHER INFORMATION: method
US-11-090-617-509
Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1277 CCACCATCTCCACAGT 1292
Db      3 CCGCCATCTCCACAGT 18

RESULT 1394
US-09-847-601B-5
; Sequence 5, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847.601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-5
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      689 TGCTGGCCTTCCCC 702
Db      1 UGCTUGGCTTCCCC 14

RESULT 1395
US-09-930-503-15/c
; Sequence 15, Application US/09930503
; Publication No. US20030060438A1
; GENERAL INFORMATION:
; APPLICANT: HENRY, JAMES
; APPLICANT: CAHILL, CATHERINE
; APPLICANT: YASHPAL, KIRAN
; TITLE OF INVENTION: APPLICATION OF ANTI-SENSE OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 39245-173913
; CURRENT APPLICATION NUMBER: US/09/930,503
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,086
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-930-503-15
Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      209 AATGATTAACGTC 222
Db      14 AATGATTAACGTC 1

RESULT 1396
US-09-866-108-6965
; Sequence 6965, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 6965
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6965
Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 CAGTCATCCAGAA 41
         |||||
```

```
Db      4 CAGTCATCCAGAA 17

RESULT 1397
US-09-866-108-6969
; Sequence 6969, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ASCOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6969
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6969

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      29 AGTCATCCAGAG 42
Db      1 AGTCATCCAGAG 14

RESULT 1398
US-09-930-423-1550/c
; Sequence 1550, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry

US-09-930-423-1550
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00-918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1550
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1550

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1277 CCACCATCTCCACA 1290
Db      16 CCACCATCTCCACA 3

RESULT 1399
US-09-780-164-867
; Sequence 867, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 867
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-867

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      803 TCTGTGTGACTGTG 816
Db      1 UCUGUGACUGUG 14

RESULT 1400
US-09-745-237A-1550/c
; Sequence 1550, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1550
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1550
```

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1277 CCACCATCTCCACA 1290  
DB 16 CCACCATCTCCACA 3

RESULT 1401  
US-10-339-782-265  
; Sequence 265, Application US/10339782  
; Publication No. US20030166026A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Goodman, Laurie J.  
; APPLICANT: Bowen, Benjamin A.  
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells  
; FILE REFERENCE: 37-000110US  
; CURRENT APPLICATION NUMBER: US/10/339,782  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 265  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-782-265

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 ATCCCTCCAGCCC 630  
DB 2 ATCCCTCCAGCCC 15

RESULT 1402  
US-10-712-672-343  
; Sequence 343, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH800-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 343  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-712-672-343

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 64.3%; Pred. No. 1e+03;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1689 CCAGCTTTCTCTCA 1702  
DB 2 CCAGCTTTCTCTCA 15

RESULT 1403  
US-10-712-672-344  
; Sequence 344, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH800-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 344  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-712-672-344

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 64.3%; Pred. No. 1e+03;  
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1689 CCAGCTTTCTCTCA 1702  
DB 1 CCAGCTTTCTCTCA 14

RESULT 1404  
US-10-723-361-6965  
; Sequence 6965, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30



Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; SEQ ID NO: 6965  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-723-361-6965

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 CAGTCATCCAGAA 41  
DB 4 CAGTCATCCAGAA 17

RESULT 1405

US-10-723-361-6969  
; Sequence 6969, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:

;; APPLICANT: JI, Yizhong  
;; APPLICANT: PENN, Sharon G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wenheng  
;; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MROSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: P0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO: 6969  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-6969

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 AGTCATCCAGAG 42  
DB 1 AGTCATCCAGAG 14

RESULT 1406

US-11-090-866-22

;; Sequence 22, Application US/11090866  
;; Publication No. US20050164294A1  
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, John P.  
;; APPLICANT: Basi, Guripal  
;; APPLICANT: Doane, Minh Tam  
;; APPLICANT: Frigon, Normand  
;; APPLICANT: John, Varghese  
;; APPLICANT: Power, Michael  
;; APPLICANT: Sinha, Sukanto  
;; APPLICANT: Tatsuno, Gwen  
;; APPLICANT: Tung, Jay  
;; APPLICANT: Wang, Shuwen  
;; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; FILE REFERENCE: 228-US-NEW2C12  
; CURRENT APPLICATION NUMBER: US/11/090,866  
; CURRENT FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 09/723,722  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/501,708  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: US 09/471,669  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: 60/119,571  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/139,172  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 22  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(17)  
;; OTHER INFORMATION: n = A,T,C or G  
US-11-090-866-22

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1306 GAGGAGGCCAGAGA 1322  
DB 1 GAGGAGGCCAGAGA 17

RESULT 1407

US-11-089-918-22  
; Sequence 22, Application US/11089918  
; Publication No. US20050164327A1  
; GENERAL INFORMATION:

;; APPLICANT: Anderson, John P.  
;; APPLICANT: Basi, Guripal  
;; APPLICANT: Doane, Minh Tam  
;; APPLICANT: Frigon, Normand  
;; APPLICANT: John, Varghese  
;; APPLICANT: Power, Michael  
;; APPLICANT: Sinha, Sukanto  
;; APPLICANT: Tatsuno, Gwen  
;; APPLICANT: Tung, Jay  
;; APPLICANT: Wang, Shuwen  
;; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; FILE REFERENCE: 228-US-NEW2C9  
; CURRENT APPLICATION NUMBER: US/11/089,918

```
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-089-918-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1408
US-11-069-377-22
; Sequence 22, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEM2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-090-872-22
```

```
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-069-377-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1409
US-11-090-872-22
; Sequence 22, Application US/11090872
; Publication No. US2005017888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEM2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-11-090-872-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1306 GAGGAGAGCCGAGGA 1322
DB      1 GAYGARAGCCGAGGA 17
      |||:|||||
RESULT 1410
US-11-090-399-22
; Sequence 22, Application US/11090399
; Publication No. US20050196839A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
```

```

; APPLICANT: Baqi, Guiribai
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varheese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C10
; CURRENT APPLICATION NUMBER: US/11/090,399
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate oligonucleotide primer
; NAME/KEY: misc feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
; US-11-090-399-22

Query Match          0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy      1306 GAGAGAGCGCAGCA 1322
Db      1 GAYGARGAGCCGAGGA 17

RESULT 1411
US-09-866-108-2756
; Sequence 2756, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2756
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-2756

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      1196 GCGACTATGAGGGCTG 1212
Db      1 GCGAGTATGAGAGCTG 17

RESULT 1412
US-09-866-108-7674/c
; Sequence 7674, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
```

PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
NUMBER OF SEQ ID NOS: 15752  
SOFTWARE: Aeonica Sequence Listing Engine  
SEQ ID NO 7674  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTCGAGCTTCTCCCA 1420  
DB 17 CTCGCTTCTTCTCA 1

RESULT 1413  
US-09-864-785-336  
Sequence 336, Application US/09864785  
Patent No. US20020177568A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Slinchemb, Dan  
APPLICANT: Draper, Ken  
APPLICANT: McSwigen, Jim  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
FILE REFERENCE: 400/022 (MHB00-812-D)  
CURRENT APPLICATION NUMBER: US/09/864,785  
CURRENT FILING DATE: 2001-05-23  
NUMBER OF SEQ ID NOS: 3929  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 336  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-336

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 CCCGAGCGCCGAC 151  
DB 1 CCCGAGCGCCGAC 17

RESULT 1414  
US-09-961-077-765/C  
Sequence 765, Application US/09961077  
Publication No. US20030014775A1  
GENERAL INFORMATION:  
APPLICANT: Zwick, Michael G.  
Edington, Brent E.  
McSwigen, James A.  
Merlo, Patricia Ann Owens  
Guo, Lining  
Skokut, Thomas A.  
Young, Scott A.

Folkerts, Otto  
Merlo, Donald J.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
MODULATION OF GENE EXPRESSION  
IN PLANTS  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/961,077  
FILING DATE: 21-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,645  
FILING DATE: July 12, 1996  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 765:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 765:  
US-09-961-077-765

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 GTCAGCCAGCGACCA 652  
DB 17 GTCAGCCAGCGACCA 1

RESULT 1415  
US-09-780-533A-1580  
Sequence 1580, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Chowrira, Bharat  
APPLICANT: Haeblerli, Peter  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MHB00,878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1580  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-1580

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 1.1e+03;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 545 CCATCGCCGCTGTCTTC 561  
DB 1 CCAUCCCGGCGUCUGC 17

RESULT 1416  
US-09-780-533A-2357/c  
Sequence 2357, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Chowitra, Bharat  
APPLICANT: Haeblerli, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH00, 878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780, 533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181, 797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2357  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-2357

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1003 CACATCTTCTTCTCTCT 1019  
DB 17 CTCCTCTTCTTCTCTCT 1

RESULT 1417  
US-09-780-533A-2363  
Sequence 2363, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Chowitra, Bharat  
APPLICANT: Haeblerli, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
FILE REFERENCE: MBH00, 878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780, 533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181, 797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2363  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-2363

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 GAGGAGGAGCAGAGCA 1322  
DB 1 GAGGAGGAGGAGAGCA 17

RESULT 1418  
US-09-877-478-2345  
Sequence 2345, Application US/09877478  
Publication No. US20030068301A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Draper, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Morrissey, Dave  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: MBH00-845-H (400/029)  
CURRENT APPLICATION NUMBER: US/09/877, 478  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US 07/882, 712  
PRIOR FILING DATE: 1992-05-14  
PRIOR APPLICATION NUMBER: US 09/531, 025  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: US 09/636, 385  
PRIOR FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: US 09/636, 347  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 08/193, 627  
PRIOR FILING DATE: 1994-02-07  
PRIOR APPLICATION NUMBER: US 08/433, 993  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 08/434, 504  
PRIOR FILING DATE: 1995-05-04  
PRIOR APPLICATION NUMBER: US 09/436, 430  
PRIOR FILING DATE: 1999-11-08  
NUMBER OF SEQ ID NOS: 6586  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2345  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Hepatitis B virus  
US-09-877-478-2345

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1.1e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1265 GCGCGCTGAGAGCACC 1281  
DB 1 GUGCAUGAGAGACACC 17

RESULT 1419  
US-09-877-478-2346  
Sequence 2346, Application US/09877478  
Publication No. US20030068301A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Draper, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwigen, Jim  
APPLICANT: Morrissey, Dave  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: MBH00-845-H (400/029)  
CURRENT APPLICATION NUMBER: US/09/877, 478  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: US 07/882, 712  
PRIOR FILING DATE: 1992-05-14

```
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2346
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
; US-09-877-478-2346
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1267 CGCCTGGAGACCAACCAT 1283
Db 1 CGCAUGGAGACCAACCGU 17
```

```
RESULT 1420
US-09-848-754A-243/c
; Sequence 243, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 243
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-243
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1313 AGCCAGAGACGCGCCC 1329
Db 17 AGCAAGAGAGCGGCC 1
```

```
RESULT 1421
US-09-848-754A-891/c
; Sequence 891, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 891
```

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-891
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1695 TTTCCTCAAGAGCCCAA 1711
Db 17 TTTCCTCAAGAGCCCA 1
```

```
RESULT 1422
US-09-848-754A-990/c
; Sequence 990, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 990
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-990
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 310 CTTTGGGAGCTGCTTA 326
Db 17 CTTTGGGAGCTGCCA 1
```

```
RESULT 1423
US-09-848-754A-1483/c
; Sequence 1483, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1483
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-848-754A-1483
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1224 CACCCGATATCCAGA 1240
Db 17 CACCCGATGCTCCAGA 1
```

```
RESULT 1424
US-09-848-754A-1525/c
; Sequence 1525, Application US/09848754A
```

```
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: Leleis of Epidermal Growth Factor Receptors
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1525

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1646 CAATCTGACTGCTTG 1662
DB      17 CAACTCAGGAACTTGG 1

RESULT 1425
US-09-776-474-250/C
; Sequence 250, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Faltacy, Ali
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-776-474-250

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1369 TCTTACGAAAGTGC 1385
DB      17 TCTTACGAAAGTGC 1

RESULT 1426
US-09-930-423-839
; Sequence 839, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00-918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
```

```
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 839
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-930-423-839

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1346 CCTGACCTGACCTCC 1362
DB      1 CCTGACACACACCUC 17

RESULT 1427
US-09-827-395A-381
; Sequence 381, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwigen
; APPLICANT: Bharat Chowitra
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Ge
; FILE REFERENCE: MHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-381

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1084 TGGCTGGCATGAGTC 1100
DB      1 UGGGUGGCGGACCC 17

RESULT 1428
US-09-740-332-964/C
; Sequence 964, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 964
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
```

US-09-740-332-964

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 GTACAAAGTCAGCGCC 1270  
DB 17 GTACAAAGTCAGCGCC 1

RESULT 1429

US-09-745-237A-839  
; Sequence 839, Application US/09745237A  
; Publication No. US20030143708A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blact, Larry  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: 400/007 (MBH00-918-A)  
; CURRENT APPLICATION NUMBER: US/09/745,237A  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 4550  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 839  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-745-237A-839

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 1.1e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1346 CCCGAGCTGAGCTCC 1362  
DB 1 CCCGAGCTGAGCTCC 17

RESULT 1430

US-09-817-879-964/c  
; Sequence 964, Application US/09817879  
; Publication No. US2003017311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 964  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-964

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 GTACAAAGTCAGCGCC 1270  
DB 17 GTACAAAGTCAGCGCC 1

RESULT 1431

US-10-060-756A-4268/c  
; Sequence 4268, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO: 4268  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-4268

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1089 GGCCATGAGCTCCACCA 1105  
DB 17 GGCCATGAGCTCCACCA 1

RESULT 1432  
US-10-156-306-6951/c  
; Sequence 6951, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwigen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 6951  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-6951

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1402 AGCTTACGCTTCTCTC 1418  
DB 17 AGCTTACGCTTCTCTC 1

RESULT 1433  
US-10-061-201-1453/c



```
; Sequence 1453, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1453
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1453

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1444 CCTTGGCAGGTGCAGC 1460
Db      17 CCTTTGCAGGTCCAGC 1

RESULT 1434
US-10-430-882-381
; Sequence 381, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chewlra
; APPLICANT: Peter Haebelri
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 381
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-381

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1084 TGCGTGGCCATGAGCTC 1100
Db      1 UGCGUGCGCCGUGACCTC 17

RESULT 1435
US-10-297-068-1039
; Sequence 1039, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1039
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture
US-10-297-068-1039

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1299 GCGCCACGAGGAGGAGC 1315
Db      1 GCGCCATGAGGCGGAGC 17

RESULT 1436
US-10-342-902-2345
; Sequence 2345, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Stima Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
```

PRIOR APPLICATION NUMBER: US 07/882,712  
 PRIOR FILING DATE: 1992-05-14  
 PRIOR APPLICATION NUMBER: US 03/436,430  
 PRIOR FILING DATE: 1999-11-08  
 NUMBER OF SEQ ID NOS: 6592  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 2345  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Hepatitis B virus  
 US-10-342-902-2345

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1265 GCGCGCTGGAGACCAACC 1281  
 Db 1 GCGCAUGGAGACCAACC 17

RESULT 1437  
 US-10-342-902-2346  
 Sequence 2346, Application US/10342302  
 Publication No. US20040054156A1  
 GENERAL INFORMATION:  
 APPLICANT: Sima Therapeutics, Inc.  
 APPLICANT: Draper, Kenneth  
 APPLICANT: Blatt, Larry  
 APPLICANT: McSwiggen, Jim  
 APPLICANT: Morrissey, Dave  
 TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
 FILE REFERENCE: 400/075 (MHB00-845-1)  
 CURRENT APPLICATION NUMBER: US/10/342,902  
 PRIOR FILING DATE: 2003-01-15  
 PRIOR APPLICATION NUMBER: US 09/877,478  
 PRIOR FILING DATE: 2001-06-08  
 PRIOR APPLICATION NUMBER: US 09/531,025  
 PRIOR FILING DATE: 2000-03-20  
 PRIOR APPLICATION NUMBER: US 09/636,385  
 PRIOR FILING DATE: 2000-08-09  
 PRIOR APPLICATION NUMBER: US 09/696,347  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 08/193,627  
 PRIOR FILING DATE: 1994-02-07  
 PRIOR APPLICATION NUMBER: US 07/882,712  
 PRIOR FILING DATE: 1992-05-14  
 PRIOR APPLICATION NUMBER: US 09/436,430  
 PRIOR FILING DATE: 1999-11-08  
 NUMBER OF SEQ ID NOS: 6592  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 2346  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Hepatitis B virus  
 US-10-342-902-2346

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 76.5%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1267 GCGCTGGAGACCAACC 1283  
 Db 1 GCGCAUGGAGACCAACC 17

RESULT 1438  
 US-10-138-674-1714/c  
 Sequence 1714, Application US/10138674  
 Publication No. US20040077565A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 FILE REFERENCE: MHB00-876-N (400/049)  
 CURRENT APPLICATION NUMBER: US/10/138,674  
 CURRENT FILING DATE: 2002-05-03  
 NUMBER OF SEQ ID NOS: 20822  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1714  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-10-138-674-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCAAGAGACCA 730  
 Db 17 CACACCAAGAGACCA 1

RESULT 1439  
 US-10-138-674-1886/c  
 Sequence 1886, Application US/10138674  
 Publication No. US20040077565A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 APPLICANT: McSwiggen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 FILE REFERENCE: MHB00-876-N (400/049)  
 CURRENT APPLICATION NUMBER: US/10/138,674  
 CURRENT FILING DATE: 2002-05-03  
 NUMBER OF SEQ ID NOS: 20822  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 1886  
 LENGTH: 17  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-10-138-674-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGACCAATCA 1521  
 Db 17 TTCATCTGGATCATGA 1

RESULT 1440  
 US-10-138-674-6345/c  
 Sequence 6345, Application US/10138674  
 Publication No. US20040077565A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 APPLICANT: Pavco, Pam  
 APPLICANT: McSwiggen, Jim  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Escobedo, Jaime  
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 FILE REFERENCE: MHB00-876-N (400/049)  
 CURRENT APPLICATION NUMBER: US/10/138,674  
 CURRENT FILING DATE: 2002-05-03  
 NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-138-674-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 ACTCAACCAAGAGACC 729

Db 17 ACACACCAAGAGAGACC 1

RESULT 1441

US-10-287-949A-1714/c

Sequence 1714, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1714

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-287-949A-1714

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCAAGAGAGCCA 730

Db 17 CACAACCAAGAGAGCCA 1

RESULT 1442

US-10-287-949A-1886/c

Sequence 1886, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1886

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-287-949A-1886

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCAAGAGAGCCA 730

Db 17 CACAACCAAGAGAGCCA 1

RESULT 1443

US-10-287-949A-6345/c

Sequence 6345, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-287-949A-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1690 CAGCTTCTCTCAAGAG 1706

Db 1 CAGCTTCTCTCAAGAG 17

RESULT 1444

US-10-712-672-345

Sequence 345, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowitra, Bharat

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/10/712,672

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US/09/653,225

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/197,769

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: PatentIn version 3.0

SEQ ID NO 345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-712-672-345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 1.1e+03;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1690 CAGCTTCTCTCAAGAG 1706

Db 1 CAGCTTCTCTCAAGAG 17

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTTCATCTGAACATCA 1521

Db 17 TTTCATCTGAATTCATGA 1

RESULT 1443

US-10-287-949A-6345/c

Sequence 6345, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-287-949A-6345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 ACTCAACCAAGAGACC 729

Db 17 ACACACCAAGAGAGACC 1

RESULT 1444

US-10-712-672-345

Sequence 345, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowitra, Bharat

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/10/712,672

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US/09/653,225

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/197,769

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: PatentIn version 3.0

SEQ ID NO 345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-712-672-345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 ACTCAACCAAGAGACC 729

Db 17 ACACACCAAGAGAGACC 1

RESULT 1445

US-10-712-672-345

Sequence 345, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Chowitra, Bharat

APPLICANT: McSwigen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/10/712,672

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US/09/653,225

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/197,769

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: PatentIn version 3.0

SEQ ID NO 345

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-712-672-345

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 1.1e+03;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1690 CAGCTTCTCTCAAGAG 1706

Db 1 CAGCTTCTCTCAAGAG 17

```
RESULT 1445
US-10-712-672-506/c
; Sequence 506, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 506
; SOFTWARE: PatentIn version 3.0
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-506

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1450 GCAGGTGCAGCCCCCACC 1466
Db      17 GCAGCAGCAGCCCCCACC 1

RESULT 1446
US-10-712-672-763
; Sequence 763, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 763
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-763

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1294 GTGGGGGCCCAAGAGGA 1310
Db      1 GTGGGGGCCCAAGAGGA 17
```

```
RESULT 1447
US-10-712-672-764
; Sequence 764, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 764
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-764

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1295 TTGGGGGCCCAAGAGAG 1311
Db      1 TTGGGGGCCCAAGAGAG 17

RESULT 1448
US-10-712-672-765
; Sequence 765, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-765

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1296 GGGGGGCCCAAGAGAG 1312
Db      1 GGGGGGCCCAAGAGAG 17
```

```
RESULT 1449
US-10-712-672-766
; Sequence 766, Application US/10712672
; Publication No. US20040102413a1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowitra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT FILING DATE: US/10/712,672
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-766

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1297 GGGGCCCGAGGAGGA 1313
Db      1 GCGGCCCGCGAGGAGA 17

RESULT 1450
US-10-669-841-2148
; Sequence 2148, Application US/10669841
; Publication No. US20040127446a1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
```

```
;; PRIOR APPLICATION NUMBER: US 09/504,321
;; PRIOR FILING DATE: 2000-02-15
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 16207
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2148
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Hepatitis B Virus
US-10-669-841-2148

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1265 GCGCCCTGAGACCAAC 1281
Db      1 GCGCAUGAGACCAACC 17

RESULT 1451
US-10-669-841-2149
; Sequence 2149, Application US/10669841
; Publication No. US20040127446a1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2149
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-2149

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1267 GCGCTGAGACCAACAT 1283
```

```
Db      1  CGCAGGAGGACCCGU 17
|||||:|||||:|||||:
RESULT 1452
US-10-669-841-3557/c
; Sequence 3557, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sima Therapeutics, Inc.
; APPLICANT: Lawrence, Blac
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggan
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3557
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-3557
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1254  GTTCAAGTCAGCGGCC 1270
          |||||:|||||:|||||:
Db      17  GTTCAAGTCAGCGGCC 1
          |||||:|||||:|||||:
RESULT 1453
US-10-723-361-2756
; Sequence 2756, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```

```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2756
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2756
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1196  GCGACTATGAGGGGCTG 1212
          |||||:|||||:|||||:
Db      1  GCGACTATGAGGGGCTG 17
          |||||:|||||:|||||:
RESULT 1454
US-10-723-361-7674/c
; Sequence 7674, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
```

;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; SEQ ID NO: 7674  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-723-361-7674

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1404 CTCAGCTCTCTCCCA 1420  
Db 17 CTCGCTCTCTCTCCA 1

RESULT 1455  
US-10-498-462-376  
; Sequence 376, Application US/10498462  
; Publication No. US20040259175A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Jinjiao  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1  
; FILE REFERENCE: PB01102  
; CURRENT APPLICATION NUMBER: US/10/498,462  
; CURRENT FILING DATE: 2004-06-10  
; PRIOR APPLICATION NUMBER: US 60/339,764  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: PCT/US02/37506  
; PRIOR FILING DATE: 2002-11-22  
; NUMBER OF SEQ ID NOS: 3320  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO: 376  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-498-462-376

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 786 TGAGAAAGTGTACCA 802  
Db 1 TGAGAAAGTGTACCA 17

RESULT 1456  
US-10-498-462-1855  
; Sequence 1855, Application US/10498462  
; Publication No. US20040259175A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Jinjiao  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1  
; FILE REFERENCE: PB01102  
; CURRENT APPLICATION NUMBER: US/10/498,462  
; CURRENT FILING DATE: 2004-06-10  
; PRIOR APPLICATION NUMBER: US 60/339,764  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: PCT/US02/37506

;; PRIOR FILING DATE: 2002-11-22  
;; NUMBER OF SEQ ID NOS: 3320  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; SEQ ID NO: 1855  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-498-462-1855

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 987 CTCGCTGCTGCTCTCC 1003  
Db 1 CTCGCTGCTGCTCTCC 17

RESULT 1457  
US-10-498-462-2044/c  
; Sequence 2044, Application US/10498462  
; Publication No. US20040259175A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Jinjiao  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1  
; FILE REFERENCE: PB01102  
; CURRENT APPLICATION NUMBER: US/10/498,462  
; CURRENT FILING DATE: 2004-06-10  
; PRIOR APPLICATION NUMBER: US 60/339,764  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: PCT/US02/37506  
; PRIOR FILING DATE: 2002-11-22  
; NUMBER OF SEQ ID NOS: 3320  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO: 2044  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-498-462-2044

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 255 CTCCTACTAACAACCTCGG 271  
Db 17 CTCCTACTAACAACCG 1

RESULT 1458  
US-10-890-776A-4268/c  
; Sequence 4268, Application US/10890776A  
; Publication No. US20050129683A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB01177  
; CURRENT APPLICATION NUMBER: US/10/890,776A  
; CURRENT FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: US 10/060,756  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669

```

; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4268
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776a-4268

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1089 GGCCTAGAGCTCCACCA 1105
DB      17  GGCCTAGAGCTCCACCA 1

RESULT 1459
US-10-951-303-1714/c
; Sequence 1714, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1714
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1714

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      714  CTCACCAAGAGACCA 730
DB      17  CACACCAAGAGACCA 1

RESULT 1460
US-10-951-303-1886/c
; Sequence 1886, Application US/10951303
; Publication No. US20050227937A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Escobedo, Jaime
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1886
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1505 TTCATCTGGAACCATCA 1521
DB      17  TTCATCTGGAACCATCA 1

RESULT 1461
US-10-492-570-396
; Sequence 396, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 396
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-492-570-396

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1336 CTGGACTTGCAAAAG 1552
DB      1  CTGGACTTGCAAAAG 17

RESULT 1462
US-10-492-570-397
; Sequence 397, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 397
; LENGTH: 17
```

```

; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/10/951,303
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/685,664
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1886
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-951-303-1886

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1505 TTCATCTGGAACCATCA 1521
DB      17  TTCATCTGGAACCATCA 1

RESULT 1461
US-10-492-570-396
; Sequence 396, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 396
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-492-570-396

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1336 CTGGACTTGCAAAAG 1552
DB      1  CTGGACTTGCAAAAG 17

RESULT 1462
US-10-492-570-397
; Sequence 397, Application US/10492570
; Publication No. US20060057666A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: PB0180
; CURRENT APPLICATION NUMBER: US/10/492,570
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US 60/329,000
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 397
; LENGTH: 17
```



TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-492-570-397

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 TGGGACTTGC AAAAGG 1553  
Db 1 TGGGACTGCGAAATAGG 17

RESULT 1463  
US-10-492-570-1002  
Sequence 1002, Application US/10492570  
Publication No. US20060057666A1  
GENERAL INFORMATION:  
APPLICANT: Zhang, Jian  
TITLE OF INVENTION: A HUMAN G PROTEIN COUPLED RECEPTOR  
FILE REFERENCE: PRO180  
CURRENT APPLICATION NUMBER: US/10/492,570  
CURRENT FILING DATE: 2004-04-12  
PRIOR APPLICATION NUMBER: US 60/329,000  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 1926  
SOFTWARE: Aeomica Sequence Listing Engine  
SEQ ID NO 1002  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-492-570-1002

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 455 CTGCATCATCACTG 471  
Db 1 CTGCATCATCACTG 17

RESULT 1464  
US-11-189-546-9/C  
Sequence 9, Application US/11189546  
Publication No. US20060057613A1  
GENERAL INFORMATION:  
APPLICANT: Nanosphere, Inc  
APPLICANT: Ramakrishnan, Ramesh  
APPLICANT: Riccielli, Peter V  
TITLE OF INVENTION: Method For Distinguishing Methicillin Resistant S. Aureus From  
FILE REFERENCE: 04-437-A  
CURRENT APPLICATION NUMBER: US/11/189,546  
CURRENT FILING DATE: 2005-07-26  
PRIOR APPLICATION NUMBER: 60/591,127  
PRIOR FILING DATE: 2004-07-26  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 9  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic sequence that is a capture probe for the MRSA gene.  
US-11-189-546-9

Db 17 AACCGCATCATCACTG 1

Search completed: June 12, 2006, 06:22:21  
Job time : 36 secs

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1111 AACCGCATCATCACTG 1127  
|||||

**THIS PAGE BLANK (SPM)**

**THIS PAGE BLANK (SPM)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:18:10 ; Search time 0.001 Seconds

(without alignments)  
533.332 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766  
Sequence: 1 aattcagagccaccgcgggc.....cgagtgctcattccagatg 1766

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 11 segs, 151 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 8  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 11 summaries

Database : us-09-930-503a-6.sl.rnpbns4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	0.9	19	US-10-533-300-10	Sequence 10, Appl
2	15.8	0.9	19	US-10-533-300-12	Sequence 12, Appl
3	12.4	0.7	14	US-11-303-896-1	Sequence 1, Appl
4	12.4	0.7	14	US-11-305-629-2	Sequence 2, Appl
5	12.4	0.7	15	US-10-559-415-172	Sequence 172, Appl
6	12	0.6	12	US-11-113-534-39	Sequence 39, Appl
7	11	0.6	11	US-11-158-209-139	Sequence 139, Appl
8	11	0.6	11	US-11-158-209-234	Sequence 234, Appl
9	11	0.6	11	US-11-158-209-936	Sequence 936, Appl
10	11	0.6	12	US-11-113-534-33	Sequence 33, Appl
11	11	0.6	13	US-11-238-162-28	Sequence 28, Appl

## ALIGNMENTS

RESULT 1  
US-10-533-300-10/c  
Sequence 10, Application US/10533300  
Publication No. US20060100145A1  
GENERAL INFORMATION:  
APPLICANT: Meder, Wolfgang  
APPLICANT: Wendland, Martin  
APPLICANT: John, Harald  
APPLICANT: Richter, Rudolf  
APPLICANT: Meyer, Markus  
APPLICANT: Forssmann, Wolf-Georg  
TITLE OF INVENTION: Human Chondrosteomodulin (TIG2), Production, and Use for the  
Treatment or Diagnosis of Bone Diseases, Cartilage Diseases,  
TITLE OF INVENTION: Obesity, Inflammatory Diseases, and Skin Diseases  
FILE REFERENCE: 2388.0010000/SRL/BL5  
CURRENT APPLICATION NUMBER: US/10/533.300  
CURRENT FILING DATE: 2005-04-29

PRIOR APPLICATION NUMBER: PCT/EP03/11799  
PRIOR FILING DATE: 2003-10-24  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 10  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence: Primer mDEZol14  
US-10-533-300-10

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.4;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 671 TCTGGGTCTGCTCTCTCT 689  
Db 19 TCTGGGTCTGCTCTCTCT 1

RESULT 2  
US-10-533-300-12/c  
Sequence 12, Application US/10533300  
Publication No. US20060100145A1  
GENERAL INFORMATION:  
APPLICANT: Meder, Wolfgang  
APPLICANT: Wendland, Martin  
APPLICANT: John, Harald  
APPLICANT: Richter, Rudolf  
APPLICANT: Meyer, Markus  
APPLICANT: Forssmann, Wolf-Georg  
TITLE OF INVENTION: Human Chondrosteomodulin (TIG2), Production, and Use for the  
Treatment or Diagnosis of Bone Diseases, Cartilage Diseases,  
TITLE OF INVENTION: Obesity, Inflammatory Diseases, and Skin Diseases  
FILE REFERENCE: 2388.0010000/SRL/BL5  
CURRENT APPLICATION NUMBER: US/10/533.300  
CURRENT FILING DATE: 2005-04-29  
PRIOR APPLICATION NUMBER: PCT/EP03/11799  
PRIOR FILING DATE: 2003-10-24  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 12  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence: Primer hDEZ\_a\_0114  
US-10-533-300-12

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.4;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 671 TCTGGGTCTGCTCTCTCT 689  
Db 19 TCTGGGTCTGCTCTCTCT 1

RESULT 3  
US-11-303-896-1  
Sequence 1, Application US/11303896  
Publication No. US20060099186A1  
GENERAL INFORMATION:  
APPLICANT: PODSAKOFF, GREGORY M.  
APPLICANT: KESSLER, PAUL D.  
APPLICANT: BYRNE, BARRY J.  
APPLICANT: KURTZMAN, GARY J.  
TITLE OF INVENTION: METHODS FOR DELIVERING DNA TO MUSCLE  
CELLS USING RECOMBINANT ADENO-ASSOCIATED VIRUS  
VIRIONS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:

us-09-930-503a-6.s1.mp3

Page 2

US-11-113-534-39/C  
Sequence 39, Application US/11113534  
Publication NO. US20060115825A1  
GENERAL INFORMATION:  
APPLICANT: Park, Hyun Gyu  
TITLE OF INVENTION: PNA CHIP USING ZIP-CODES AND FABRICATION METHOD THEREOF

FILE REFERENCE: 4240-120  
CURRENT APPLICATION NUMBER: US/11/113,534  
CURRENT FILING DATE: 2005-04-25  
PRIOR APPLICATION NUMBER: KR 10-2004-0099514  
PRIOR FILING DATE: 2004-11-30  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 39  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-11-113-534-39

Query Match 0.7%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 940 CGCAGGTGTC 951  
DB 12 CGCAGGTGTC 1

RESULT 7  
US-11-158-209-139  
Sequence 139, Application US/11/158209  
Publication No. US20060088852A1  
GENERAL INFORMATION:  
APPLICANT: Dirk Petersohn  
APPLICANT: Kordula Schlotmann  
APPLICANT: Thomas Gassenmeier  
APPLICANT: Olaf Holtkotter  
APPLICANT: Marcus Conradt  
APPLICANT: Kay Hofmann  
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin  
FILE REFERENCE: H 05667 PCT  
CURRENT APPLICATION NUMBER: US/11/158,209  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: PCT/EP2003/014070  
PRIOR FILING DATE: 2003-12-11  
PRIOR APPLICATION NUMBER: 102 60 931.4-41  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 1335  
SOFTWARE: SeqWin99, version 1.02  
SEQ ID NO 139  
LENGTH: 11  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-158-209-139

Query Match 0.6%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1674 AAATAAAGCT 1684  
DB 1 AAATAAAGCT 11

RESULT 8  
US-11-158-209-234  
Sequence 234, Application US/11/158209  
Publication No. US20060088852A1  
GENERAL INFORMATION:  
APPLICANT: Dirk Petersohn  
APPLICANT: Kordula Schlotmann  
APPLICANT: Thomas Gassenmeier  
APPLICANT: Olaf Holtkotter  
APPLICANT: Marcus Conradt  
APPLICANT: Kay Hofmann  
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin  
FILE REFERENCE: H 05667 PCT

CURRENT APPLICATION NUMBER: US/11/158,209  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: PCT/EP2003/014070  
PRIOR FILING DATE: 2003-12-11  
PRIOR APPLICATION NUMBER: 102 60 931.4-41  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 1335  
SOFTWARE: SeqWin99, version 1.02  
SEQ ID NO 234  
LENGTH: 11  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-158-209-234

Query Match 0.6%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 969 GGGTGACCT 979  
DB 1 GGGTGACCT 11

RESULT 9  
US-11-158-209-936  
Sequence 936, Application US/11/158209  
Publication No. US20060088852A1  
GENERAL INFORMATION:  
APPLICANT: Dirk Petersohn  
APPLICANT: Kordula Schlotmann  
APPLICANT: Thomas Gassenmeier  
APPLICANT: Olaf Holtkotter  
APPLICANT: Marcus Conradt  
APPLICANT: Kay Hofmann  
TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin  
FILE REFERENCE: H 05667 PCT  
CURRENT APPLICATION NUMBER: US/11/158,209  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: PCT/EP2003/014070  
PRIOR FILING DATE: 2003-12-11  
PRIOR APPLICATION NUMBER: 102 60 931.4-41  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 1335  
SOFTWARE: SeqWin99, version 1.02  
SEQ ID NO 936  
LENGTH: 11  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-158-209-936

Query Match 0.6%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 355 GGCACGTGCT 365  
DB 1 GGCACGTGCT 11

RESULT 10  
US-11-113-534-33/C  
Sequence 33, Application US/11/113534  
Publication No. US20060115825A1  
GENERAL INFORMATION:  
APPLICANT: Park, Hyun Gyu  
APPLICANT: Song, Jae Yang  
TITLE OF INVENTION: PNA CHIP USING ZIP-CODES AND FABRICATION METHOD THEREOF  
FILE REFERENCE: 4240-120  
CURRENT APPLICATION NUMBER: US/11/113,534  
CURRENT FILING DATE: 2005-04-25  
PRIOR APPLICATION NUMBER: KR 10-2004-0099514  
PRIOR FILING DATE: 2004-11-30  
NUMBER OF SEQ ID NOS: 55

```

; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-113-534-33

```

```

Query Match          0.6%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1062 GCAGGCTCTACC 1072
      |||||
Db       11 GCAGGCTCTACC 1

```

```

RESULT 11
US-11-238-162-28
; Sequence 28, Application US/11238162
; Publication No. US20060099618A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: DETECTION, IDENTIFICATION AND DIFFERENTIATION OF SERRATIA SPECIES
; TITLE OF INVENTION: THE SPACER REGION.
; FILE REFERENCE: 2551-177
; CURRENT APPLICATION NUMBER: US/11/238,162
; PRIOR FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 04447218.1
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 60/634,106
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: DNA
; ORGANISM: S. marcescens
US-11-238-162-28

```

```

Query Match          0.6%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      576 CATGACGGCTG 586
      |||||
Db       1 CATGACGGCTG 11

```

Search completed: June 12, 2006, 06:18:11  
Job time : 0.001 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:15:31 ; Search time 12 Seconds

(without alignments)

3.239 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766

Sequence: 1 aattcagagccaccgcgggc.....cgagtcctcattcagagatg 1766

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 612 seqs, 11005 residues

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 621 summaries

Database : us-09-930-503a-6.sl.rng4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	1.7	30	1	ADN12185
2	28	1.6	28	1	AED31523
3	27	1.5	27	1	ABS60998
4	27	1.5	27	1	ADN12184
5	27	1.5	27	1	ADN12182
6	27	1.5	27	1	AED31524
7	26	1.5	27	1	ABS61087
8	25.8	1.5	30	1	ADN12193
9	25	1.4	25	1	AAH26071
10	25	1.4	25	1	AAH26070
11	25	1.4	25	1	ABS60907
12	25	1.4	25	1	ABS61082
13	25	1.4	27	1	ABS61088
14	24	1.4	24	1	AAO37209
15	24	1.4	24	1	AED51264
16	24	1.4	27	1	ABS61086
17	24	1.4	29	1	AAH26738
18	24	1.4	29	1	AAV02408
19	24	1.4	29	1	AAV81238
20	24	1.4	29	1	AAH15513
21	23.6	1.3	24	1	ABS60997
22	23.4	1.3	29	1	ABX95641
23	23.4	1.3	29	1	ABX95641
24	23	1.3	29	1	ABX95641
25	23	1.3	29	1	ABX95641
26	23	1.3	24	1	AAQ30776
27	23	1.3	24	1	ABK63862
28	22.4	1.3	24	1	AAO30777
29	22	1.2	22	1	ABS60912
30	22	1.2	22	1	ABS61083
31	21.8	1.2	27	1	AAH18348
32	21.8	1.2	27	1	AAH18348
33	21.8	1.2	27	1	AAH18348

C 34	21.8	1.2	27	1	AAV02406	Receptor protein d
C 35	21.8	1.2	27	1	AAV81236	Human G-protein co
C 36	21.8	1.2	27	1	AAH83875	G-protein-coupled
C 37	21.8	1.2	27	1	AAH15511	Probe used to scre
C 38	21	1.2	21	1	AAQ30782	PCR primer hsp13a1
C 39	21	1.2	21	1	AAQ30790	PCR primer hsp13a2
C 40	21	1.2	21	1	AAQ30785	PCR primer hsp15a1
C 41	21	1.2	21	1	AAQ30789	PCR primer hsp15a1
C 42	21	1.2	21	1	AAQ30787	PCR primer hsp15a1
C 43	21	1.2	21	1	AAQ29678	hsp13a1 primer 1
C 44	21	1.2	21	1	AAQ29679	hsp13a1 primer 868
C 45	21	1.2	21	1	AAQ29674	hsp13a1 primer 768
C 46	21	1.2	21	1	AAQ29676	hsp13a1 primer 888
C 47	21	1.2	21	1	AAQ29671	hsp13a1 primer 491
C 48	21	1.2	21	1	AAQ29678	hsp13a1 primer 836
C 49	21	1.2	21	1	AAQ29678	hsp13a1 primer 836
C 50	21	1.2	21	1	ABS60219	Human polymorphism
C 51	21	1.2	21	1	ABS60218	Human polymorphism
C 52	21	1.2	21	1	ABS60277	Human polymorphism
C 53	21	1.2	21	1	ABS60343	Human polymorphism
C 54	21	1.2	21	1	ABS60999	Human genotyping p
C 55	21	1.2	21	1	ABS60214	Human polymorphism
C 56	21	1.2	21	1	ABS60345	Human polymorphism
C 57	21	1.2	21	1	ABS60217	Human polymorphism
C 58	21	1.2	21	1	ABS60283	Human polymorphism
C 59	21	1.2	21	1	ABS60344	Human polymorphism
C 60	21	1.2	21	1	ABS60994	Human genotyping p
C 61	21	1.2	21	1	ABK63856	Neurokinin 1 recep
C 62	21	1.2	21	1	ABK63871	Neurokinin 1 recep
C 63	21	1.2	21	1	ABK63894	Neurokinin 1 recep
C 64	21	1.2	21	1	ABK63875	Neurokinin 1 recep
C 65	21	1.2	21	1	ABK63890	Neurokinin 1 recep
C 66	21	1.2	21	1	ABK63904	Neurokinin 1 recep
C 67	21	1.2	21	1	ABK63851	Neurokinin 1 recep
C 68	21	1.2	21	1	ABK63885	Neurokinin 1 recep
C 69	21	1.2	21	1	ABK63889	Neurokinin 1 recep
C 70	21	1.2	21	1	ABK63870	Neurokinin 1 recep
C 71	21	1.2	21	1	ABK63878	Neurokinin 1 recep
C 72	21	1.2	21	1	ABK63866	Neurokinin 1 recep
C 73	21	1.2	21	1	ABK63880	Neurokinin 1 recep
C 74	21	1.2	21	1	ABK63887	Neurokinin 1 recep
C 75	21	1.2	21	1	ABK63868	Neurokinin 1 recep
C 76	21	1.2	21	1	ABK63897	Neurokinin 1 recep
C 77	21	1.2	21	1	ABK63852	Neurokinin 1 recep
C 78	21	1.2	21	1	ABK63852	Neurokinin 1 recep
C 79	21	1.2	21	1	ABK63906	Neurokinin 1 recep
C 80	21	1.2	21	1	ABK63854	Neurokinin 1 recep
C 81	21	1.2	21	1	ABK63873	Neurokinin 1 recep
C 82	21	1.2	21	1	ABK63861	Neurokinin 1 recep
C 83	21	1.2	21	1	ABK63881	Neurokinin 1 recep
C 84	21	1.2	21	1	ABK63859	Neurokinin 1 recep
C 85	21	1.2	21	1	ABK63892	Neurokinin 1 recep
C 86	21	1.2	21	1	ABK63900	Neurokinin 1 recep
C 87	21	1.2	21	1	ADU26730	Knock-down target
C 88	21	1.2	21	1	ADU26729	Knock-down target
C 89	21	1.2	26	1	AAQ37208	PCR primer #1 to a
C 90	20.8	1.2	24	1	AAQ30778	PCR primer rspr7a1
C 91	20.6	1.2	21	1	ABS60911	Human genotyping p
C 92	20.6	1.2	24	1	AAH18361	G-protein coupled
C 93	20	1.1	20	1	AAQ30792	PCR primer hsp15a2
C 94	20	1.1	20	1	AAQ30788	PCR primer hsp15a2
C 95	20	1.1	20	1	AAQ30791	PCR primer hsp15a2
C 96	20	1.1	20	1	AAQ30786	PCR primer hsp15a2
C 97	20	1.1	20	1	AAQ30783	PCR primer hsp13a4
C 98	20	1.1	20	1	AAQ30784	PCR primer hsp13a5
C 99	20	1.1	20	1	AAQ29672	hsp13a4 primer 532
C 100	20	1.1	20	1	AAQ29675	hsp15a2 primer 793
C 101	20	1.1	20	1	AAQ29680	hsp15a2 primer 912
C 102	20	1.1	20	1	AAQ29677	hsp15a2 primer 943
C 103	20	1.1	20	1	AAQ29681	hsp15a2 primer 935
C 104	20	1.1	20	1	AAQ29673	hsp15a4 primer 568
C 105	20	1.1	20	1	AAZ92287	Allele specific pr
C 106	20	1.1	20	1	ABS60995	Human genotyping p

107	20	1.1	20	1	ABSG0996	Human genotyping p	180	17.4	1.0	19	1	ABSG5990	Human DNA represen
C 108	20	1.1	20	1	ABK63858	Neurokinin 1 recep	181	17	1.0	20	1	ABE77637	Human dopamine rec
C 109	20	1.1	20	1	ABK63876	Neurokinin 1 recep	182	17	1.0	20	1	AAE77702	Human dopamine rec
C 110	20	1.1	20	1	ABK63857	Neurokinin 1 recep	C 183	17	1.0	21	1	AAQ36818	Oligomer SM 82 use
C 111	20	1.1	20	1	ABK63893	Neurokinin 1 recep	C 184	17	1.0	21	1	AAQ36820	Oligomer SM 86 use
C 112	20	1.1	20	1	ABK63895	Neurokinin 1 recep	C 185	17	1.0	21	1	AAQ36822	Oligomer SM 88 use
C 113	20	1.1	20	1	ABK63869	Neurokinin 1 recep	C 186	17	1.0	21	1	AAQ94986	SSP Oligonucleoti
C 114	20	1.1	20	1	ABK63877	Neurokinin 1 recep	C 187	17	1.0	21	1	AAQ94984	SSP Oligonucleoti
C 115	20	1.1	20	1	ABK63891	Neurokinin 1 recep	C 188	17	1.0	21	1	AAQ94976	SSP Oligonucleoti
C 116	20	1.1	20	1	ABK63850	Neurokinin 1 recep	C 189	17	1.0	21	1	AAV99519	Oligonucleotide SM
C 117	20	1.1	20	1	ABK63888	Neurokinin 1 recep	C 190	17	1.0	21	1	AAV99509	Oligonucleotide SM
C 118	20	1.1	20	1	ABK63853	Neurokinin 1 recep	C 191	17	1.0	21	1	ADA15931	Oligonucleotide SM
C 119	20	1.1	20	1	ABK63874	Neurokinin 1 recep	C 192	17	1.0	21	1	ADA15939	Synthetic storage
C 120	20	1.1	20	1	ABK63896	Neurokinin 1 recep	C 193	17	1.0	21	1	ADA15937	Synthetic storage
C 121	20	1.1	20	1	ABK63872	Neurokinin 1 recep	C 194	17	1.0	21	1	ADA15921	Synthetic storage
C 122	20	1.1	20	1	ABK63855	Neurokinin 1 recep	C 195	17	1.0	21	1	ACH03695	Ear I-based lysine
C 123	20	1.1	20	1	ABT16453	Human neurokinin 1	C 196	17	1.0	21	1	ACH03685	Ear I-based lysine
C 124	20	1.1	20	1	ABT16465	Human neurokinin 1	C 197	17	1.0	21	1	ACH03693	Oligonucleotide SM
C 125	20	1.1	20	1	ABT16467	Human neurokinin 1	C 198	17	1.0	21	1	ADW71666	Oligonucleotide SM
C 126	20	1.1	20	1	ABT16466	Human neurokinin 1	C 199	17	1.0	21	1	ADW71648	Oligonucleotide SM
C 127	20	1.1	20	1	ABD51262	Human tachykinin r	C 200	17	1.0	21	1	ADW71664	Chimeric antisense
C 128	20	1.1	21	1	AAQ30781	Probe hsp3a2 to h	C 201	16.8	1.0	20	1	ABT44412	Human selenophosph
C 129	20	1.1	21	1	AAQ29670	hep3a2 primer 455	C 202	16.8	1.0	20	1	ADB90814	Human dopamine rec
C 130	20	1.1	21	1	ABK63898	Neurokinin 1 recep	C 203	16.8	1.0	20	1	ABE77695	Human dopamine rec
C 131	20	1.1	21	1	ABK63879	Neurokinin 1 recep	C 204	16.8	1.0	20	1	ABE77704	Human dopamine rec
C 132	20	1.1	21	1	ABK63860	Neurokinin 1 recep	C 205	16.8	1.0	20	1	ABE77703	Human dopamine rec
C 133	20	1.1	21	1	ABQ81645	Oligonucleotide se	C 206	16.8	1.0	20	1	ABE77696	Human dopamine rec
C 134	19.8	1.1	21	1	ADU41834	Knock-down target	C 207	16.8	1.0	20	1	ABE77705	Human dopamine rec
C 135	19.4	1.1	21	1	ADU41833	Knock-down target	C 208	16.8	1.0	21	1	AAZ50619	PCR primer 3-AS fo
C 136	19.2	1.1	24	1	AAQ67148	Primer for amplify	C 209	16.4	0.9	18	1	AAQ30774	PCR primer rspr284
C 137	19.2	1.1	24	1	AAT00836	HIV-1 strains TSP	C 210	16.4	0.9	18	1	AAWX73459	Mouse flk-1 VEGF r
C 138	19	1.1	19	1	ABSG5989	Human DNA represen	C 211	16.4	0.9	19	1	AD147994	Human OGR-1 probe1
C 139	19	1.1	19	1	ABSG5989	Human DNA represen	C 212	16.4	0.9	20	1	ACCT0594	Sphingosine-1-phos
C 140	19	1.1	19	1	ABSG5985	Human DNA represen	C 213	16.4	0.9	20	1	ADP83183	IGF1R antisense ol
C 141	19	1.1	19	1	ABSG59901	Human DNA represen	C 214	16.4	0.9	20	1	ADP83001	Antisense oligonuc
C 142	19	1.1	19	1	ABSG59959	Human DNA represen	C 215	16	0.9	20	1	ABK03471	Human CD20 Zinzyne
C 143	19	1.1	19	1	ABK63901	Neurokinin 1 recep	C 216	16	0.9	20	1	ABL53529	Human SM1b antis
C 144	19	1.1	19	1	ABK63865	Neurokinin 1 recep	C 217	16	0.9	20	1	ACF79553	Mouse SAM1b antis
C 145	19	1.1	19	1	ABK63882	Neurokinin 1 recep	C 218	16	0.9	20	1	ACF79551	Oligonucleotide an
C 146	19	1.1	19	1	ABK63863	Neurokinin 1 recep	C 219	16	0.9	20	1	ADH49395	MAS-signaliling tra
C 147	19	1.1	19	1	ABK63903	Neurokinin 1 recep	C 220	16	0.9	20	1	ADH49397	MAS-signaliling tra
C 148	19	1.1	19	1	ABK63884	Neurokinin 1 recep	C 221	16	0.9	20	1	AAV01172	Adrenergic recepto
C 149	19	1.1	19	1	ABE829146	Human siRNA molecu	C 222	15.8	0.9	19	1	ADO6346	Haemofiltrate-chon
C 150	19	1.1	19	1	ABE84827	Human siRNA molecu	C 223	15.8	0.9	19	1	ADO6346	Haemofiltrate-chon
C 151	19	1.1	19	1	ABE51263	Human tachykinin r	C 224	15.8	0.9	19	1	ADO6348	STAT-3 siRNA anti
C 152	19	1.1	20	1	ABE77699	Human dopamine rec	C 225	15.8	0.9	19	1	ABE90637	STAT-3 siRNA targe
C 153	19	1.1	20	1	AAE77700	Human dopamine rec	C 226	15.8	0.9	19	1	ABE90637	RNAi sense strand,
C 154	18.4	1.0	20	1	AAQ47254	Sequence of PCR pr	C 227	15.8	0.9	19	1	ABE73577	Human hairless hom
C 155	18.2	1.0	20	1	AAQ55048	Oligo probe hsp3a	C 228	15.8	0.9	19	1	ABE41028	Human hairless hom
C 156	18	1.0	18	1	AAQ30793	hsp3a65 primer 950	C 230	15.8	0.9	19	1	ABE75464	Human NGO-A trans
C 157	18	1.0	18	1	AAQ29682	Substance P recep	C 231	15.8	0.9	19	1	ABE75690	Human NGO-A siRNA
C 158	18	1.0	18	1	AAT76448	Substance P recep	C 232	15.4	0.9	17	1	AAK72794	Mouse flk-1 VEGF r
C 159	18	1.0	18	1	AAAX54239	Low adenosine anti	C 233	15.4	0.9	17	1	ABK01841	Human NGO Zinzyne
C 160	18	1.0	18	1	AAAX33683	Human substance p	C 234	15.4	0.9	17	1	ADU94309	Human OGR1 gene sp
C 161	18	1.0	18	1	AAFI9805	Human genotyping p	C 235	15.4	0.9	18	1	ADU94309	Human OGR1 gene sp
C 162	18	1.0	18	1	ABSG61000	Human genotyping p	C 236	15.4	0.9	18	1	ADU94309	Human HGPBMY9 PCR
C 163	18	1.0	18	1	ABSG60906	Human genotyping p	C 237	15.4	0.9	18	1	ADU94309	Common marmoset 18
C 164	18	1.0	18	1	ABK63886	Neurokinin 1 recep	C 238	15.4	0.9	19	1	ABE82508	Human VEGFR3 short
C 165	18	1.0	18	1	ABK63905	Neurokinin 1 recep	C 239	15.4	0.9	19	1	ADP37473	Human VEGFR3 short
C 166	18	1.0	18	1	ABK63867	Neurokinin 1 recep	C 240	15.4	0.9	19	1	ADP37472	Human VEGFR3 short
C 167	18	1.0	18	1	ABT16451	Human neurokinin 1	C 241	15.4	0.9	19	1	ADP3468	Human TERT transcr
C 168	18	1.0	18	1	ABZ95499	Human substance p	C 242	15.4	0.9	19	1	ADP3468	Human TERT transcr
C 169	18	1.0	18	1	ABD19638	Human substance p	C 243	15.4	0.9	19	1	ADK97381	Primer of the inve
C 170	18	1.0	20	1	ABE77698	Human dopamine rec	C 244	15.4	0.9	19	1	ADK97381	Anti-TERT siRNA SE
C 171	18	1.0	20	1	ABE77701	Human dopamine rec	C 245	15.4	0.9	19	1	ADK97381	Ribosome binding s
C 172	18	1.0	22	1	ABSG61085	Human automated ge	C 246	15.4	0.9	19	1	ADY88479	VEGFR siRNA SEQ ID
C 173	17.8	1.0	21	1	ABT4Q254	Human Chem23 PCR p	C 247	15.4	0.9	19	1	ADY88476	VEGFR siRNA SEQ ID
C 174	17.8	1.0	22	1	ADW43814	Human Chem23 PCR p	C 248	15.4	0.9	19	1	AEA06712	G protein-coupled
C 175	17.8	1.0	22	1	AAQ47385	Substance P recep	C 249	15.4	0.9	19	1	AEA06625	G protein-coupled
C 176	17.4	1.0	19	1	ABSG5964	Human DNA represen	C 250	15.4	0.9	19	1	AEA21650	Short interfering
C 177	17.4	1.0	19	1	ABSG5962	Human DNA represen	C 251	15.4	0.9	19	1	AEA21651	Short interfering
C 178	17.4	1.0	19	1	ABSG5986	Human DNA represen	C 252	15.4	0.9	19	1	AEA21649	Short interfering
C 179	17.4	1.0	19	1	ABSG5958	Human DNA represen	C 252	15.4	0.9	19	1	ABE15725	Human telomerase-t



C 253	15.4	0.9	19	1	ABE15948	Human telomerase-t
C 254	15.4	0.9	19	1	AED37961	VEGF or VEGFR-spec
C 255	15.4	0.9	19	1	AED37714	VEGF or VEGFR-spec
C 256	15.4	0.9	19	1	AEF75485	Human NOGO-A trans
C 257	15.4	0.9	19	1	AEF75711	Human NOGO-A siRNA
C 258	15	0.8	15	1	AAT76449	Substance P recept
C 259	15	0.8	15	1	AAT76450	Substance P recept
C 260	15	0.8	15	1	AAK54240	Substance P recept
C 261	15	0.8	15	1	AAK54241	Substance P recept
C 262	15	0.8	15	1	AAA33685	Low adenosine anti
C 263	15	0.8	15	1	AAA33684	Low adenosine anti
C 264	15	0.8	15	1	AAFI9807	Human substance P
C 265	15	0.8	15	1	AAFI9806	Human substance P
C 266	15	0.8	15	1	ABZ95501	Human substance P
C 267	15	0.8	15	1	ABZ95500	Human substance P
C 268	15	0.8	15	1	ABD19639	Human substance P
C 269	15	0.8	15	1	ABD19640	Human substance P
C 270	15	0.8	17	1	ABK03403	Human CD20 G-cleav
C 271	15	0.8	17	1	AAK54501	Degenerate primer f
C 272	15	0.8	17	1	ABN06976	Human GDMLP-1 17-m
C 273	15	0.8	17	1	ABN06974	Human GDMLP-1 17-m
C 274	15	0.8	17	1	ABN06975	Human GDMLP-1 17-m
C 275	15	0.8	17	1	ACN70065	Human GDMLP-1 prob
C 276	15	0.8	17	1	ACN70066	Human GDMLP-1 prob
C 277	15	0.8	17	1	ACN70064	Human GDMLP-1 prob
C 278	15	0.8	18	1	AAA99603	Rat D4 receptor ol
C 279	15	0.8	18	1	ABK12223	Rat dopamine D2 an
C 280	15	0.8	18	1	ADF29051	Rat dopaminergic D4 re
C 281	15	0.8	18	1	ADK41404	Human autoimmune d
C 282	15	0.8	18	1	ADW71322	Human p53 target spe
C 283	15	0.8	18	1	ADW71312	Human p53 exon spe
C 284	15	0.8	18	1	AAQ35431	GFP-R primer (EXT
C 285	14.8	0.8	18	1	AAV34526	Chemokine receptor
C 286	14.8	0.8	18	1	AAV49658	Human SRCR protein
C 287	14.8	0.8	18	1	AAZ40901	Human CD40 phospho
C 288	14.8	0.8	18	1	AAZ47734	Human CD40 antisen
C 289	14.8	0.8	18	1	AAK06638	Human alpha1-antile
C 290	14.8	0.8	18	1	AAAF75209	Human/mouse NTRK3
C 291	14.8	0.8	18	1	ABQ73036	Human chloride cha
C 292	14.8	0.8	18	1	ABK64461	Human TGF-beta bin
C 293	14.8	0.8	18	1	ADY75584	Antisense oligonuc
C 294	14.8	0.8	18	1	ADY75702	Antisense oligonuc
C 295	14.8	0.8	18	1	AEC52834	Antisense oligonuc
C 296	14.8	0.8	18	1	AEC51657	Antisense oligonuc
C 297	14.8	0.8	18	1	AEC52974	Antisense oligonuc
C 298	14.8	0.8	18	1	AEC27781	Human allele-speci
C 299	14.6	0.8	15	1	ABK12174	Human Tachykinin R
C 300	14.6	0.8	15	1	ABK12178	Human Tachykinin R
C 301	14.6	0.8	15	1	ABK12184	Human Tachykinin R
C 302	14.6	0.8	15	1	ABK12192	Human Tachykinin R
C 303	14.6	0.8	15	1	ABK12193	Human Tachykinin R
C 304	14.6	0.8	15	1	ABK12194	Human Tachykinin R
C 305	14.6	0.8	15	1	ABK12195	Human Tachykinin R
C 306	14.6	0.8	15	1	ABK12187	Human Tachykinin R
C 307	14.6	0.8	15	1	ABK12177	Human Tachykinin R
C 308	14.6	0.8	15	1	ABK12186	Human Tachykinin R
C 309	14.4	0.8	16	1	ADU94981	Human TERT G-cleav
C 310	14.4	0.8	16	1	ABK63842	Neurokinin 1 recep
C 311	14.4	0.8	17	1	AAV93332	Human B-raf subscr
C 312	14.4	0.8	17	1	ABK03470	Human CD20 zinyne
C 313	14.4	0.8	17	1	ABK00920	Human NOGO inozyme
C 314	14.4	0.8	17	1	ADV06518	Human BACE DNAzyme
C 315	14.4	0.8	17	1	ADU06311	Human TERT hammetz
C 316	14.4	0.8	17	1	ABK63841	Neurokinin 1 recep
C 317	14.4	0.8	17	1	ACA07747	NFKB sub-unit modu
C 318	14.4	0.8	17	1	ABZ61190	Human K-Ras DNAzym
C 319	14.4	0.8	17	1	ADK13263	Human glioma endot
C 320	14.4	0.8	17	1	ADN00720	Human SIRT related
C 321	14.4	0.8	17	1	ADZ30264	Human K-Ras subscr
C 322	14.4	0.8	17	1	AED88220	Human Leukocyte An
C 323	14.4	0.8	18	1	AAQ85449	PCR primer for HAR
C 324	14.4	0.8	18	1	AAT41606	Oligonucleotide co
C 325	14.4	0.8	18	1	AAK73505	Mouse ftk-1 VEGF r
C 326	14.4	0.8	18	1	AAK84480	PCR primer for Hum
C 327	14.4	0.8	18	1	AAK07036	Human integrin bet
C 328	14.4	0.8	18	1	AAZ48483	Human TNFR1 mRNA 1
C 329	14.4	0.8	18	1	AAZ59805	Human Smad3 phosph
C 330	14.4	0.8	18	1	AAZ76614	Human biallelic ma
C 331	14.4	0.8	18	1	AAH37701	SNP specific upper
C 332	14.4	0.8	18	1	ABT04979	TNFR1 expression m
C 333	14.4	0.8	18	1	ABK63840	Neurokinin 1 recep
C 334	14.4	0.8	18	1	ADD40778	Human tenascin-W p
C 335	14.4	0.8	18	1	ADK33426	HLA class I allele
C 336	14.4	0.8	18	1	ADL09276	HLA locus-specific
C 337	14.4	0.8	18	1	ADN35828	Human NSCLC gene a
C 338	14.4	0.8	18	1	ADN06011	Human TNFR1 antise
C 339	14.2	0.8	17	1	ADK58092	Primer Gamma 15 fo
C 340	14	0.8	17	1	AAT76447	Substance P recept
C 341	14	0.8	14	1	AAK54238	Substance P recept
C 342	14	0.8	14	1	AAA33682	Low adenosine anti
C 343	14	0.8	14	1	AAK289118	Rice OPK17 PCR pri
C 344	14	0.8	14	1	AAFI9804	Human substance P
C 345	14	0.8	14	1	ABZ72765	Rod opsin hairpin
C 346	14	0.8	14	1	ABZ95498	Human substance P
C 347	14	0.8	14	1	ABD19637	Human substance P
C 348	14	0.8	15	1	AAQ90578	Encodes recombinan
C 349	14	0.8	15	1	AAV93851	Target sequence wi
C 350	14	0.8	15	1	ABK63843	Neurokinin 1 recep
C 351	14	0.8	16	1	AAT94355	Human DRP4 sequenc
C 352	14	0.8	17	1	AAV11865	Mus musculus Tnd 1
C 353	14	0.8	17	1	AAV93331	Human B-raf subscr
C 354	14	0.8	17	1	AAK59530	PCR primer used to
C 355	14	0.8	17	1	ABK03568	Human CD20 DNAzyme
C 356	14	0.8	17	1	ADV07675	Human BACE ambery
C 357	14	0.8	17	1	ADU06313	Human TERT hammetz
C 358	14	0.8	17	1	ADU06312	Human TERT hammetz
C 359	14	0.8	17	1	ABN06977	Human GDMLP-1 17-m
C 360	14	0.8	17	1	ABN06973	Human GDMLP-1 17-m
C 361	14	0.8	17	1	ADMS4123	Human GRID mRNA su
C 362	14	0.8	17	1	ADL62292	Human ER- breast c
C 363	14	0.8	17	1	ADR31412	Bovine RORC2 DNA
C 364	14	0.8	17	1	ACN70067	Human GDMLP-1 prob
C 365	14	0.8	17	1	ACN70063	Human GDMLP-1 prob
C 366	14	0.8	17	1	ADK41403	Human autoimmune d
C 367	13.8	0.8	17	1	AAQ30775	PCR primer respr284
C 368	13.8	0.8	17	1	AAK47255	PCR primer for amp
C 369	13.8	0.8	17	1	AAK71369	Human KDR VEGF rec
C 370	13.8	0.8	17	1	AAK72795	Mouse ftk-1 VEGF r
C 371	13.8	0.8	17	1	AAK72944	Mouse ftk-1 VEGF r
C 372	13.8	0.8	17	1	AAK71197	Human KDR VEGF rec
C 373	13.8	0.8	17	1	AAK62890	Delta-9 desaturase
C 374	13.8	0.8	17	1	AAV97463	Human BGF-R target
C 375	13.8	0.8	17	1	AAA00669	Integrin alpha 6 b
C 376	13.8	0.8	17	1	AAH94825	Human CHK1 ribozym
C 377	13.8	0.8	17	1	ABK01580	Human NOGO G-Cleav
C 378	13.8	0.8	17	1	ABK02357	Human NOGO Ambery
C 379	13.8	0.8	17	1	ABK02363	Human NOGO Ambery
C 380	13.8	0.8	17	1	ADU93087	Human TERT NCH rib
C 381	13.8	0.8	17	1	ADU93088	Human TERT NCH rib
C 382	13.8	0.8	17	1	ADU06314	Human TERT hammetz
C 383	13.8	0.8	17	1	ADU92547	Human TERT NCH rib
C 384	13.8	0.8	17	1	ADU93086	Human TERT NCH rib
C 385	13.8	0.8	17	1	ADV62161	HBV amberyyme ribo
C 386	13.8	0.8	17	1	ADV62160	HBV amberyyme ribo
C 387	13.8	0.8	17	1	ADV03744	Human BACE NCH rib
C 388	13.8	0.8	17	1	ADU03089	Human TERT NCH rib
C 389	13.8	0.8	17	1	ABN07082	Human GDMLP-1 17-m
C 390	13.8	0.8	17	1	ABN02764	Human GDMLP-1 17-m
C 391	13.8	0.8	17	1	ABO63570	Human KTM1a portc
C 392	13.8	0.8	17	1	ABV83022	Human HRP1 scannin
C 393	13.8	0.8	17	1	ABV00740	Human POSH1 scann
C 394	13.8	0.8	17	1	ABL21550	Human HLA genotypi
C 395	13.8	0.8	17	1	ABQ76743	TNF-aseassociated PCR
C 396	13.8	0.8	17	1	ACN01554	WNV inozyme subscr
C 397	13.8	0.8	17	1	ACN13517	WNV minus strand 2
C 398	13.8	0.8	17	1	ACN01555	WNV inozyme subscr

C 399	13.8	0.8	17	1	ACN01273	472	13	0.7	13	1	ABC10988	Oligonucleotide SE
C 400	13.8	0.8	17	1	ACN07407	473	13	0.7	13	1	ABF29163	Oligonucleotide SE
C 401	13.8	0.8	17	1	ACN12112	474	13	0.7	13	1	ABF98356	Oligonucleotide SE
C 402	13.8	0.8	17	1	ACN07336	475	13	0.7	13	1	ABC34324	Oligonucleotide SE
C 403	13.8	0.8	17	1	ACN09339	476	13	0.7	13	1	ABF73245	Oligonucleotide SE
C 404	13.8	0.8	17	1	ACN13675	477	13	0.7	13	1	AAT33386	Human vascular end
C 405	13.8	0.8	17	1	ACN03237	478	13	0.7	13	1	AAT48401	Oligonucleotide H-
C 406	13.8	0.8	17	1	ACN15211	479	13	0.7	13	1	AAK33621	Thrombin inhibitor
C 407	13.8	0.8	17	1	ACD00505	480	13	0.7	13	1	ABK55500	Selectin L lymphoc
C 408	13.8	0.8	17	1	ACA98879	481	13	0.7	13	1	ABK95827	Solute Carrier Fam
C 409	13.8	0.8	17	1	ACA99880	482	13	0.7	13	1	ABK95804	Solute Carrier Fam
C 410	13.8	0.8	17	1	ABT35050	483	13	0.7	13	1	ABN80579	Pyridoxal (Pyridox
C 411	13.8	0.8	17	1	ABT36411	484	13	0.7	13	1	ABN80579	Human P450(cytochr
C 412	13.8	0.8	17	1	ACA06517	485	13	0.7	13	1	ABK92616	ASO primer #14 to
C 413	13.8	0.8	17	1	ADBA9853	486	13	0.7	13	1	ABLS2021	Human CRYBB1 gene
C 414	13.8	0.8	17	1	ADB03782	487	13	0.7	13	1	AAK97335	Human APOA4 allele
C 415	13.8	0.8	17	1	ACD55641	488	13	0.7	13	1	AAK16726	Human CASP5 gene a
C 416	13.8	0.8	17	1	ACD55640	489	13	0.7	13	1	ABK81517	CCR5 allele-specific
C 417	13.8	0.8	17	1	ACD58714	490	13	0.7	13	1	ABA97329	Human lysosomal ac
C 418	13.8	0.8	17	1	ACC62777	491	13	0.7	13	1	ABT6318	SMOH polymorphism
C 419	13.8	0.8	17	1	ACA89898	492	13	0.7	13	1	AAK39772	Allele-specific ol
C 420	13.8	0.8	17	1	ADBA4298	493	13	0.7	13	1	ADP74524	Hyperlipidemia tre
C 421	13.8	0.8	17	1	ADP64140	494	13	0.7	13	1	ADN89026	Primer for second
C 422	13.8	0.8	17	1	ADP63951	495	13	0.7	13	1	ADS88857	Tachykinin recepto
C 423	13.8	0.8	17	1	ADP62472	496	13	0.7	13	1	ADN12185	Endothelial nitric
C 424	13.8	0.8	17	1	ADT51353	497	13	0.7	13	1	AAV70488	Control probe hybr
C 425	13.8	0.8	17	1	ACC53250	498	12.8	0.7	13	1	AAZ09807	p53 exon 8 PCR pri
C 426	13.8	0.8	17	1	ACC53982	499	12.8	0.7	13	1	AAZ09807	Inducible nitric o
C 427	13.8	0.8	17	1	ADL46848	500	12.8	0.7	13	1	AAK54320	Endothelial nitric o
C 428	13.8	0.8	17	1	ADL46896	501	12.8	0.7	13	1	AAK54275	Inducible nitric o
C 429	13.8	0.8	17	1	ADM60212	502	12.8	0.7	13	1	AAK54321	Low adenosine anti
C 430	13.8	0.8	17	1	ADM60212	503	12.8	0.7	13	1	AAK33764	Low adenosine anti
C 431	13.8	0.8	17	1	ACN70772	504	12.8	0.7	13	1	AAK33765	HIV-1 protease gen
C 432	13.8	0.8	17	1	ACN65854	505	12.8	0.7	13	1	AAZ97920	Human inducible ni
C 433	13.8	0.8	17	1	ADW29146	506	12.8	0.7	13	1	AAK19886	Human inducible ni
C 434	13.8	0.8	17	1	AEK23914	507	12.8	0.7	13	1	AAK19887	Human endothelial
C 435	13.8	0.8	17	1	AEK88144	508	12.8	0.7	13	1	AAK19841	Human TRRT G-cleav
C 436	13.8	0.8	17	1	AEK42068	509	12.8	0.7	13	1	ADU94873	Human TRRT G-cleav
C 437	13.6	0.8	15	1	AAK15285	510	12.8	0.7	13	1	ADU94732	Human TRRT G-cleav
C 438	13.6	0.8	15	1	AEK77703	511	12.8	0.7	13	1	ADU94557	Control probe SEQ
C 439	13.4	0.8	15	1	AAK66607	512	12.8	0.7	13	1	ABL46099	Human CPY501A2 Ex
C 440	13.4	0.8	15	1	AAK66606	513	12.8	0.7	13	1	ABK97178	Human H1A genocyp1
C 441	13.4	0.8	15	1	AAK49867	514	12.8	0.7	13	1	ABK131409	Human H1A genocyp1
C 442	13.4	0.8	15	1	AAK45173	515	12.8	0.7	13	1	ABK131307	Human hypoxia-indu
C 443	13.4	0.8	15	1	AAK49642	516	12.8	0.7	13	1	AAK56914	Human inducible ni
C 444	13.4	0.8	15	1	AAK52680	517	12.8	0.7	13	1	AAK55580	Human inducible ni
C 445	13.4	0.8	15	1	AAK52481	518	12.8	0.7	13	1	ABZ95535	Human inducible ni
C 446	13.4	0.8	15	1	AAK45224	519	12.8	0.7	13	1	ABZ95581	Human endothelial
C 447	13.4	0.8	15	1	AAK45223	520	12.8	0.7	13	1	ABD19740	Human endothelial
C 448	13.4	0.8	15	1	ABK5643	521	12.8	0.7	13	1	ABD19685	Human inducible ni
C 449	13.4	0.8	15	1	ABK88284	522	12.8	0.7	13	1	ABD19739	Human inducible ni
C 450	13.4	0.8	16	1	AAQ95705	523	12.8	0.7	13	1	ADK82289	Nucleic acid analy
C 451	13.4	0.8	16	1	ADK84377	524	12.8	0.7	13	1	ADK82289	Glutathione S-tran
C 452	13.4	0.8	16	1	ADP44279	525	12.8	0.7	13	1	ADK015394	Human VRI exon 1d
C 453	13.4	0.8	16	1	ADU76209	526	12.8	0.7	13	1	ADQ30169	Aptamer-related pe
C 454	13.4	0.8	16	1	ABK56195	527	12.8	0.7	13	1	ADQ62808	Aptamer-related DN
C 455	13	0.7	13	1	ABF73244	528	12.8	0.7	13	1	ADQ62809	Oligonucleotide of
C 456	13	0.7	13	1	ABH37834	529	12.8	0.7	13	1	ADY03782	Hepatitis C virus-
C 457	13	0.7	13	1	ABK89691	530	12.8	0.7	13	1	AEK50577	Human nucleic acid
C 458	13	0.7	13	1	ABH06065	531	12.8	0.7	13	1	ABK52878	Human leukocyte an
C 459	13	0.7	13	1	ABF59772	532	12.8	0.7	13	1	ABF46499	Oligonucleotide SE
C 460	13	0.7	13	1	ABF29162	533	12.6	0.7	13	1	ABH39848	Oligonucleotide SE
C 461	13	0.7	13	1	ABK98834	534	12.6	0.7	13	1	ABH39849	Oligonucleotide SE
C 462	13	0.7	13	1	ABK98835	535	12.6	0.7	13	1	ABF46498	Oligonucleotide SE
C 463	13	0.7	13	1	ABK77569	536	12.6	0.7	13	1	ABK96358	SCN2B gene polymor
C 464	13	0.7	13	1	ABK96357	537	12.6	0.7	13	1	ABK77519	Human CTLA4 gene a
C 465	13	0.7	13	1	ABK89690	538	12.6	0.7	13	1	ABK70728	ASO primer #9 to d
C 466	13	0.7	13	1	ABK77568	539	12.6	0.7	13	1	AAH99963	PCR primer for det
C 467	13	0.7	13	1	ABK10989	540	12.6	0.7	13	1	AAO30786	hsp75a2 primer 793
C 468	13	0.7	13	1	ABH06064	541	12.6	0.7	13	1	AAQ28675	Neurokinin 1 recep
C 469	13	0.7	13	1	ABF59773	542	12.6	0.7	13	1	ABK63893	
C 470	13	0.7	13	1	ABH37835	543	12.6	0.7	13	1	ABK63893	
C 471	13	0.7	13	1	ABC34325	544	12.6	0.7	13	1	ABK63874	

545	12.6	0.7	20	1	ABK63855	Neurokinin 1 recep
C 546	12.6	0.7	20	1	ABE77702	Human dopamine rec
C 547	12.6	0.7	20	1	ABE77704	Human dopamine rec
C 548	12.4	0.7	14	1	ABZ58817	Nucleotide sequenc
C 549	12.4	0.7	14	1	AAZ79147	Human VEGF cDNA an
C 550	12.4	0.7	14	1	AAZ54378	NK-kb antisense ol
C 551	12.4	0.7	14	1	AAA33822	Low adenosine anti
C 552	12.4	0.7	14	1	AAZ64750	Substrate for hair
C 553	12.4	0.7	14	1	AAZ65593	Immunosuppressant
C 554	12.4	0.7	14	1	ABX19944	Human NF-kB polyru
C 555	12.4	0.7	14	1	ABX01587	Hepatitis C virus
C 556	12.4	0.7	14	1	ABZ76511	Hepatitis C virus
C 557	12.4	0.7	14	1	ABZ72766	Rod opsin hairpin
C 558	12.4	0.7	14	1	ABZ95638	Human NF-kappaB an
C 559	12.4	0.7	14	1	ABD15802	Human NF-kB DNA fr
C 560	12.4	0.7	14	1	ADZ85160	MODY 3 diabetes-as
C 561	12.4	0.7	14	1	ABE01280	VEGF inhibition ol
C 562	12.4	0.7	14	1	AEC63812	Novel microarray-r
C 563	12.4	0.7	15	1	AAO70347	Antisense oligonuc
C 564	12.4	0.7	15	1	AAZ66605	Human CD40 hamme
C 565	12.4	0.7	15	1	AAZ66802	Mouse CD40 hamme
C 566	12.4	0.7	15	1	AAZ65304	Mouse B7-1 hamme
C 567	12.4	0.7	15	1	AAZ66801	Mouse CD40 hamme
C 568	12.4	0.7	15	1	AAZ65303	Mouse B7-1 hamme
C 569	12.4	0.7	15	1	AAT15256	Antisense sequence
C 570	12.4	0.7	15	1	AAT50255	Rabbit CERP HH rib
C 571	12.4	0.7	15	1	AAV49771	Transcriptional sy
C 572	12.4	0.7	15	1	AAV48607	jund gene antisens
C 573	12.4	0.7	15	1	AAAX3113	Tag sequence of a
C 574	12.4	0.7	15	1	AAAX07158	Probe for XELF1-al
C 575	12.4	0.7	15	1	AAA65946	Human leukocyte an
C 576	12.4	0.7	15	1	AAZ45174	ICG1BP2 oligonucleo
C 577	12.4	0.7	15	1	AAZ49868	ICG-1 oligonucleo
C 578	12.4	0.7	15	1	AAZ52635	ICG-1 oligonucleo
C 579	12.4	0.7	15	1	AAZ54012	ICG-1 oligonucleo
C 580	12.4	0.7	15	1	AAZ49641	ICG-1 oligonucleo
C 581	12.4	0.7	15	1	AAZ49643	ICG-1 oligonucleo
C 582	12.4	0.7	15	1	AAZ54013	ICG-1 oligonucleo
C 583	12.4	0.7	15	1	AAZ45225	ICG1BP2 oligonucleo
C 584	12.4	0.7	15	1	AAZ54280	ICG-1 oligonucleo
C 585	12.4	0.7	15	1	AAZ52681	ICG-1 oligonucleo
C 586	12.4	0.7	15	1	AAZ54011	ICG-1 oligonucleo
C 587	12.4	0.7	15	1	AAZ49866	ICG-1 oligonucleo
C 588	12.4	0.7	15	1	AAZ52634	ICG-1 oligonucleo
C 589	12.4	0.7	15	1	AAZ54010	ICG-1 oligonucleo
C 590	12.4	0.7	15	1	AAZ54222	ICG1BP2 oligonucleo
C 591	12.4	0.7	15	1	AAZ52679	ICG-1 oligonucleo
C 592	12.4	0.7	15	1	AAZ45172	ICG1BP2 oligonucleo
C 593	12.4	0.7	15	1	AAZ5482	ICG-1 oligonucleo
C 594	12.4	0.7	15	1	AAZ70390	Human DRD2 allele
C 595	12.4	0.7	15	1	AAZ65430	Human IL4R1pha ge
C 596	12.4	0.7	15	1	AAZ65387	Human IL4R1pha ge
C 597	12.4	0.7	15	1	AAZ65937	Human IL4R1pha ge
C 598	12.4	0.7	15	1	AAZ73926	Human SLC6A4 allele
C 599	12.4	0.7	15	1	AAZ73930	Human SLC6A4 allele
C 600	12.4	0.7	15	1	ADZ35833	Human anti-HER2 NC
C 601	12.4	0.7	15	1	ABZ46309	Mouse scavenger re
C 602	12.4	0.7	15	1	AAZ43755	Human AGR2 gene p
C 603	12.4	0.7	15	1	ABK32066	Human colon cancer
C 604	12.4	0.7	15	1	ACA09887	Necrosis factor ka
C 605	12.4	0.7	15	1	ACA09888	Necrosis factor ka
C 606	12.4	0.7	15	1	ABX94796	Beta-actin PCR pri
C 607	12.4	0.7	15	1	ADL50873	Human PCR substat
C 608	12.4	0.7	15	1	ADP64570	Human PKR substat
C 609	12.4	0.7	15	1	ADQ31062	VIC probe for typl
C 610	12.4	0.7	15	1	ADQ31062	C-fos mRNA detecti
C 611	12.4	0.7	15	1	ADSI2596	Poly Gly linker co
C 612	12.4	0.7	15	1	ADV95329	Reverse RT-PCR pri
C 613	12.4	0.7	15	1	ADV26280	Sequence #1 from h
C 614	12.4	0.7	15	1	ADY25936	Human beta-actin c
C 615	12.4	0.7	15	1	ADY50285	Exemplary vector a
C 616	12.4	0.7	15	1	ADY52800	Randomized DNA poo
C 617	12.4	0.7	15	1	ADZ45541	Human CHRNA2 gene
C 617	12.4	0.7	15	1	ADZ45541	Murine factor IX d

C 618 12.4 0.7 15 1 AEA40005  
 C 619 12.4 0.7 15 1 AEB21700  
 C 620 12.4 0.7 15 1 AEB08734  
 621 12.4 0.7 15 1 ABE99140

## ALIGNMENTS

RESULT 1	ADN12185/c	ADN12185 standard; DNA; 30 BP.	DNA encoding TNF r
AC	ADN12185;		Anti-Nogo-antibody
XX	01-JUL-2004 (first entry)		antibody 2A10 heav
XX			Human c-fos FRRT q
XX			
DE	Tachykinin receptor NK1 amplifying primer NK13' (nested).		
XX			
KM	Tachykinin; vascular disease; platelet aggregation; vulnery;		
KM	thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;		
XX	NK3; tachykinin receptor; ss.		
OS	Synthetic.		
XX	WO2004030695-A1.		
PN	15-APR-2004.		
XX			
PD	06-OCT-2003; 2003WO-GB004335.		
XX	04-OCT-2002; 2002GB-00023077.		
PF			
XX	(VYRE-) UNIV READING.		
XX			
PA	Gibbins JM, Lowry PJ, Graham GJ, Page NM;		
XX	WPI; 2004-330076/30.		
DR			
XX			
PT	Use of tachykinin antagonist or agonist for treating diseases mediated by		
PT	binding of tachykinin ligand to its platelet associated receptor and		
PT	failure of platelet having tachykinin receptor to aggregate normally in		
PT	presence of tachykinin.		
XX			
PS	Disclosure; Page 21; 46pp; English.		
XX			
CC	The invention relates to the use of a tachykinin antagonist in the		
CC	manufacture of a medicament for treating e.g. a disease mediated by		
CC	binding of a tachykinin ligand to its platelet associated receptor. A		
CC	method of identifying an antagonist or agonist of tachykinin having a		
CC	platelet associated tachykinin receptor involves contacting a compound to		
CC	be evaluated with platelets expressing the tachykinin receptor in the		
CC	presence of the tachykinin and monitoring for an increase or decrease of		
CC	platelet aggregation. The agonist is useful in the manufacture of a		
CC	medicament in bulk quantities for treating a disease or conditions		
CC	mediated by binding of a tachykinin ligand to its platelet-associated		
CC	receptor (e.g. thrombosis), and by a failure of or a reduced ability of		
CC	platelet having a tachykinin receptor to aggregate normally in the		
CC	presence of the tachykinin; antagonizing or stimulating the effect of		
CC	tachykinin on platelet associated tachykinin receptor; and stimulating		
CC	platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193		
CC	represent PCR primers for amplifying tachykinin receptors NK1, NK2 and		
CC	NK3.		
XX			
XX			
SQ	Sequence 30 BP; 7 A; 8 C; 14 G; 1 T; 0 U; 0 Other;		
Query Match	1.7%; Score 30; DB 1; Length 30;		
Best Local Similarity	100.0%; Pred. No. 3.5;		
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	678 CTTGGCTCTCTCTGCTGCTTCCCGAGG 707		
Db	30 CTTGGCTCTCTCTGCTGCTTCCCGAGG 1		

RESULT 2  
 AED31523 standard; DNA; 28 BP.  
 XX AED31523;  
 AC AED31523;  
 XX  
 DT 15-DEC-2005 (first entry)  
 XX  
 DE Gerbil neurokinin 1 receptor (GNK1r) PCR primer SEQ ID NO:3.  
 XX  
 KW ss; gerbil neurokinin 1 receptor; GNK1r; schizophrenia; neuroleptic;  
 KW psychiatric disorder; micronutrient disorder; uropathic;  
 KW genitourinary disease; asthma; antiasthmatic; immune disorder;  
 KW inflammation; respiratory disease; pain; analgesic; neurological disease;  
 KW major depressive disorder; antidepressant; anxiety disorder;  
 KW tranquilizer; emesis; antiemetic; gastrointestinal disease;  
 KW inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;  
 KW gastrointestinal disease; irritable bowel syndrome; dyspepsia; migraine;  
 KW antiinflammatory; primer; PCR.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Cavia sp.  
 OS Synthetic.  
 XX  
 PN WO2005090401-A1.  
 XX  
 PD 29-SEP-2005.  
 XX  
 PF 16-MAR-2005; 2005WO-GB001008.  
 XX  
 PR 20-MAR-2004; 2004GB-00006342.  
 XX  
 PA (ASTR ) ASTRAZENCA AB.  
 PA (ASTR ) ASTRAZENCA UK LTD.  
 XX  
 PI Drmotla T, Engberg S, Von Wentzer B;  
 XX  
 DR WPI; 2005-702670/72.  
 XX  
 PT New polynucleotide comprising a sequence encoding gerbil neurokinin 1  
 PT receptor (GNK1r) polypeptide, useful in preparing a composition for  
 PT treating e.g., asthma, pain, depression, emesis, urine incontinence or  
 PT schizophrenia.  
 XX  
 PS Example 1; SEQ ID NO 3; 37pp; English.  
 XX  
 CC The invention relates to a new isolated polynucleotide molecule  
 CC comprising a nucleic acid sequence which encodes gerbil neurokinin 1  
 CC receptor (GNK1r) polypeptide or a polypeptide having at least 98%  
 CC sequence identity with AED31522. Also included are the following: an  
 CC expression vector comprising the polynucleotide molecule; a host cell  
 CC transformed or transfected with the expression vector; a method for  
 CC producing a polypeptide; an isolated or purified polypeptide comprising  
 CC the GNK1r amino acid sequence (see AED31522) or its variant having at  
 CC least 98% identity to the sequence, or its N-terminal or C-terminal  
 CC fragment of at least 350 amino acids in length; a method for identifying  
 CC a chemical compound capable of modulating the activity of GNK1r; a method  
 CC for identifying a therapeutic agent capable of modulating the activity of  
 CC GNK1r; a method of making a pharmaceutical composition; and a  
 CC pharmaceutical composition comprising a GNK1r modulator, or its salt in  
 CC association with a diluent or carrier. The polynucleotide is useful in  
 CC preparing a composition for treating asthma, pain, depression, anxiety,  
 CC emesis, inflammatory bowel disease, irritable bowel syndrome, functional  
 CC dyspepsia, migraine, urine incontinence or schizophrenia. The present  
 CC sequence represents a PCR primer based on conserved regions identified by  
 CC alignment of human, mouse and guinea pig NK1r sequences and used to clone  
 CC gerbil neurokinin 1 receptor (GNK1r) cDNA.  
 XX  
 SQ Sequence 28 BP; 2 A; 13 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 1.6%; Score 28; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 6.1;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 993 GCTGCCCTTCACATCTCTCTCCTG 1020  
 DB 1 GCTGCCCTTCACATCTCTCTCCTG 28  
 RESULT 3  
 ABS60998  
 ID ABS60998 standard; DNA; 27 BP.  
 XX  
 AC ABS60998;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human genotyping PCR primer #151.  
 XX  
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
 KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;  
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUII/) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX  
 DR WPI; 2002-619265/66.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Example 3; Page 913; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2), or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids

CC : (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angiodema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachoma, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is a genotyping PCR primer  
CC for the gene encoding one of the proteins listed above  
XX  
SQ Sequence 27 BP; 9 A; 8 C; 0 G; 10 T; 0 U; 0 Other;  
Query Match 1.5%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DY 1590 TCAAAAATCTCAATCTCTCCCTATCT 1616  
DB 1 TCAAAAATCTCAATCTCTCCCTATCT 27  
RESULT 4  
ADN12184  
XX ADN12184 standard; DNA, 27 BP.  
AC ADN12184;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Tachykinin receptor NK1 amplifying primer NK15' (nested).  
XX  
XX Tachykinin; vascular disease; platelet aggregation; vulnery;  
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;  
KM NK3; tachykinin receptor; 88.  
XX  
OS Synthetic.  
XX  
PN WO2004030695-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 06-OCT-2003; 2003WO-GB004335.  
XX  
PR 04-OCT-2002; 2002GB-00023077.  
XX  
PA (UYRE-) UNIV READING.  
XX  
PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;  
XX  
XX WPI; 2004-330076/30.  
XX  
XX  
XX Use of tachykinin antagonist or agonist for treating diseases mediated by  
XX binding of tachykinin ligand to its platelet associated receptor and  
XX failure of platelet having tachykinin receptor to aggregate normally in  
XX presence of tachykinin.  
XX  
XX Disclosure; Page 21; 46pp; English.  
XX  
XX The invention relates to the use of a tachykinin antagonist in the

CC manufacture of a medicament for treating e.g. a disease mediated by  
CC binding of a tachykinin ligand to its platelet associated receptor. A  
CC method of identifying an antagonist or agonist of tachykinin having a  
CC platelet associated tachykinin receptor involves contacting a compound to  
CC be evaluated with platelets expressing the tachykinin receptor in the  
CC presence of the tachykinin and monitoring for an increase or decrease of  
CC platelet aggregation. The agonist is useful in the manufacture of a  
CC medicament in bulk quantities for treating a disease or conditions  
CC mediated by binding of a tachykinin ligand to its platelet-associated  
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of  
CC platelet having a tachykinin receptor to aggregate normally in the  
CC presence of the tachykinin; antagonizing or stimulating the effect of  
CC tachykinin on platelet associated tachykinin receptors; and stimulating  
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193  
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and  
CC NK3.  
XX  
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 1.5%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DY 213 GGATACGTCCTCCCGGTGACTCAGA 239  
DB 1 GGATACGTCCTCCCGGTGACTCAGA 27  
RESULT 5  
ADN12182/c  
XX ADN12182 standard; DNA, 27 BP.  
XX  
AC ADN12182;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Tachykinin receptor NK1 amplifying primer NK15'.  
XX  
XX Tachykinin; vascular disease; platelet aggregation; vulnery;  
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;  
KM NK3; tachykinin receptor; 88.  
XX  
OS Synthetic.  
XX  
PN WO2004030695-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 06-OCT-2003; 2003WO-GB004335.  
XX  
PR 04-OCT-2002; 2002GB-00023077.  
XX  
PA (UYRE-) UNIV READING.  
XX  
PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;  
XX  
XX WPI; 2004-330076/30.  
XX  
XX  
XX Use of tachykinin antagonist or agonist for treating diseases mediated by  
XX binding of tachykinin ligand to its platelet associated receptor and  
XX failure of platelet having tachykinin receptor to aggregate normally in  
XX presence of tachykinin.  
XX  
XX Disclosure; Page 21; 46pp; English.  
XX  
XX  
XX The invention relates to the use of a tachykinin antagonist in the  
XX manufacture of a medicament for treating e.g. a disease mediated by  
XX binding of a tachykinin ligand to its platelet associated receptor. A  
XX method of identifying an antagonist or agonist of tachykinin having a  
XX platelet associated tachykinin receptor involves contacting a compound to  
XX be evaluated with platelets expressing the tachykinin receptor in the  
XX presence of the tachykinin and monitoring for an increase or decrease of  
XX platelet aggregation. The agonist is useful in the manufacture of a

CC medicament in bulk quantities for treating a disease or conditions  
CC mediated by binding of a tachykinin ligand to its platelet-associated  
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of  
CC platelet having a tachykinin receptor to aggregate normally in the  
CC presence of the tachykinin; antagonizing or stimulating the effect of  
CC tachykinin on platelet associated tachykinin receptor; and stimulating  
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193  
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and  
CC NK3.  
XX  
SQ Sequence 27 BP; 3 A; 4 C; 11 G; 9 T; 0 U; 0 Other;  
Query Match 1.5%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 711 CTACTCAACCAAGACCATGCCAG 737  
Db 27 CTACTCAACCAAGACCATGCCAG 1  
RESULT 6  
AED31524/c  
ID AED31524 standard; DNA; 27 BP.  
XX  
AC AED31524;  
XX  
DT 15-DEC-2005 (first entry)  
XX  
DE Gerbil neurokinin 1 receptor (GNK1r) PCR primer SEQ ID NO:4.  
XX  
XX ss; gerbil neurokinin 1 receptor; GNK1r; schizophrenia; neuroleptic;  
KW psychiatric disorder; micturition disorder; uropathic;  
KW genitourinary disease; asthma; antiasthmatic; immune disorder;  
KW inflammation; respiratory disease; pain; analgesic; neurological disease;  
KW major depressive disorder; antidepressant; anxiety disorder;  
KW tranquilizer; emesis; antiemetic; gastrointestinal disease;  
KW inflammatory bowel disease; antiinflammatory; gastrointestinal gen.;  
KW gastrointestinal disease; irritable bowel syndrome; dyspepsia; migraine;  
KW antimigraine; primer; PCR.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Synthetic.  
XX  
XX WO2005090401-A1.  
XX  
XX 29-SEP-2005.  
XX  
XX 16-MAR-2005; 2005WO-GB001008.  
XX  
XX 20-MAR-2004; 2004GB-00006342.  
XX  
XX (ASTR ) ASTRAZENECA AB.  
XX (ASTR ) ASTRAZENECA UK LTD.  
XX  
XX Drmotca T, Engberg S, Von Mentzer B;  
XX  
XX WPI; 2005-702670/72.  
XX  
XX New polynucleotide comprising a sequence encoding gerbil neurokinin 1  
XX receptor (GNK1r) polypeptide, useful in preparing a composition for  
XX treating e.g., asthma, pain, depression, emesis, urine incontinence or  
XX schizophrenia.  
XX  
XX Example 1; SEQ ID NO 4; 37bp; English.  
XX  
XX The invention relates to a new isolated polynucleotide molecule  
XX comprising a nucleic acid sequence which encodes gerbil neurokinin 1  
XX receptor (GNK1r) polypeptide or a polypeptide having at least 98%  
XX sequence identity with AED31522. Also included are the following: an  
XX expression vector comprising the polynucleotide molecule; a host cell

CC transformed or transfected with the expression vector; a method for  
CC producing a polypeptide; an isolated or purified polypeptide comprising  
CC the GNK1r amino acid sequence (see AED31522) or its variant having at  
CC least 98% identity to the sequence, or its N-terminal or C-terminal  
CC fragment of at least 350 amino acids in length; a method for identifying  
CC a chemical compound capable of modulating the activity of GNK1r; a method  
CC for identifying a therapeutic agent capable of modulating the activity of  
CC GNK1r; a method of making a pharmaceutical composition; and a  
CC pharmaceutical composition comprising a GNK1r modulator, or its salt in  
CC association with a diluent or carrier. The polynucleotide is useful in  
CC preparing a composition for treating asthma, pain, depression, anxiety,  
CC emesis, inflammatory bowel disease, irritable bowel syndrome, functional  
CC dyspepsia, migraine, urine incontinence or schizophrenia. The present  
CC sequence represents a PCR primer based on conserved regions identified by  
CC alignment of human, mouse and rat NK1r sequences and used to clone gerbil  
CC neurokinin 1 receptor (GNK1r) cDNA.  
XX  
SQ Sequence 27 BP; 8 A; 8 C; 10 G; 1 T; 0 U; 0 Other;  
Query Match 1.5%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 669 CATCTGGGTCCTGCTCTCTCTCTGCTGAC 695  
Db 27 CATCTGGGTCCTGCTCTCTCTCTGCTGAC 1  
RESULT 7  
ABS61087/c  
ID ABS61087 standard; DNA; 27 BP.  
XX  
AC ABS61087;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
XX Human automated genomic bit analysis (GBA) PCR primer #64.  
XX  
XX Human; ss; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;  
KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; CINH;  
KW kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KW polypeptidase; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
KW autoimmune disease; inflammatory arthritis; cancer; genotyping;  
KW viral infection; bacterial infection; fungal infection; COPD; GBA;  
KW Chronic obstructive pulmonary disease; enterocolitis;  
KW automated genetic bit analysis.  
XX  
XX Homo sapiens.  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 03-DEC-2001; 2001WO-US047235.  
XX  
XX 04-DEC-2000; 2000US-0251015P.  
XX 23-JAN-2001; 2001US-0263678P.  
XX 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX (TSUC/) TSUCHIHASHI Z.  
XX (HUTL/) HUT L.  
XX  
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX Swanson BN, Powell JR,  
XX WPI; 2002-619265/66.  
XX

PT New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.

XX Example 3; Page 932; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is a genotyping PCR primer  
CC for the gene encoding one of the proteins listed above, using the method  
CC of automated genetic bit analysis, GBA

XX Sequence 27 BP; 6 A; 10 C; 3 G; 7 T; 0 U; 1 Other;

Query Match 1.5%; Score 26; DB 1; Length 27;  
Best Local Similarity 96.3%; Pred. No. 12;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1539 GGACTTGCAAAAAGGTCAGTATGGGT 1565

Db 27 GGACTTGCAAAAAGGTCAGTATGGGT 1

RESULT 8  
ADN12193/c  
ID ADN12193 standard; DNA; 30 BP.

AC ADN12193;

XX 01-JUL-2004 (first entry)

XX Tachykinin receptor NK3 amplifying primer NK3' (nested).

XX Tachykinin; vascular disease; platelet aggregation; vulnary;

KW thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;

XX NK3; NK3; tachykinin receptor; ss.

OS Synthetic.

XX WO2004030695-A1.

XX 15-APR-2004.

XX 06-OCT-2003; 2003WO-GB004335.

XX 04-OCT-2002; 2002GB-00023077.

XX (UTRE-) UNIV READING.

XX Gibbins JM, Lowry PJ, Graham GJ, Page NM;

DR WPI; 2004-330076/30.

PT Use of tachykinin antagonist or agonist for treating diseases mediated by  
PT binding of tachykinin ligand to its platelet associated receptor and  
PT failure of platelet having tachykinin receptor to aggregate normally in  
PT presence of tachykinin.

PS Disclosure; Page 21; 46pp; English.

XX The invention relates to the use of a tachykinin antagonist in the  
CC manufacture of a medicament for treating e.g. a disease mediated by  
CC binding of a tachykinin ligand to its platelet associated receptor. A  
CC method of identifying an antagonist or agonist of tachykinin having a  
CC platelet associated tachykinin receptor involves contacting a compound to  
CC be evaluated with platelets expressing the tachykinin receptor in the  
CC presence of the tachykinin and monitoring for an increase or decrease of  
CC platelet aggregation. The agonist is useful in the manufacture of a  
CC medicament in bulk quantities for treating a disease or conditions  
CC mediated by binding of a tachykinin ligand to its platelet-associated  
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of  
CC platelet having a tachykinin receptor to aggregate normally in the  
CC presence of the tachykinin; antagonizing or stimulating the effect of  
CC tachykinin on platelet associated tachykinin receptor; and stimulating  
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193  
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and  
CC NK3.

XX Sequence 30 BP; 7 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 25.8; DB 1; Length 30;  
Best Local Similarity 93.1%; Pred. No. 17;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 556 GTCTTCGCCAGTATCTCACTGACGCGC 584

Db 30 GTCTTCGCCAGTATCTCACTGACGCGC 2

RESULT 9  
AAH26071  
ID AAH26071 standard; DNA; 25 BP.

AC AAH26071;

XX 05-SEP-2001 (first entry)

XX Human NK-1 gene antisense PCR primer.

XX NK-1; neurokinin receptor; PPT-1; human; preprotachykinin; cytostatic;  
KW analgesic; antiarthritic; antiasthmatic; antidepressant; breast cancer;  
KW metastasis; pain; arthritis; aggression; depression;  
KW haematopoietic disorder; gene therapy; PCR primer; ss.

XX Homo sapiens.

XX WO200146399-A1.

XX 28-JUN-2001.

XX 23-DEC-2000; 2000WO-US035047.

XX 23-DEC-1999; 99US-0171970P.



XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
PA Rameshwar P, Gascon P;  
PI WPI; 2001-408640/43.  
XX  
DR Novel promoters and 3' regulatory region of preprotrachykinin gene, useful  
XX for treating pain, asthma, arthritis, aggressive behavior, depression,  
PT bone marrow metastasis, and hematopoietic disorders.  
XX  
PS Example; Page 35; 78pp; English.  
XX The present sequence is that of the antisense primer used in the PCR  
CC amplification of a fragment of the human neurokinin NK-1 receptor gene.  
CC The sense primer is given in AAH26070. Quantitative PCR was performed on  
CC total RNA extracted from breast cancer cells. The results showed that NK-  
CC 1 expression is up-regulated in breast cancers. Agonists and antagonists  
CC that influence expression of NK-1 can be used for the treatment of breast  
CC cancer, bone marrow metastasis, pain, asthma, arthritis, aggressive  
CC behaviour and depression associated with NK-1 imbalance  
CC  
CC  
SQ Sequence 25 BP; 7 A; 4 C; 7 G; 7 T; 0 U; 0 Other;  
Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 400 AGGACAGTGCAGCACTATTCTTCTGG 424  
DB 1 AGGACAGTGCAGCACTATTCTTCTGG 25  
RESULT 10  
AAH26070/c  
ID AAH26070 standard; DNA; 25 BP.  
XX  
XX AAH26070;  
AC  
XX  
DT 05-SRP-2001 (first entry)  
XX  
XX Human NK-1 gene sense PCR primer.  
DE  
XX NK-1; neurokinin receptor; PPT-1; human; preprotrachykinin; cytostatic;  
KW analgesic; antiarthritic; antiasthmatic; antidepressant; breast cancer;  
KW metastasis; pain; arthritis; aggression; depression;  
KW haematopoietic disorder; gene therapy; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200146399-A1.  
XX  
XX 28-JUN-2001.  
PD  
XX 23-DEC-2000; 2000WO-US035047.  
PF  
XX 23-DEC-1999; 99US-0171970P.  
PR  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
PA  
XX Rameshwar P, Gascon P;  
PI  
XX WPI; 2001-408640/43.  
DR  
XX Novel promoters and 3' regulatory region of preprotrachykinin gene, useful  
PT for treating pain, asthma, arthritis, aggressive behavior, depression,  
PT bone marrow metastasis, and hematopoietic disorders.  
XX  
XX Example; Page 35; 78pp; English.  
XX The present sequence is that of the sense primer used in the PCR  
CC amplification of a fragment of the human neurokinin NK-1 receptor gene.  
CC The antisense primer is given in AAH26071. Quantitative PCR was performed

CC on total RNA extracted from breast cancer cells. The results showed that  
CC NK-1 expression is up-regulated in breast cancers. Agonists and  
CC antagonists that influence expression of NK-1 can be used for the  
CC treatment of breast cancer, bone marrow metastasis, pain, asthma,  
CC arthritis, aggressive behaviour and depression associated with NK-1  
CC imbalance  
CC  
CC  
SQ Sequence 25 BP; 6 A; 5 C; 6 G; 8 T; 0 U; 0 Other;  
Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1041 CTACTGGAAGAACTTTATCCAGCAG 1065  
DB 25 CTACTGGAAGAACTTTATCCAGCAG 1  
RESULT 11  
ABS60907/c  
ID ABS60907 standard; DNA; 25 BP.  
XX  
XX ABS60907;  
AC  
XX  
DT 05-NOV-2002 (first entry)  
XX  
XX Human genotyping PCR primer #60.  
DE  
XX  
XX Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;  
KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
KW viral infection; bacterial infection; fungal infection; COPD;  
KW Chronic obstructive pulmonary disease; enterocolitis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
PD  
XX  
XX 03-DEC-2001; 2001WO-US047235.  
PF  
XX  
XX 04-DEC-2000; 2000US-0251015P.  
PR  
XX 23-JAN-2001; 2001US-0263678P.  
PR  
XX 02-MAR-2001; 2001US-0273037P.  
PR  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA  
XX (TSUC/) TSUCHIHASHI Z.  
PA  
XX (HUTL/) HUT L.  
XX  
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR;  
XX  
XX WPI; 2002-619265/66.  
DR  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX Example 3; Page 898; 977pp; English.  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme



2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a nucleotide polymorphism comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasoepitope inhibitor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hyperextension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hyperextension, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence is a genotyping PCR primer for the gene encoding one of the proteins listed above

Sequence 25 BP; 4 A; 3 C; 9 G; 9 T; 0 U; 0 Other;  
Query Match 1.4%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

707 GCTACTACTCAACCAAGACCAT 731  
Db 25 GCTACTACTCAACCAAGACCAT 1

RESULT 12  
ABS61082/c  
ID ABS61082 standard; DNA; 25 BP.

AC ABS61082;

XX 05-NOV-2002 (first entry)

DE Human automated genomic bit analysis (GBA) PCR primer #59.

XX Human; ss; antipeptidase P; XPNRP2; bradykinin receptor B1; primer;  
KM BDKRB1; tachykinin receptor B1; TRACR1; Cl esterase inhibitor; C1NH;  
KM kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KM cardiovascular disease; angina pectoris; hyperextension; heart failure;  
KM myocardial infarction; ventricular hypertrophy; vascular disease;  
KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
KM arteriosclerosis; atherosclerosis; hyperextension; sepsis; PCR;  
KM autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
KM viral infection; bacterial infection; fungal infection; COPD; GBA;  
KM Chronic obstructive pulmonary disease; enterocolitis;  
KM automated genetic bit analysis.

XX Homo sapiens.  
XX OS  
XX WO200261131-A2.  
XX PD 08-AUG-2002.

XX 03-DEC-2001, 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.  
XX 23-JAN-2001; 2001US-0263678P.  
XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.  
XX (TSUC/) TSUCHIHASHI Z.  
XX (HUI/L) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX Swanson BN, Powell JR;  
XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful  
XX for detecting, diagnosing and treating disorders such as angioedema,  
XX cancer, viral, bacterial or fungal infection, cardiovascular and  
XX autoimmune diseases.

XX Example 3; Page 931; 977p; English.

XX The invention relates to an isolated nucleic acid from a human gene  
XX encoding antipeptidase P (XPNRP2), bradykinin receptor B1 (BDKRB1),  
XX tachykinin receptor B1 (TRACR1), Cl esterase inhibitor (C1NH), kallikrein  
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
XX polymorphic position. Also included are (1) a probe that hybridises to a  
XX nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
XX obtaining the sample from one or more individuals and determining the  
XX nucleic acid sequence at one or more polymorphic positions in a gene  
XX encoding a protein selected from the group above; (3) constructing (M2)  
XX haplotypes using the genes comprising grouping at least two nucleic acids  
XX; (4) identifying (M3) an individual at risk of developing a disorder  
XX upon administration of an ACE inhibitor and/or vasoepitope inhibitor  
XX using the polymorphic data; (5) a library of nucleic acids, each of which  
XX comprises one or more polymorphic positions within a gene encoding a  
XX human protein selected from the group above; and (6) genotyping (M4) an  
XX individual comprising obtaining a nucleic acid sample, determining the  
XX nucleotide present in at least one polymorphic position, and comparing at  
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)  
XX and compositions are useful for detecting, diagnosing, treating,  
XX preventing various disorders such as angioedema and diseases which  
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
XX disease, trachomas, and cardiovascular diseases like angina pectoris,  
XX hypertension, heart failure, myocardial infarction, ventricular  
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
XX artery disease, arteriosclerosis and/or atherosclerosis, and  
XX hyperextension, cancer, wounds, viral, bacterial or fungal infection, Chronic  
XX obstructive pulmonary disease (COPD) and enterocolitis (many other  
XX diseases and disorders are listed in the specification). The  
XX polynucleotides are also useful for chromosome identification. Antibodies  
XX against the proteins may be utilised for immunophenotyping of cell lines  
XX and biological samples. The present sequence is a genotyping PCR primer  
XX for the gene encoding one of the proteins listed above, using the method  
XX of automated genetic bit analysis, GBA

XX Sequence 25 BP; 6 A; 5 C; 11 G; 3 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 25; DB 1; Length 25;  
XX Best Local Similarity 100.0%; Pred. No. 14;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 544 CCCATGCGCGCTGCTTCCGACGTA 568  
XX Db 25 CCCATGCGCGCTGCTTCCGACGTA 1

RESULT 13



SO Sequence 24 BP; 9 A; 3 C; 9 G; 3 T; 0 U; 0 Other;  
Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1411 TTCTCCCAATGTCCTCTCTAG 1434  
Db 24 TTCTCCCAATGTCCTCTCTAG 1  
RESULT 15  
AED51264  
ID AED51264 standard; DNA; 24 BP.  
XX AED51264;  
AC  
XX  
XX  
DT 29-DEC-2005 (first entry)  
XX  
XX Human tachykinin receptor 1 (TACR1) cDNA probe.  
DE  
XX Screening; diagnosis; tachykinin receptor 1; TACR1;  
KW cardiovascular disease; infection; dermatological disease;  
KW gastrointestinal disease; cancer; neoplasm; inflammation;  
KW metabolic disorder; hematological disease; respiratory disease;  
KW musculoskeletal disease; neurological disease; gynecological disorder;  
KW gynecology and obstetrics; genitourinary disease; cardiovascular disorder;  
KW cardiant; hypotensive; antimicrobial; antibacterial; fungicide; virucide;  
KW dermatological; antiparasitic; gastrointestinal-gen.; antineoplastic;  
KW cytotoxic; immunosuppressive; anorectic; antidiabetic; antianemic;  
KW respiratory-gen.; asthmatic; muscular-gen.; osteopathic;  
KW antiarthritic; neuroprotective; nootropic; antiparkinsonian;  
KW gynecological; antifertility; nephrotropic; metabolic; uropathic;  
KW probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX W02005100986-A1.  
PN  
XX 27-OCT-2005.  
PD  
XX 02-APR-2005; 2005WO-EP003465.  
PF  
XX 15-APR-2004; 2004EP-00008923.  
PR  
XX (FARB ) BAYER HEALTHCARE AG.  
PA  
XX Golz S, Brueggemeier U, Geerts A;  
PI  
XX WPI; 2005-758663/77.  
DR  
XX Screening for therapeutic agents, useful for treating a disease, e.g.  
PT cardiovascular, infections, dermatological, cancer, inflammation,  
PT respiratory, or neurological, comprises contacting a test compound with a  
PT tachykinin receptor 1.  
XX  
XX Example 2; SEQ ID NO 5; 118bp; English.  
PS  
XX The invention relates to a method of screening for therapeutic agents  
CC useful for treating a disease, comprising contacting a test compound with  
CC a tachykinin receptor 1 (TACR1) polypeptide or polynucleotide, detecting  
CC binding of the polypeptide or polynucleotide, determining the activity of  
CC TACR1 at a certain concentration of the test compound, in the absence of  
CC the compound or in the presence of a known regulator of the TACR1  
CC polypeptide. The invention also relates to a method of diagnosing a  
CC disease in a mammal comprising determining the amount of a TACR1  
CC polynucleotide in a sample taken from the mammal and determining the  
CC amount of TACR1 polynucleotide in healthy and/or diseased mammals, a  
CC pharmaceutical composition for treating diseases in a mammal comprising a  
CC TACR1 polynucleotide or polypeptide or a therapeutic agent which binds to  
CC or regulates the activity of a TACR1 polypeptide, and preparing a  
CC pharmaceutical composition useful for treating diseases in a mammal. The  
CC disease is chosen from cardiovascular diseases, infections,

CC dermatological diseases, gastrointestinal diseases, cancer, inflammation,  
CC metabolic disorders, hematological diseases, respiratory diseases,  
CC musculoskeletal diseases, neurological diseases, gynecological disorders  
CC and genitourinary diseases. This sequence represents a probe used in  
CC expression profiling of the human TACR1 cDNA of the invention. The probe  
CC is labeled with FAM (carboxyfluorescein succinimidyl ester) as a reporter  
CC dye and TAMRA (carboxytetramethylrhodamine) as a quencher.  
XX  
SO Sequence 24 BP; 4 A; 6 C; 7 G; 7 T; 0 U; 0 Other;  
Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 296 CTTGGCAATTGTCCTTTGGGCGAG 319  
Db 1 CTTGGCAATTGTCCTTTGGGCGAG 24  
RESULT 16  
ABS61086  
ID ABS61086 standard; DNA; 27 BP.  
XX  
AC ABS61086;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
XX Human automated genomic bit analysis (GBA) PCR primer #63.  
DE  
XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;  
KW kallikrein 1; KUK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
KW viral infection; bacterial infection; fungal infection; COPD; GBA;  
KW Chronic obstructive pulmonary disease; enterocolitis;  
KW automated genetic bit analysis.  
XX  
XX Homo sapiens.  
OS  
XX W0200261131-A2.  
PN  
XX 08-AUG-2002.  
PD  
XX 03-DEC-2001; 2001WO-US047235.  
PF  
XX 04-DEC-2000; 2000US-0251015P.  
PR 23-JAN-2001; 2001US-0263678P.  
PR 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUI/) HUI L.  
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR.  
XX WPI; 2002-619265/66.  
DR  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX Example 3; Page 932; 977bp; English.  
PS  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),

CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KAL1), bradykinin receptor B2 (BKR2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is a genotyping PCR primer  
 CC for the gene encoding one of the proteins listed above, using the method  
 CC of automated genetic bit analysis, GBA

XX  
 XX Sequence 27 BP; 3 A; 8 C; 3 G; 10 T; 0 U; 3 Other;

Query Match 1.4%; Score 24; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 24;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1608 TCCCATCTTTGGCACCCCTCAGCTGT 1634  
 DB 1 TCCCATCTTTGCMACCTNATGCTGT 27

RESULT 17  
 AAT36738/c  
 ID AAT36738 standard; DNA; 29 BP.

AC AAT36738;  
 XX  
 XX  
 DT 15-OCT-1996 (first entry)

DE G-protein conjugate receptor protein cDNA degenerate PCR primer.

XX G-protein; conjugate receptor; drug; development; antibody;  
 KW ligand determination; antiserum; production; construction;  
 KW expression system; screening; receptor binding assay system;  
 KW drug candidate screening; drug design; probe; primer; preparation;  
 KW genetic analysis; gene therapy; PCR; polymerase chain reaction;  
 KW degenerate; ss.

XX Synthetic.  
 OS

XX JP08154682-A.  
 PN

XX 18-JUN-1996.  
 PD

XX 02-DEC-1994; 94JP-00299792.  
 PF

XX 02-DEC-1994; 94JP-00299792.  
 PR

XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 XX WPI; 1996-336572/34.  
 DR

XX G protein conjugate receptor protein - useful in ligand determination,  
 PT antibody prodn., drug screening and design and receptor binding assay  
 PT system development.  
 PT

PS Example 1; Page 22; 23pp; Japanese.

XX The present sequence is a degenerate PCR primer for a G-protein conjugate  
 CC receptor (GPCR) protein, cDNA, structure elucidation of which may lead to  
 CC the development of unique drugs. The GPCR protein and its cDNA can be  
 CC used in ligand determination, antibody and antiserum prodn., recombinant  
 CC receptor protein expression system construction (which can be used in  
 CC receptor binding assay system development), drug candidate screening,  
 CC drug design based on comparisons among structurally similar ligand  
 CC receptors and probe and PCR primer prepn., for use in genetic analysis  
 CC and gene therapy

XX Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;

Query Match 1.4%; Score 24; DB 1; Length 29;  
 Best Local Similarity 72.4%; Pred. No. 29;  
 Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCGCTGCCCTTCCACAT 1007  
 DB 29 TTCCRYSMTCGTGCTGCTGCCCTTCCAT 1

RESULT 18  
 AAV02408/c  
 ID AAV02408 standard; DNA; 29 BP.

AC AAV02408;  
 XX

DT 06-APR-1998 (first entry)

DE Mouse MINE-derived G protein-coupled receptor PCR primer 2.

KW G-protein-coupled receptor; ligand binding; pharmaceutical; modulator;  
 KW pituitary; central nervous system; pancreas; prophylactic;  
 KW therapeutic agent; PCR primer; ss.

OS Synthetic.  
 OS Mus sp.

XX Key Location/Qualifiers  
 FH modified\_base 23 /tag= a  
 FT /mod\_base= i  
 FT /note= "inositol"

PN WO9724436-A2.

XX 10-JUL-1997.

PD 26-DEC-1996; 96WO-JP003821.

XX 28-DEC-1995; 95JP-00343371.

PR 15-MAR-1996; 96JP-00059419.

PR 12-AUG-1996; 96JP-00211805.

PR 18-SEP-1996; 96JP-00246573.

PA (TAKE ) TAKEDA CHEM IND LTD.

XX Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;

XX Kitada C;  
 DR WPI; 1997-363672/33.

PT Ligand peptide for G protein-coupled receptor - acts by modulating  
PT function in the central nervous system, pancreas and pituitary gland.  
XX  
PS Example 4, Page 104, 258pp; English.  
XX  
CC AAV02408 and AAV02407 are PCR primers used to amplify a region of the G  
CC protein-coupled receptor from mouse pancreatic beta-cell strain MIN6. The  
CC resulting fragment is used in an assay to monitor ligand binding to  
CC receptor proteins. Pharmaceutical compositions containing such ligands  
CC may be used as a pituitary function modulator, a central nervous system  
CC modulator or a pancreatic function modulator. These ligands could have  
CC specific applications as a prophylactic or therapeutic agent for  
CC dementia, depression, hyperkinetic syndrome, disturbance of  
CC consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone  
CC secretory disease, hyper- and polyphagia, hypercholesterolaemia,  
CC hyperglycaemia, hyperlipidaemia, hyperprolactinaemia, diabetes,  
CC cancer, pancreatitis, renal disease, Turner's syndrome, neurosis,  
CC rheumatoid arthritis, spinal injury, transient brain ischaemia, asthma,  
CC amyotrophic lateral sclerosis, acute myocardial infarction, epilepsy,  
CC spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,  
CC osteoporosis, infertility and/or oligosaccharia. Assays can also be  
CC developed to screen compounds which are capable of altering the binding  
CC activity of the ligand thus affecting activation of the G protein-coupled  
CC receptor protein  
XX  
SQ Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 29;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCCCTTCCACAT 1007  
|||:::|||||:|||||:|:|  
Db 29 TTCRYSNCTGCTGCTGCCCTTCCACAT 1

RESULT 19  
AAV81238/C  
ID AAV81238 standard; DNA; 29 BP.  
XX  
AC AAV81238;  
XX  
DT 10-MAR-1999 (first entry)  
XX  
DE Mouse MIN6-derived G-protein coupled receptor cDNA amplifying primer.  
XX  
KM Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;  
KM GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;  
KM tissue; screen; therapeutic; binding; senile dementia; ligand; murine;  
KM Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;  
KM Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;  
KM secretion; diabetes; cancer; Rheumatoid arthritis; epilepsy; vasopressor;  
KM gene therapy; transgenic animal; mouse; PCR primer; ss.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
PN WO9849295-A1.  
XX  
PD 05-NOV-1998.  
XX  
PE 27-APR-1998; 98WO-JP001923.  
XX  
PR 28-APR-1997; 97JP-00109974.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Hinuma S, Fukusumi S;  
XX  
XX WPI; 1999-009423/01.  
XX  
PT New polypeptide ligand for orphan G protein coupled receptors - used for  
PT treating disorders of central nervous system, pituitary and pancreas, and

PT for drug screening.  
XX  
PS Example 4, Page 98, 206pp; English.  
XX  
CC The invention relates to a murine pituitary-derived ligand polypeptide  
CC which is a ligand for the G-protein coupled orphan receptor designated  
CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing  
CC the ligand polypeptide encoding DNA are used to produce a recombinant  
CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate  
CC function of the pituitary, central nervous system, pancreas and other  
CC tissues and can be used to screen for agents that modulate binding of the  
CC polypeptide to the receptor; to quantify the amount of receptor in a  
CC sample and to raise antibodies. They may also be used therapeutically,  
CC e.g. to treat senile dementia, Alzheimer's, Parkinson's or Huntington's  
CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;  
CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;  
CC rheumatoid arthritis, epilepsy and many others, also to improve post-  
CC operative nutritional status and as vasopressor. Transgenic animals  
CC carrying the ligand polypeptide encoding DNA or its mutin are used to  
CC study the function of the polypeptide-expressing genes, as models of  
CC disease, for drug screening and as source of cell lines. The ligand  
CC polypeptide DNA is used as a source of probes and primers; to identify  
CC related sequences; in receptor-binding assays; for production of Ab and  
CC antisera; in drug development; for gene therapy and to develop transgenic  
CC animals. Primers AAV81237-238 are used for the PCR amplification of the  
CC cDNA encoding a mouse MIN6-derived G-protein coupled receptor protein  
XX  
SQ Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 29;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCCCTTCCACAT 1007  
|||:::|||||:|||||:|:|  
Db 29 TTCRYSNCTGCTGCTGCCCTTCCACAT 1

RESULT 20  
AAK15513/C  
ID AAK15513 standard; DNA; 29 BP.  
XX  
AC AAK15513;  
XX  
DT 06-MAY-1999 (first entry)  
XX  
DE PCR primer used to amplify cDNA encoding a G protein-coupled receptor.  
XX  
KM G protein-coupled receptor; GPCR; hypovarianism; gonocyte carcinoma;  
KM menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;  
KM pituitary adenomatosis; brain tumour; emmenorrhoea; autoimmune disease;  
KM prolactinoma; infertility; impotence; amenorrhoea; galactorrhoea;  
KM acromegaly; Chiari-Frommel syndrome; Argonza-del Castillo syndrome;  
KM Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;  
KM contraceptive; placental function; chorioncarcinoma; hydatid mole;  
KM abortion; unthrifty fetus; abnormal saccharometabolism;  
KM abnormal lipidmetabolism; oxytocia; prolactin secretion; PCR primer; ss.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
PN WO9858962-A1.  
XX  
PD 30-DEC-1998.  
XX  
PE 22-JUN-1998; 98WO-JP002765.  
XX  
PR  
XX  
PA  
XX  
PI  
XX  
XX WPI; 1999-009423/01.  
XX  
PT New polypeptide ligand for orphan G protein coupled receptors - used for  
PT treating disorders of central nervous system, pituitary and pancreas, and

PR 23-JUN-1997; 97JP-00165437.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 XX  
 PI Hinuma S, Kawamata Y, Fujii R, Matsumoto H;  
 XX WPI; 1999-105614/09.  
 DR  
 XX Use of G protein-coupled receptor ligands - for modulating prolactin  
 PT secretion or placental function, e.g. for treating menopausal syndrome,  
 PT tumours, autoimmune disease or abnormal pregnancy.  
 PT  
 XX Example 4; Page 74; 241pp; English.  
 PS  
 XX PCR primers AAX15512-13 were used to amplify cDNA encoding a G protein-  
 CC coupled receptor protein. The specification describes an agent for  
 CC modulating prolactin secretion which comprises a ligand polypeptide or a  
 CC salt, for a G protein-coupled receptor (GPCR) protein. The agents for  
 CC promoting prolactin secretion can be used for treating or preventing  
 CC hypovarianism, gonocyte carcinogenesis, menopausal syndrome, euthyroid or  
 CC mammal and as an aphrodisiac. The agents for inhibiting prolactin  
 CC secretion can be used for treating or preventing pituitary adenomatosis,  
 CC brain tumour, emmenorrhoea, amenorrhoea, galactorrhea, acromegaly, Chiari-  
 CC infertility, impotence, menorrhoea, galactosia, acromegaly, Chiari-  
 CC lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can  
 CC also be used as contraceptives. The agents for modulating placental  
 CC function can be used for treating or preventing chorionicarcoma, hydatid  
 CC mole, irruption mole, abortion, unfertilized fetus, abnormal  
 CC saccharometabolism, abnormal lipidmetabolism or oxytocia  
 CC  
 XX Sequence 29 BP; 9 A; 4 C; 9 G; 0 T; 0 U; 7 Other;  
 SQ  
 Query Match 1.4%; Score 24; DB 1; Length 29;  
 Best Local Similarity 72.4%; Pred. No. 29;  
 Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 979 TTGGCATCTGCTGGCTGGCTTCCACAT 1007  
 Db 29 TTCTGATCTGCTGGCTGGCTTCCACAT 1  
 RESULT 21  
 ABS60997  
 ID ABS60997 standard; DNA; 24 BP.  
 XX  
 AC ABS60997;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human genotyping PCR primer #150.  
 XX  
 KW Human; ss; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;  
 KW BKRPB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;  
 KW Kallikrein 1; KKL1; bradykinin receptor B2; BKRPB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; heart failure;  
 KW cardiovascular disease; angina pectoris; hypertension; vascular disease;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease; angioedema;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic Obstructive Pulmonary disease; enterocolitis.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX WO200261131-A2.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 03-DEC-2001; 2001WO-US047235.  
 XX PF

XX 04-DEC-2000; 2000US-0251015P.  
 XX 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/L/) HUI L.  
 XX  
 XX Tsuchinashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone ME;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 PT  
 XX Example 3; Page 912; 977pp; English.  
 PS  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BKRPB1),  
 CC tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein  
 CC 1 (KKL1), bradykinin receptor B2 (BKRPB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC upon administration of an ACE inhibitor and/or vasopressin inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiotensin like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases, like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and the specification). The  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is a genotyping PCR primer  
 CC for the gene encoding one of the proteins listed above  
 XX  
 SQ Sequence 24 BP; 8 A; 7 C; 2 G; 6 T; 0 U; 1 Other;  
 Query Match 1.3%; Score 23.6; DB 1; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 21;  
 Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1631 CTGTGTGACTCAACCAACCAATCACT 1654  
 Db 1 CTGTGTGACTCAACCAACCAATCACT 24  
 RESULT 22  
 ABX95641/C  
 ID ABX95641 standard; DNA; 29 BP.  
 XX  
 XX





XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
 XX myocardial infarction; ventricular hypertrophy; vascular disease;  
 XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 XX autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 XX viral infection; bacterial infection; fungal infection; COPD;  
 XX Chronic obstructive pulmonary disease; enterocolitis.  
 XX Homo sapiens.  
 XX OS  
 XX PN W0200261131-A2.  
 XX FD 08-AUG-2002.  
 XX PF 03-DEC-2001; 2001WO-US047235.  
 XX PR 04-DEC-2000; 2000US-0251015P.  
 XX PR 23-JAN-2001; 2001US-0263678P.  
 XX PR 02-MAR-2001; 2001US-0273037P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PA (TSUC/) TSUCHIHASHI Z.  
 XX PA (HUIL/) HUI L.  
 XX PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 XX PI Swanson BN, Powell JR;  
 XX DR WPI; 2002-619265/66.  
 XX PT New isolated nucleic acid with at least one polymorphic position, useful  
 XX PT for detecting, diagnosing and treating disorders such as angioedema,  
 XX PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 XX PT autoimmune diseases.  
 XX PT  
 XX Example 3; Page 899; 977bp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 XX encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),  
 XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 XX 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
 XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 XX polymorphic position. Also included are (1) a probe that hybridises to a  
 XX polymorphic position as provided in the detailed summary of single  
 XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 XX obtaining the sample from one or more individuals and determining the  
 XX nucleic acid sequence at one or more polymorphic positions in a gene  
 XX encoding a protein selected from the group above; (3) constructing (M2)  
 XX haplotypes using the genes comprising grouping at least two nucleic acids  
 XX ; (4) identifying (M3) an individual at risk of developing a disorder  
 XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 XX using the polymorphic data; (5) a library of nucleic acids, each of which  
 XX comprises one or more polymorphic positions within a gene encoding a  
 XX human protein selected from the group above; and (6) genotyping (M4) an  
 XX individual comprising obtaining a nucleic acid sample, determining the  
 XX nucleotide present in at least one polymorphic position, and comparing at  
 XX least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 XX and compositions are useful for detecting, diagnosing, treating,  
 XX preventing various disorders such as angioedema and diseases which  
 XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 XX disease, trachoma, and cardiovascular diseases like angina pectoris,  
 XX hypertension, heart failure, myocardial infarction, ventricular  
 XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 XX artery disease, arteriosclerosis and/or atherosclerosis, and  
 XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 XX obstructive pulmonary disease (COPD) and enterocolitis (many other  
 XX diseases and disorders are listed in the specification). The  
 XX polynucleotides are also useful for chromosome identification. Antibodies  
 XX against the proteins may be utilised for immunophenotyping of cell lines  
 XX and biological samples. The present sequence is a genotyping PCR primer

CC for the gene encoding one of the proteins listed above  
 XX  
 XX Sequence 23 BP; 6 A; 5 C; 4 G; 8 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.3%; Score 23; DB 1; Length 23;  
 XX Best Local Similarity 100.0%; Pred. No. 23;  
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1675 AATAAAGGTGCGACCACTTTT 1697  
 XX ||||||||||||||||||||  
 XX Db 23 AATAAAGGTGCGACCACTTTT 1  
 XX  
 XX RESULT 25  
 XX AAQ30776/c  
 XX ID AAQ30776 standard; DNA; 24 BP.  
 XX  
 XX AC AAQ30776;  
 XX  
 XX DT 25-MAR-2003 (revised)  
 XX DT 22-MAR-1993 (first entry)  
 XX  
 XX PCR primer rspr7a2 to amplify human NK1R 5' core region.  
 XX  
 XX Neurokinin-1 receptor short form; arthritis; Substance P;  
 XX polymerase chain reaction; rat NK1R; ss.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN EP514207-A2.  
 XX  
 XX PD 19-NOV-1992.  
 XX  
 XX PF 15-MAY-1992; 92EP-00304432.  
 XX  
 XX PR 17-MAY-1991; 91US-00701930.  
 XX PR 17-MAY-1991; 91US-00701935.  
 XX PR 17-MAY-1991; 91US-00701937.  
 XX  
 XX PA (MERI ) MERCK & CO INC.  
 XX  
 XX PI Strader CD, Fong TM;  
 XX  
 XX DR WPI; 1992-384034/47.  
 XX  
 XX PT New human neurokinin-1 receptor short form protein - useful for  
 XX PT identifying and determining substance P antagonists in arthritic  
 XX PT patients.  
 XX  
 XX Example 1; Page 8; 36bp; English.  
 XX  
 XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1  
 XX and U87MG. First strand cDNA was synthesised and used as template with  
 XX rat primers rspr7a4, rspr7a4h and rspr7a2 (AAQ30774-6) in first round PCR  
 XX amplification. Secondary PCR was performed on the amplified product using  
 XX the same 3 primers prior to a third round of amplification, this time  
 XX using the primers rspr2a4, rspr2a4h, rspr7a1 (AAQ30777) and rspr7a1h  
 XX (AAQ30778). The tertiary PCR product was sequenced and was found to have  
 XX 90% identity at the nucleotide level with the central core region of the  
 XX rat NK1R from amino acid 91 to 280. Primer rspr7a2 is an antisense primer  
 XX based on the rat NK1R sequence 918-894 (numbering as in J.Biol.Chem. 264:  
 XX 17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX SQ Sequence 24 BP; 7 A; 2 C; 8 G; 7 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.3%; Score 23; DB 1; Length 24;  
 XX Best Local Similarity 100.0%; Pred. No. 26;  
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1105 ATGTACAAACCCATCATCTACTG 1127  
 XX ||||||||||||||||||||  
 XX Db 24 ATGTACAAACCCATCATCTACTG 2



RESULT 26  
ID ABK63862/c  
ABK63862 standard; DNA; 24 BP.  
AC ABK63862;  
XX 18-JUN-2002 (first entry)  
DT  
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #13.  
DE  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX MO300213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-IB001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
XX Henry JI, Cahill CM, Yaehpal K;  
XX WPI; 2002-241835/29.  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Claim 24; Page 20; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosia, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (e.g. chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative

disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 24 BP; 7 A; 2 C; 8 G; 7 T; 0 U; 0 Other;  
Query Match 1.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1105 ATGTACACCCCATCTACTCTG 1127  
DB 24 ATGTACACCCCATCTACTCTG 2  
RESULT 27  
ID AAQ30777/c  
AAQ30777 standard; DNA; 24 BP.  
XX  
XX AAQ30777;  
XX  
XX 25-MAR-2003 (revised)  
DT 22-MAR-1993 (first entry)  
XX  
XX PCR primer rspr7a1 to amplify human NK1R 5' core region.  
XX  
XX Neurokinin-1 receptor short form; arthritis; Substance P;  
KM polymerase chain reaction; rat NK1R; ss.  
XX  
XX Synthetic.  
XX  
XX BP514207-A2.  
XX  
XX 19-NOV-1992.  
XX  
XX 15-MAY-1992; 92EP-00304432.  
XX  
XX 17-MAY-1991; 91US-00701930.  
PR 17-MAY-1991; 91US-00701935.  
PR 17-MAY-1991; 91US-00701937.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Strader CD, Fong TM;  
XX WPI; 1992-384034/47.  
XX  
XX New human neurokinin-1 receptor short form protein - useful for  
PT identifying and determining substance P antagonists in arthritic  
PT patients.  
XX  
XX Example 1; Page 8; 36pp; English.  
XX  
XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1  
CC and U87MG. First strand cDNA was synthesised and used as template with  
CC rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR  
CC amplification. Secondary PCR was performed on the amplified product using  
CC the same 3 primers prior to a third round of amplification, this time  
CC using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h  
CC (AAQ30778). The tertiary PCR product was sequenced and was found to have  
CC 90% identity at the nucleotide level with the central core region of the  
CC rat NK1R from amino acid 91 to 280. Primer rspr7a1 is an antisense primer  
CC based on the rat NK1R sequence 864-841 (numbering as in J.Biol.Chem. 264:  
CC 17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 24 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 22.4; DB 1; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 32;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1051 AAGTTATCCAGCAGGTCTACTG 1074  
 24 AAGTTATCCAGCAGGTCTACTG 1

RESULT 28  
 ABS60912/c  
 ID ABS60912 standard; DNA; 22 BP.  
 XX  
 AC ABS60912;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human genotyping PCR primer #65.  
 XX  
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonde M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 PI  
 DR WPI; 2002-619265/66.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Example 3; Page 899; 977pp; English.  
 XX  
 OS The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wound, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is a genotyping PCR primer  
 CC for the gene encoding one of the proteins listed above

Sequence 22 BP; 3 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1373 CACGAAGTGACTCCAGACCAT 1394  
 22 CACGAAGTGACTCCAGACCAT 1

RESULT 29  
 ABS61083/c  
 ID ABS61083 standard; DNA; 22 BP.  
 XX  
 AC ABS61083;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human automated genomic bit analysis (GBA) PCR primer #60.  
 XX  
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 KW viral infection; bacterial infection; fungal infection; COPD; GBA;  
 KW Chronic obstructive pulmonary disease; enterocolitis;  
 KW automated genetic bit analysis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.  
PA (HUI/) HUI L.  
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR;  
XX WPI: 2002-619265/66.  
DR  
XX  
PT New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
PS Example 3: Page 931, 977pp; English.  
XX  
CC The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
CC 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridizes to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analyzing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polymorphisms are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilized for immunophenotyping of cell lines  
CC and biological samples. The present sequence is a genotyping PCR primer  
CC for the gene encoding one of the proteins listed above, using the method  
CC of automated genetic bit analysis, GBA  
XX  
SQ Sequence 22 BP; 7 A; 8 C; 7 G; 0 T; 0 U; 0 Other;  
OY Query Match 1.2%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 673 TGGGTCCTGGCTCTCTCTCTG 694  
DB 22 TGGGTCCTGGCTCTCTCTCTG 1

RESULT 30  
AAT18348/c  
ID AAT18348 standard; DNA; 27 BP.  
XX  
AC AAT18348;  
XX  
DT 26-AUG-1996 (first entry)  
XX  
DE G-protein coupled receptor protein DNA primer HS-2.

XX  
KM G-protein coupled receptor protein; G-PCR; agonist; antagonist;  
KM cystic fibrosis; incontinence; diabetes; diagnosis; gene therapy;  
KM transgenic animal; polymerase chain reaction; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN W09605302-A1.  
XX  
PD 22-FEB-1996.  
XX  
PF 10-AUG-1995; 95WO-JP001599.  
XX  
PR 11-AUG-1994; 94JP-00189272.  
PR 11-AUG-1994; 94JP-00189273.  
PR 11-AUG-1994; 94JP-00189274.  
PR 30-SEP-1994; 94JP-00236356.  
PR 30-SEP-1994; 94JP-00236357.  
PR 02-NOV-1994; 94JP-00270017.  
PR 28-DEC-1994; 94JP-00326611.  
PR 20-JAN-1995; 95JP-00007177.  
PR 16-MAR-1995; 95JP-00057186.  
PR 19-APR-1995; 95JP-00093989.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Hinuma S, Hosoya M, Fujii R, Ohtaki T, Fukusumi S, Ohgi K;  
PI WPI: 1996-139698/14.  
DR  
XX  
PT G-protein coupled receptor protein DNA and protein - also methods for  
PT isolating (ant) agonists for treatment of cystic fibrosis, incontinence  
PT and diabetes.  
XX  
PS Claim 1; Page 238; 360pp; English.  
XX  
CC PCR primer HS-2 (AAT18348) is complementary to DNA coding for a region  
CC corresponding to, or near, the sixth transmembrane domain of known G-  
CC protein coupled receptor proteins (G-PCRs). HS-2 and other primers (see  
CC also AAT18347 and AAT18349-65) based on G-PCR transmembrane domains are  
CC used for the PCR amplification of mammalian DNAs to obtain G-PCR-  
CC encoding sequences (see also AAT18366-73 and AAT13901-09)  
XX  
SQ Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;  
OY Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 54;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
OY 979 TTGGCCATCTGCTGCTGCTGCTTCCAC 1005  
DB 27 TTGGCCATCTGCTGCTGCTGCTTCCAC 1

RESULT 31  
AAT27220/c  
ID AAT27220 standard; cDNA; 27 BP.  
XX  
AC AAT27220;  
XX  
DT 29-OCT-1996 (first entry)  
XX  
DE Degenerate primer for G protein coupled receptor protein sequence.  
XX  
KM G protein coupled receptor protein; GCR; identification; detection;  
KM ligands; physiological response; arachidonic acid; acetylcholine;  
KM calcium; cyclic adenosine monophosphate; cAMP; inositol;  
KM membrane potential; phosphorylation; c-fos; antibodies;  
KM transgenic animals; ss.  
XX  
OS Synthetic.  
XX  
PN EP711831-A2.

```

XX 15-MAY-1996.
XX 11-NOV-1995; 95EP-00117786.
XX 14-NOV-1994; 94JP-00279545.
XX 24-AUG-1995; 95JP-00215798.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Hinuma S, Fujii R, Kawamata Y;
XX WPI; 1996-232096/24.
XX New isolated rabbit G protein receptor protein - used partic. to identify
XX agonists or antagonists which can promote or inhibit physiological
XX responses.
XX Disclosure; Page 27; 40pp; English.
XX G protein coupled receptor (GCR) proteins can be used to identify ligands
XX which act as antagonists of GCR/ligand binding. Such ligands can be used
XX for promoting or inhibiting physiological responses such as liberation of
XX arachidonic acid, acetylcholine and endocellular calcium, endocellular
XX cyclic AMP production, production of inositol, changes in cell membrane
XX potential, phosphorylation of endocellular proteins, activation of c-fos,
XX lowering of pH, activation of G protein and cell promulgation. The GCR
XX products can also be used for the detection of ligands and in the
XX production of antibodies and transgenic animals. Two degenerate primers
XX (AAT27219, AAT27220) were synthesised based on other receptor protein
XX coding sequences in an attempt to amplify the G protein coupled receptor.
XX The resulting amplified fragment was amplified from both sides by the
XX single primer described in AAT27219
SQ Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 979 TTGGCATTCTGCTGCTGCGCCCTTCAC 1005
DB 27 TTGGCCMTCTGCTGANTGCCCTTCAC 1
RESULT 32
AAT29438/c
ID AAT29438 standard; cDNA; 27 BP.
XX AAT29438;
XX 27-OCT-1996 (first entry)
XX Galanin receptor DNA primer.
XX Galanin receptor; stomach ulcer; antidiabetic; antidiabetic;
XX dementia; neuropeptide; sedative; Alzheimer's disease; obesity;
XX DNA primer; oligonucleotide; polymerase chain reaction; PCR; ss.
XX Synthetic.
XX EP711830-A2.
XX 15-MAY-1996.
XX 11-OCT-1995; 95EP-00115996.
XX 13-OCT-1994; 94JP-00247599.
XX 28-DEC-1994; 94JP-00326610.
XX 31-MAY-1995; 95JP-00134412.
XX (TAKE ) TAKEDA CHEM IND LTD.

```

```

PI Hinuma S, Fujii R, Fukusumi S, Ohtaki T, Hosoya M, Ohgi K;
PI Onda H;
XX WPI; 1996-232095/24.
XX Isolated galanin receptor proteins - used partic. to identify agonists or
XX antagonists, which can be used to treat, e.g. ulcers, diabetes or
XX dementia.
XX Disclosure; Page 35; 71pp; English.
XX This DNA primer is used for amplifying DNA coding for G protein coupled
XX receptor protein
CC Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
SQ Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 979 TTGGCATTCTGCTGCTGCGCCCTTCAC 1005
DB 27 TTGGCCMTCTGCTGANTGCCCTTCAC 1
RESULT 33
AAT98800/c
ID AAT98800 standard; cDNA; 27 BP.
XX AAT98800;
XX 19-MAR-1998 (first entry)
XX Primer #2 for G protein coupled receptor coding sequence.
XX G protein coupled receptor; amygdaloid nucleus-derived protein; amplify;
XX agonist identification; antagonist; human; PCR primer; gene therapy; ss.
XX Homo sapiens.
XX EP789076-A2.
XX 13-AUG-1997.
XX 05-FEB-1997; 97EP-00101767.
XX 07-FEB-1996; 96JP-00021562.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Hinuma S, Sakamoto J, Hosoya M;
XX WPI; 1997-395571/37.
XX Human amygdaloid nucleus-derived G protein coupled receptor - useful for
XX identifying (ant)agonists used in the treatment of, e.g., Alzheimer's
XX disease, dementia, angina or epilepsy.
XX Example 1; Page 33; 58pp; English.
XX This sequence represents a primer for the coding sequence for the human
XX amygdaloid nucleus-derived G protein coupled receptor (see AAW34512) of
XX the invention. The protein and peptide can be used to identify agonists
XX or antagonists useful for creating spinal injury, Alzheimer's disease,
XX asthma, hyperphagia, neuropathy, dementia, pain, cerebral thrombosis,
XX encephalitis, cerebral infarction, cerebrovascular spasm, spondylitis,
XX angina, neurosis, drug dependence, drug and alcohol withdrawal symptoms,
XX schizophrenia, phobia, stroke, anxiety, depression, respiratory distress
XX syndrome, emesis, epilepsy, etc. The DNA encoding it can be used to
XX produce the recombinant protein or peptide, to construct diagnostic
XX probes and primers, and for gene therapy. An antibody directed against
XX the G protein coupled receptor can be used in immunoassays for the

```

```
XX Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
SQ Best Local Similarity 1.2%; Score 21.8; DB 1; Length 27;
Query Match 74.1%; Pred. No. 54;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 979 TTGGCATTGCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGCTGCTGCCCTTCAC 1

RESULT 34
AAV02406/c
ID AAV02406 standard; DNA; 27 BP.
XX
AC AAV02406;
XX
DT 06-APR-1998 (first entry)
XX
DE Receptor protein degenerate PCR primer 2.
XX
KW G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
KW pituitary; central nervous system; pancreas; prophylactic;
KW therapeutic agent; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO9724436-A2.
XX
PD 10-JUL-1997.
XX
PF 26-DEC-1996; 96WO-JP003821.
XX
PR 28-DEC-1995; 95JP-00343371.
PR 15-MAR-1996; 96JP-00059419.
PR 12-AUG-1996; 96JP-00211805.
PR 18-SEP-1996; 96JP-00246573.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
PI Kitada C;
XX
DR WPI; 1997-363672/33.
XX
PT Ligand peptide for G protein-coupled receptor - acts by modulating
PT function in the central nervous system, pancreas and pituitary gland.
XX
PS Example 1; Page 101; 258pp; English.
XX
XX AAV02406 and AAV02405 are degenerate PCR primers designed to amplify a
XX large number of G protein-coupled receptor protein sequences for
XX comparative sequence study. Such sequences are used in ligand assays to
XX monitor ligand binding to receptor proteins. Pharmaceutical compositions
XX containing such ligands may be used as a pituitary functional modulator, a
XX central nervous system modulator or a pancreatic function modulator.
XX These ligands could have specific applications as a prophylactic or
XX therapeutic agent for dementia, depression, hyperkinetic syndrome,
XX disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
XX growth hormone secretory disease, hyper- and polyphagia, diabetes,
XX hypercholesterolemia, hyperglycaemia, hyperlipidaemia, renal disease
XX hyperprolactinaemia, pancreatitis, cancer, Turner's syndrome, neurosis,
XX rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy,
XX amyotrophic lateral sclerosis, acute myocardial infarction, infertility,
XX spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
XX osteoporosis, asthma, and/or oligosaccharia. Assays can also be developed
XX to screen compounds which are capable of altering the binding activity of
XX the ligand thus affecting activation of the G protein-coupled receptor
XX protein
XX
XX Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
```

```
Oy 979 TTGGCATTGCTGCTGCTGCCCTTCAC 1005
Db 27 TTGGCMTCTGCTGCTGCTGCCCTTCAC 1

RESULT 35
AAV81236/c
ID AAV81236 standard; DNA; 27 BP.
XX
AC AAV81236;
XX
DT 10-MAR-1999 (first entry)
XX
DE Human G-protein coupled receptor cDNA amplifying primer.
XX
KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
KW GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
KW Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
KW secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
KW gene therapy; transgenic animal; human; PCR primer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN MO9849295-A1.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-JP001923.
XX
PR 28-APR-1997; 97JP-00109974.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fukusumi S;
XX
DR WPI; 1999-009423/01.
XX
PT New polypeptide ligand for orphan G protein coupled receptors - used for
PT treating disorders of central nervous system, pituitary and pancreas, and
PT for drug screening.
XX
PS Example 1; Page 95; 206pp; English.
XX
XX The invention relates to a murine pituitary-derived ligand polypeptide
XX which is a ligand for the G-protein coupled orphan receptor designated
XX GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
XX the ligand polypeptide encoding DNA are used to produce a recombinant
XX ligand polypeptide. The ligand polypeptide, and its fragments, modulate
XX function of the pituitary, central nervous system, pancreas and other
XX tissues and can be used to screen for agents that modulate binding of the
XX polypeptide to the receptor; to quantify the amount of receptor in a
XX sample and to raise antibodies. They may also be used therapeutically,
XX e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
XX diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
XX diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
XX rheumatoid arthritis; epilepsy and many others, also to improve post-
XX operative nutritional status and as vasopressor. Transgenic animals
XX carrying the ligand polypeptide encoding DNA or its mutant are used to
XX study the function of the polypeptide-expressing genes, as models of
XX disease, for drug screening and as source of cell lines. The ligand
XX polypeptide DNA is used as a source of probes and primers; to identify
XX related sequences; in receptor-binding assays; for production of Ab and
XX antisera. Primers AAV81235-236 are used for the PCR amplification of the
XX cDNA encoding a human pituitary-derived G-protein coupled receptor
```

```

SQ      Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
Query Match
Best Local Similarity 74.1%; Score 21.8; DB 1; Length 27;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy      979 TTGGCCATCTGCTGCTGCTGCTTCAC 1005
      |||||:|||||:|||||:|||||:
Db      27 TTGGCCMTCTGCTGANTGCTTCAC 1

RESULT 36
AAK83875/c
ID      AAK83875 standard; DNA; 27 BP.
XX
XX      AAK83875;
AC
XX
XX      09-SEP-1999 (first entry)
DT
XX
XX      G protein-coupled receptor protein PCR primer SEQ ID NO:6.
DE
XX      G protein-coupled receptor protein; APJ; central nervous system;
XX      circulation; immune function; gastrointestinal function; reproduction;
XX      metabolic function; HIV; infection; AIDS; PCR primer; SS.
KM
XX
XX      Synthetic.
OS
XX      WO9333976-A1.
PN
XX      08-JUL-1999.
PD
XX
XX      22-DEC-1998; 98WO-JP005805.
PF
XX
XX      24-DEC-1997; 97JP-00353955.
PR      16-FEB-1998; 98JP-00032577.
PR      04-AUG-1998; 98JP-00220853.
PR      25-SEP-1998; 98JP-00271645.
XX
XX      (TAKEDA ) TAKEDA CHEM IND LTD.
PA
XX
XX      Hinuma S, Tatemoto K, Hosoya M, Habata Y, Fujii R, Kitada C;
PI
XX      WPI; 1999-405507/34.
DR
XX
XX      New ligand polypeptide for the G protein-coupled receptor, APJ, useful
PT      for modulating central nervous system.
PT
XX
XX      Disclosure; Page 79; 163PP; English.
PS
XX
XX      The present invention describes a ligand polypeptide for the G protein-
CC      coupled receptor, APJ. The APJ ligand can modulate central nervous system
CC      function, circulatory function, immune function, gastrointestinal
CC      function, metabolic function and reproductive function. An antibody
CC      against the APJ ligand can be used in diagnosis. The APJ ligand can be
CC      used in an assay to screen for compounds that change its binding activity
CC      to its receptor. The ligand can also be used for treating HIV infection
CC      and AIDS. The present sequence represents a PCR primer for a G protein-
CC      coupled receptor protein
XX
XX      Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;
SQ

Query Match
Best Local Similarity 74.1%; Score 21.8; DB 1; Length 27;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy      979 TTGGCCATCTGCTGCTGCTTCAC 1005
      |||||:|||||:|||||:|||||:
Db      27 TTGGCCMTCTGCTGANTGCTTCAC 1

RESULT 37
AAK15511/c
ID      AAK15511 standard; DNA; 27 BP.

```

XX	AA115511;	
XX		
DT	06-MAY-1999	(first entry)
XX		
DE	Probe used to screen for G protein-coupled receptor cDNA.	
XX		
KM	G protein-coupled receptor; GPCR; hypocoarctanism; gonocyst cacogenesis;	
KM	menopausal syndrome; euthyroid; hypometabolism; lactation; modulation;	
KM	pituitary adenomatosis; brain tumour; emmenopathy; autoimmune disease;	
KM	prolactinoma; infertility; impotence; amenorrhea; galactorrhea;	
KM	acromegaly; Chiari-Frommel syndrome; lymphoma; Sheehan syndrome;	
KM	Forbes-Albright syndrome; Argonz-del Castillo syndrome;	
KM	contraceptive; placental function; chorioncarcinoma; hydatid mole;	
KM	irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;	
KM	abnormal lipidmetabolism; oxytocia; prolactin secretion; probe; ss.	
XX		
OS	Synthetic.	
PN		
XX	W09858962-A1.	
XX		
PD	30-DEC-1998.	
XX		
PF	22-JUN-1998; 98WO-JP002765.	
XX		
PR	23-JUN-1997; 97JP-00165437.	
XX		
PA	(TAKE ) TAKEDA CHEM IND LTD.	
PI		
XX	Hinuma S, Kawamata Y, Fujii R, Matsumoto H;	
DR	WPI, 1999-105614/09.	
XX		
PT	Use of G protein-coupled receptor ligands - for modulating prolactin	
PT	secretion or placental function, e.g. for treating menopausal syndrome,	
PT	tumours, autoimmune disease or abnormal pregnancy.	
XX		
PS	Disclosure; Page 71; 241pp; English.	
XX		
CC	The present sequence represents a probe used to screen for cDNA encoding	
CC	a G protein-coupled receptor protein. The specification describes an	
CC	agent for modulating prolactin secretion which comprises a ligand	
CC	polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein.	
CC	The agents for promoting prolactin secretion can be used for treating or	
CC	preventing hypovarianism, gonocyst cacogenesis, menopausal syndrome, in	
CC	euthyroid or hypometabolism. They can be used for promoting lactation in	
CC	a domestic mammal and as an aphrodisiac. The agents for inhibiting	
CC	prolactin secretion can be used for treating or preventing pituitary	
CC	adenomatosis, brain tumour, emmenopathy, autoimmune disease,	
CC	prolactinoma, infertility, impotence, amenorrhea, galactorrhea,	
CC	acromegaly, Chiari-Frommel syndrome, Argonz-del Castillo syndrome, Forbes-	
CC	Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The	
CC	modulating agents can also be used as contraceptives. The agents for	
CC	inhibiting placental function can be used for treating or preventing	
CC	chorioncarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,	
CC	abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia	
XX		
XX	Sequence 27 BP; 7 A; 5 C; 8 G; 1 T; 0 U; 6 Other;	
Q0		
Query Match	1.2%;	Score 21.8; DB 1; Length 27;
Best Local Similarity	74.1%;	Pred. No. 54;
Matches 20; Conservative	4;	Mismatches 3; Indels 0; Gaps 0;
QY	979 TTGGCATTGCTGCTGCTGCTTCAC 1005	
DB	27 TTTCGCTGCTGCTGCTGCTTCAC 1	
XX		
XX		
AC	AAQ30782;	

```
XX
DT 25-MAR-2003 (revised)
XX
DT 22-MAR-1993 (first entry)
XX
DE PCR primer hsp341 to amplify human NK1R sf N-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
XX polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
XX
PR 17-MAY-1991; 91US-00701935.
XX
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Strader CD, Fong TM;
XX
PS WPI; 1992-384034/47.
XX
PT New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC The core region of human NK1R sf was isolated by PCR and sequenced (see
CC AAQ30774-Q30778). The antisense primers hsp345, hsp341, hsp342,
CC hsp341 and hsp342 (AAQ30784-Q30788) were synthesised based on the human
CC core sequence. Human glioblastoma mRNA and each of these primers were
CC used in first strand cDNA synthesis to produce the template for a primary
CC PCR amplification. Primer hsp345 was used with 2 rat sense primers r3p1n
CC and r3p1n (AAQ30779 and AAQ30780) for the primary amplification. The PCR
CC product was then used as template for secondary PCR with the same rat
CC primers and the human antisense primer hsp344 (AAQ30783). The secondary
CC PCR product was the template for tertiary PCR amplification, again using
CC the same rat sense primers but with human antisense primer hsp341
CC (AAQ30782). The amplified DNA fragment hybridised to hsp342 (AAQ30781),
CC indicating it is not a non-specific by-product. The DNA was sequenced and
CC found to encode the human NK1R sf N-terminal region and also contains a
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 559 TTGGCCAGTACTACTGCATG 579
DB 21 TTGGCCAGTACTACTGCATG 1
RESULT 39
AAQ30790
ID AAQ30790 standard; DNA; 21 BP.
XX
AC AAQ30790;
XX
XX 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DB PCR primer hsp342 to amplify human NK1R sf C-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
XX anchored polymerase chain reaction; rat NK1R; ss.
```

```
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
PR 17-MAY-1991; 91US-00701930.
XX
PR 17-MAY-1991; 91US-00701935.
XX
PR 17-MAY-1991; 91US-00701937.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Strader CD, Fong TM;
XX
PS WPI; 1992-384034/47.
XX
PT New human neurokinin-1 receptor short form protein - useful for
PT identifying and determining substance P antagonists in arthritic
PT patients.
XX
PS Example 1; Page 8; 36pp; English.
XX
CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-
CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then
CC ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC primary PCR amplification with human primers hsp341 and hsp342
CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC "Stratagene"). The primary PCR product was used as template for secondary
CC PCR with the human primer hsp343 (AAQ30791) and t3. The product of this
CC reaction was amplified in a tertiary PCR amplification with hsp344
CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC 400bp DNA fragment was detected which hybridised to human oligoprobe
CC hsp345 (AAQ30793). This fragment was subcloned and sequenced. It was
CC found to encode the C-terminal region of human NK1R sf and also contains
CC 3' UTR. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 956 TGATGATTGTCGTGTCGCA 976
DB 1 TGATGATTGTCGTGTCGCA 21
RESULT 40
AAQ30785/C
ID AAQ30785 standard; DNA; 21 BP.
XX
AC AAQ30785;
XX
XX 25-MAR-2003 (revised)
DT 22-MAR-1993 (first entry)
XX
DB PCR primer hsp341 to amplify human NK1R sf N-terminal region.
XX
KM Neurokinin-1 receptor short form; arthritis; Substance P;
XX polymerase chain reaction; rat NK1R; ss.
XX
OS Synthetic.
XX
PN EP514207-A2.
XX
PD 19-NOV-1992.
XX
PF 15-MAY-1992; 92EP-00304432.
XX
```

PR 17-MAY-1991; 91US-00701930.  
 PR 17-MAY-1991; 91US-00701935.  
 PR 17-MAY-1991; 91US-00701937.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Strader CD, Fong TM;  
 XX  
 DR WPI; 1992-384034/47.  
 XX  
 PT New human neurokinin-1 receptor short form protein - useful for  
 PT identifying and determining substance P antagonists in arthritic  
 PT patients.  
 PS  
 PS Example 1; Page 8; 36pp; English.  
 XX  
 CC The core region of human NK1R sf was isolated by PCR and sequenced (see  
 CC AAQ30774-Q30778). The antisense primers hsp3a5, hsp3a1, hsp3a2,  
 CC hsp3a6 and hsp3a2 (AAQ30784-Q30788) were synthesised based on the human  
 CC core sequence. Human glioblastoma mRNA and each of these primers were  
 CC used in first strand cDNA synthesis to produce the template for a primary  
 CC PCR amplification. Primer hsp3a5 was used with 2 rat sense primers reprim  
 CC and reprim (AAQ30779 and AAQ30780) for the primary amplification. The PCR  
 CC product was then used as template for secondary PCR with the same rat  
 CC primers and the human antisense primer hsp3a4 (AAQ30783). The secondary  
 CC PCR product was the template for tertiary PCR amplification, again using  
 CC the same rat sense primers but with human antisense primer hsp3a1  
 CC (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),  
 CC indicating it is not a non-specific by-product. The DNA was sequenced and  
 CC found to encode the human NK1R sf N-terminal region and also contains a  
 CC 5' UTR. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 836 TGCTGGTGAATTGCTATGTCAT 856  
 |||||  
 Db 21 TGCTGGTGAATTGCTATGTCAT 1

RESULT 41  
 AAQ30789  
 ID AAQ30789 standard; DNA; 21 BP.  
 XX  
 AC AAQ30789;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-MAR-1993 (first entry)  
 XX  
 DE PCR primer hsp3a1 to amplify human NK1R sf C-terminal region.  
 XX  
 KM Neurokinin-1 receptor short form; arthritis; Substance P;  
 KM anchored polymerase chain reaction; rat NK1R; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN EP514207-A2.  
 XX  
 PD 19-NOV-1992.  
 PF 15-MAY-1992; 92EP-00304432.  
 XX  
 PR 17-MAY-1991; 91US-00701930.  
 PR 17-MAY-1991; 91US-00701935.  
 PR 17-MAY-1991; 91US-00701937.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Strader CD, Fong TM;  
 XX

DR WPI; 1992-384034/47.  
 XX  
 XX New human neurokinin-1 receptor short form protein - useful for  
 PT identifying and determining substance P antagonists in arthritic  
 PT patients.  
 PS  
 PS Example 1; Page 8; 36pp; English.  
 XX  
 CC Double-stranded cDNA was prepared from human glioblastoma mRNA and large-  
 CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then  
 CC ligated to the calf intestinal phosphatase-treated EcoRI site of the  
 CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a  
 CC primary PCR amplification with human primers hsp3a1 and hsp3a2  
 CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from  
 CC "Stratagene"). The primary PCR product was used as template for secondary  
 CC PCR with the human primer hsp3a3 (AAQ30791) and t3. The product of this  
 CC reaction was amplified in a tertiary PCR amplification with hsp3a4  
 CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A  
 CC 400bp DNA fragment was detected which hybridised to human Oligoprobe  
 CC hsp3a5 (AAQ30793). This fragment was subcloned and sequenced. It was  
 CC found to encode the C-terminal region of human NK1R sf and also contains  
 CC 3'UTR. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 924 GCAAGTCTGCGAAGCGCAA 944  
 |||||  
 Db 1 GCAAGTCTGCGAAGCGCAA 21

RESULT 42  
 AAQ30787/C  
 ID AAQ30787 standard; DNA; 21 BP.  
 XX  
 AC AAQ30787;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-MAR-1993 (first entry)  
 XX  
 DE PCR primer hsp3a1 to amplify human NK1R sf N-terminal region.  
 XX  
 KM Neurokinin-1 receptor short form; arthritis; Substance P;  
 KM polymerase chain reaction; rat NK1R; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN EP514207-A2.  
 XX  
 PD 19-NOV-1992.  
 PF 15-MAY-1992; 92EP-00304432.  
 XX  
 PR 17-MAY-1991; 91US-00701930.  
 PR 17-MAY-1991; 91US-00701935.  
 PR 17-MAY-1991; 91US-00701937.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Strader CD, Fong TM;  
 XX  
 DR WPI; 1992-384034/47.  
 XX  
 PT New human neurokinin-1 receptor short form protein - useful for  
 PT identifying and determining substance P antagonists in arthritic  
 PT patients.  
 PS  
 PS Example 1; Page 8; 36pp; English.  
 XX  
 CC The core region of human NK1R sf was isolated by PCR and sequenced (see



CC AAQ030774-Q30778) . The antisense primers hsp325, hsp52a1, hsp52a2, hsp52a3 and hsp52a4 (AAQ030784-Q30788) were synthesised based on the human CC core sequence. Human glioblastoma mRNA and each of these primers were CC used in first strand cDNA synthesis to produce the template for a primary CC PCR amplification. Primer hsp325 was used with 2 rat sense primers reprim CC and reprimh (AAQ030779 and AAQ030780) for the primary amplification. The PCR CC product was then used as template for secondary PCR with the same rat CC primers and the human antisense primer hsp324 (AAQ030783). The secondary CC PCR product was the template for tertiary PCR amplification, again using CC the same rat sense primers but with human antisense primer hsp32a1 (AAQ030782). The amplified DNA fragment hybridised to hsp32a2 (AAQ030781), CC indicating it is not a non-specific by-product. The DNA was sequenced and CC found to encode the human NKIR sf N-terminal region and also contains a CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTCGCA 976  
|||  
21 TGATGATTGTCGTGTCGCA 1

Db

RESULT 43  
AAQ29783/c  
ID AAQ29783 standard; DNA; 21 BP.  
XX  
XX AAQ29783;  
XX  
XX 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
XX hsp32a5 primer 1499-1479.  
DE  
XX  
XX Human, neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
KW amplify; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP510878-A1.  
PN  
XX  
XX 28-OCT-1992.  
PD  
XX  
XX 16-APR-1992; 92EP-00303457.  
PF  
XX  
XX 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
XX (MERI ) MERCK & CO INC.  
PA  
XX  
XX Fong TM, Strader CD;  
PI  
XX  
XX WPI; 1992-359073/44.  
DR  
XX  
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
XX Disclosure; Page 8; 35pp; English.

CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NKIR cDNA and also regions of the rat NKIR which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NKIR cDNA was obtained from a human cDNA library utilising portions of

CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGGAACAATTCATCTTG 1587  
|||  
21 AGGGAACAATTCATCTTG 1

Db

RESULT 44  
AAQ29679  
ID AAQ29679 standard; DNA; 21 BP.  
XX  
XX AAQ29679;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
XX hsp62 primer 868-888.  
DE  
XX  
XX Human, neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
KW amplify; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP510878-A1.  
PN  
XX  
XX 28-OCT-1992.  
PD  
XX  
XX 16-APR-1992; 92EP-00303457.  
PF  
XX  
XX 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
XX (MERI ) MERCK & CO INC.  
PA  
XX  
XX Fong TM, Strader CD;  
PI  
XX  
XX WPI; 1992-359073/44.  
DR  
XX  
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
XX Disclosure; Page 8; 35pp; English.

CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NKIR cDNA and also regions of the rat NKIR which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NKIR cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTCGCA 976  
|||  
1 TGATGATTGTCGTGTCGCA 21

Db

RESULT 45  
AAQ29674/C  
ID AAQ29674 standard; DNA; 21 BP.  
XX  
AC AAQ29674;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
DE hsp95a1 primer 768-748.  
XX  
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
KW amplify; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP510878-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 16-APR-1992; 92EP-00303457.  
XX  
PR 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Strader CD;  
XX  
DR WPI; 1992-359073/44.  
XX  
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NKIR cDNA and also regions of the rat NKIR which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NKIR cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 836 TCGTGGTGAATGCGTATGCA 856  
DB 21 TCGTGGTGAATGCGTATGCA 1  
RESULT 46  
AAQ29676/C  
ID AAQ29676 standard; DNA; 21 BP.  
XX  
AC AAQ29676;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
DE hsp95a1 primer 888-868.

XX  
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
KW amplify; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP510878-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 16-APR-1992; 92EP-00303457.  
XX  
PR 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Strader CD;  
XX  
DR WPI; 1992-359073/44.  
XX  
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NKIR cDNA and also regions of the rat NKIR which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NKIR cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 956 TGATGATTTGCTGCTGTGCA 976  
DB 21 TGATGATTTGCTGCTGTGCA 1  
RESULT 47  
AAQ29677/C  
ID AAQ29677 standard; DNA; 21 BP.  
XX  
AC AAQ29677;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
DE hsp95a1 primer 491-471.  
XX  
KW Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
KW amplify; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP510878-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 16-APR-1992; 92EP-00303457.

XX 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Strader CD;  
XX  
DR WPI; 1992-359073/44.  
XX  
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AA029670-82, AA029783 and AA029746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AA029749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
XX  
Query March 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 559 TTGCGCAGTATCTACTCGATG 579  
Db 21 TTGCGCAGTATCTACTCGATG 1  
XX  
RESULT 48  
AA029678  
ID AA029678 standard; DNA; 21 BP.  
XX  
AC AA029678;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
XX hepr6el primer 836-856.  
XX  
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;  
KW amplify; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP510878-A1.  
XX  
XX 28-OCT-1992.  
XX  
XX 16-APR-1992; 92EP-00303457.  
XX  
XX 25-APR-1991; 91US-00691197.  
XX 25-APR-1991; 91US-00691198.  
XX 25-APR-1991; 91US-00691200.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Fong TM, Strader CD;  
XX  
XX WPI; 1992-359073/44.  
XX  
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate

PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AA029670-82, AA029783 and AA029746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AA029749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
Query March 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 924 GCAAGTCTGCGCAGCGCAA 944  
Db 1 GCAAGTCTGCGCAGCGCAA 21  
XX  
RESULT 49  
ABS60219  
ID ABS60219 standard; DNA; 21 BP.  
XX  
AC ABS60219;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
XX Human polymorphism associated DNA sequence #113.  
XX  
DE Human polymorphism associated DNA sequence #113.  
XX  
XX Aminoacylase P; XPRNP2; bradykinin receptor B1; de; BDKRB1;  
KW tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;  
KW KKT1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW aneurysm; embolism; thrombosis; coronary artery disease; trachoma;  
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
KW autoimmune disease; inflammatory arthritis; cancer; wound;  
KW viral infection; bacterial infection; fungal infection; COPD;  
KW Chronic obstructive pulmonary disease; enterocolitis.  
XX  
XX Homo sapiens.  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 03-DEC-2001; 2001WO-US047235.  
XX  
XX 04-DEC-2000; 2000US-0251015P.  
XX 23-JAN-2001; 2001US-0263678P.  
XX 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX (TSUC/) TSUCHIHASHI Z.  
XX (HUI/) HUI L.  
XX  
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR;  
XX  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,

PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.

PS Disclosure; Page 717; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TRACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
CC 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopressin inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
CC listing but is not referred to anywhere else in the specification

XX Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1360 TCCAACTGCTCTTCGAGAGT 1380

DB 1 TCCAACTGCTCTTCGAGAGT 21

RESULT 50

ABS60157/c

ID ABS60157 standard; DNA; 21 BP.

AC ABS60157;

DT 05-NOV-2002 (first entry)

DE Human polymorphism associated DNA sequence #51.

XX Aminopeptidase P, XPNP2, bradykinin receptor B1; de; BDKRB1;  
XX tachykinin receptor B1; TRACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
XX K1K1; bradykinin receptor B2; BDKRB2; gene therapy;  
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
XX polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; ventricular hypertrophy; vascular disease;  
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
XX autoimmune disease; inflammatory arthritis; cancer; wound;

KW viral infection; bacterial infection; fungal infection; COPD;  
KW Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

PN WO200261131-A2.

PD 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

PR 23-JAN-2001; 2001US-0263678P.

PR 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.

PA (HUI/) HUI L.

PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MR;

PI Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX Disclosure; Page 707; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TRACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopressin inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
CC listing but is not referred to anywhere else in the specification

SQ Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1545 GCAAAAAGGTCAGTATGGCT 1565  
 |||||  
 Db 21 GCAAAAAGGTCAGTATGGCT 1  
 |||||  
 RESULT 51  
 ABS60218  
 ID ABS60218 standard; DNA; 21 BP.  
 AC  
 XX ABS60218;  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human polymorphism associated DNA sequence #112.  
 XX  
 KM Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
 KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;  
 KM KUK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KM myocardial infarction; ventricular hypertrophy; vascular disease;  
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KM autoimmune disease; inflammatory arthritis; cancer; wound;  
 KM viral infection; bacterial infection; fungal infection; COPD;  
 KM Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX  
 DR WPI; 2002-619265/66.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 717; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein  
 CC 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC / (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcoma, Crohn's  
 CC disease, trachoma, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is included in the sequence  
 CC listing but is not referred to anywhere else in the specification  
 XX  
 SQ Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1360 TCCAACTGCTCTTCACGAGCT 1380  
 |||||  
 Db 1 TCCAACTGCTCTTCACGAGCT 21  
 |||||  
 RESULT 52  
 ABS60277/C  
 ID ABS60277 standard; DNA; 21 BP.  
 XX  
 AC ABS60277;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human polymorphism associated DNA sequence #171.  
 XX  
 KM Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
 KM tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;  
 KM KUK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KM myocardial infarction; ventricular hypertrophy; vascular disease;  
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KM autoimmune disease; inflammatory arthritis; cancer; wound;  
 KM viral infection; bacterial infection; fungal infection; COPD;  
 KM Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;

XX  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX Disclosure; Page 726; 977bp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
XX listing but is not referred to anywhere else in the specification  
XX  
SQ Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Fred. NO. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 GTGGATCATCTTAGCCACAA 392  
Db 21 GTGGATCATCTTAGCCACAA 1

RESULT 53  
ABS60343  
ID ABS60343 standard; DNA; 21 BP.  
XX  
XX ABS60343;  
XX  
XX 05-NOV-2002 (first entry)  
XX  
XX Human polymorphism associated DNA sequence #237.  
XX  
XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
XX tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; Kallikrein 1;  
XX K1K1; bradykinin receptor B2; BDKRB2; gene therapy;  
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; ventricular hypertrophy; vascular disease;  
XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
XX autoimmune disease; inflammatory arthritis; cancer; wound;  
XX viral infection; bacterial infection; fungal infection; COPD;  
XX Chronic obstructive pulmonary disease; enterocolitis.  
XX  
XX Homo sapiens.  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 03-DEC-2001; 2001MO-US047235.  
XX  
XX 04-DEC-2000; 2000US-0251015P.  
XX 23-JAN-2001; 2001US-0263678P.  
XX 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX (TSUC/) TSUCHIHASHI Z.  
XX (HUI/L/) HUI L.  
XX  
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX Swanson BN, Powell JR; Ma-Edmonds M, Perrone MH;  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX Disclosure; Page 736; 977bp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (K1K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
XX listing but is not referred to anywhere else in the specification  
XX





PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUII/) HUI L.  
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 P1 Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 716; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (CINH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC nucleotide position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polymucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is included in the sequence  
 CC listing but is not referred to anywhere else in the specification  
 XX  
 SQ Sequence 21 BP; 6 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 252 CATCTCCACTTAACACCTCGGA 272  
 Db 1 CATCTCCACTTAACACCTCGGA 21  
 RESULT 56  
 ABS60345  
 ID ABS60345 standard; DNA; 21 BP.  
 XX  
 AC ABS60345;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human polymorphism associated DNA sequence #239.  
 XX

KW Aminopeptidase P; XPNEP2; bradykinin receptor B1; de; BDKRB1;  
 KW tachykinin receptor B1; TACR1; CI esterase inhibitor; CINH; kallikrein 1;  
 KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy; PI4;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 XX 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUII/) HUI L.  
 P1 Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 P1 Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 PT  
 PS Disclosure; Page 737; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (CINH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC nucleotide position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The



CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
CC listing but is not referred to anywhere else in the specification  
XX

SO Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1399 GAGAGCTTCAGCTTCCTCC 1419  
Db 1 GAGAGCTTCAGCTTCCTCC 21

RESULT 57  
ABS60217  
ID ABS60217 standard; DNA; 21 BP.

AC ABS60217;  
XX  
DT 05-NOV-2002 (first entry)

XX Human polymorphism associated DNA sequence #111.

XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;  
XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;  
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; ventricular hypertrophy; vascular disease;  
XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
XX autoimmune disease; inflammatory arthritis; cancer; wound;  
XX viral infection; bacterial infection; fungal infection; COPD;  
XX chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-026378P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PA (TSUC/) TSUCHIHASHI Z.

XX PI (HUI/L) HUI L.

XX PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX Swanson BW, Powell JR;

XX DR WPI; 2002-619265/66.

XX PT New isolated nucleic acid with at least one polymorphic position, useful  
XX for detecting, diagnosing and treating disorders such as angioedema,  
XX cancer, viral, bacterial or fungal infection, cardiovascular and  
XX autoimmune diseases.

XX PT disclosure; Page 716; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene  
XX encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
XX tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein  
XX 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
XX 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
XX polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
CC listing but is not referred to anywhere else in the specification  
XX

SO Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1360 TCCACGCTGCTTCACGAGT 1380  
Db 1 TCCACGCTGCTTCACGAGT 21

RESULT 58

ABS60283/C  
ID ABS60283 standard; DNA; 21 BP.

XX ABS60283;

XX 05-NOV-2002 (first entry)

XX Human polymorphism associated DNA sequence #177.

XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;  
XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;  
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; ventricular hypertrophy; vascular disease;  
XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
XX autoimmune disease; inflammatory arthritis; cancer; wound;  
XX viral infection; bacterial infection; fungal infection; COPD;  
XX chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/L/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.

Disclosure; Page 727; 977pp; English.

CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases, like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins are also useful for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is included in the sequence  
 CC listing but is not referred to anywhere else in the specification  
 XX  
 XX  
 SQ Sequence 21 BP, 7 A, 2 C, 7 G, 5 T, 0 U, 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 ATTCCTTCATCTCGAACCAT 1519  
 DB 21 ATTCCTTCATCTCGAACCAT 1

RESULT 59  
 ABS60344  
 ID ABS60344 standard; DNA; 21 BP.  
 XX  
 AC ABS60344;

XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 XX Human polymorphism associated DNA sequence #238.  
 DE  
 XX Aminopeptidase P; XPNP2; bradykinin receptor B1; ds; BDKRB1;  
 XX tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
 XX KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 XX KLK1; bradykinin receptor B2; ACE2; protease inhibitor 4; PI4;  
 XX angiotensin converting enzyme 2; ACE2; angiotensin converting enzyme 2;  
 XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 XX cardiovascular disease; angina pectoris; hypertension; heart failure;  
 XX myocardial infarction; ventricular hypertrophy; vascular disease;  
 XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 XX autoimmune disease; inflammatory arthritis; cancer; wound;  
 XX viral infection; bacterial infection; fungal infection; COPD;  
 XX Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W0200261131-A2.  
 EN  
 XX  
 XX 08-AUG-2002.  
 PD  
 XX  
 XX 03-DEC-2001; 2001WO-US047235.  
 PF  
 XX  
 XX 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 PR

(BRIM ) BRISTOL-MYERS SQUIBB CO.  
 (TSUC/) TSUCHIHASHI Z.  
 (HUI/L/) HUI L.  
 PA Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PA Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.

XX  
 XX  
 PS Disclosure; Page 736; 977pp; English.  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

artery disease, arteriosclerosis and/or atherosclerosis, and  
hyperinsensitivity reactions, sepsis, autoimmune diseases, inflammatory  
arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
obstructive pulmonary disease (COPD) and enterocolitis (many other  
diseases and disorders are listed in the specification). The  
polynucleotides are also useful for chromosome identification. Antibodies  
against the proteins may be utilized for immunophenotyping of cell lines  
and biological samples. The present sequence is included in the sequence  
listing but is not referred to anywhere else in the specification

Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1399 GAGAGCTTCAGCTTCTCTCC 1419  
1 GAGAGCTTCAGCTTCTCTCC 21

RESULT 60  
ABS60994  
ID ABS60994 standard; DNA; 21 BP.  
XX  
AC ABS60994;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Human genotyping PCR primer #147.  
XX  
Human, ss; aminopeptidase P, XPNR2; bradykinin receptor B1; primer;  
BDRB1; bradykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
kallikrein 1; K1; bradykinin receptor B2; BDRB2; gene therapy;  
angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
cardiovascular disease; angina pectoris; hypertension; heart failure;  
myocardial infarction; ventricular hypertrophy; vascular disease;  
aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
viral infection; bacterial infection; fungal infection; COPD;  
Chronic obstructive pulmonary disease; enterocolitis.

Homo sapiens.  
XX  
OS  
XX  
PN WO200261131-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 03-DEC-2001; 2001WO-US047235.  
XX  
PR 04-DEC-2000; 2000US-0251015P.  
XX  
PR 23-JAN-2001; 2001US-0263678P.  
XX  
PR 02-MAR-2001; 2001US-0273037P.  
XX  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
XX  
PA (TSCC/) TSUCHIHASHI Z.  
XX  
PA (HUI/) HUI L.  
XX  
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
XX  
PI Swanson BM, Powell JR;  
XX  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
XX for detecting, diagnosing and treating disorders such as angiodaema,  
XX cancer, viral, bacterial or fungal infection, cardiovascular and  
XX autoimmune diseases.  
XX  
XX Example 3; Page 912; 977pp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene

encoding aminopeptidase P (XPNR2), bradykinin receptor B1 (BDRB1),  
tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
1 (K1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
polymorphic position. Also included are (1) a probe that hybridises to a  
polymorphic position as provided in the detailed summary of single  
nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
obtaining the sample from one or more individuals and determining the  
nucleic acid sequence at one or more polymorphic positions in a gene  
encoding a protein selected from the group above; (3) constructing (M2)  
haplotypes using the genes comprising grouping at least two nucleic acids  
; (4) identifying (M3) an individual at risk of developing a disorder  
upon administration of an ACE inhibitor and/or vasopressin inhibitor  
using the polymorphic data; (5) a library of nucleic acids, each of which  
comprises one or more polymorphic positions within a gene encoding a  
human protein selected from the group above; and (6) genotyping (M4) an  
individual comprising obtaining a nucleic acid sample, determining the  
nucleotide present in at least one polymorphic position, and comparing at  
least one position with a known data set. The genes, (M1, M2, M3 and M4)  
and compositions are useful for detecting, diagnosing, treating,  
preventing various disorders such as angiodaema and diseases which  
involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
disease, trachomas, and cardiovascular diseases like angina pectoris,  
hypertension, heart failure, myocardial infarction, ventricular  
hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
artery disease, arteriosclerosis and/or atherosclerosis, and  
hyperinsensitivity reactions, sepsis, autoimmune diseases, inflammatory  
arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
obstructive pulmonary disease (COPD) and enterocolitis (many other  
diseases and disorders are listed in the specification). The  
polynucleotides are also useful for chromosome identification. Antibodies  
against the proteins may be utilised for immunophenotyping of cell lines  
and biological samples. The present sequence is a genotyping PCR primer  
for the gene encoding one of the proteins listed above

Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

493 CACAACGAATGCTACTACGGC 513  
1 CACAACGAATGCTACTACGGC 21

RESULT 61  
ABK63856/c  
ID ABK63856 standard; DNA; 21 BP.  
XX  
AC ABK63856;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #7.  
XX  
XX Human, neurokinin receptor-1; NK-1; dermatological disorder;  
XX immune disorder; autoimmune disorder; cardiovascular disorder;  
XX vascular disorder; airway disorder; neuropathic disorder; pain;  
XX psychiatric disorder; central nervous system disorder; inflammation;  
XX respiratory condition; ophthalmic condition; intestinal condition;  
XX demyelinating disease; small cell lung cancer; depression;  
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
XX neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX

PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 20; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX  
 SQ Sequence 21 BP; 8 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 QY  
 Best Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 836 TGCTGGTGGATTGGCTATGCAT 856  
 21 TGCTGGTGGATTGGCTATGCAT 1  
 RESULT 62  
 ABK63871/c  
 ID ABK63871 standard; DNA; 21 BP.  
 XX  
 AC ABK63871;

XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #16.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 65; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 924 GCAAGTCTCTGCCAAGCCAA 944  
DB 21 GCAAGTCTCTGCCAAGCCAA 1  
|||||  
RESULT 63  
ABR63894 ID ABR63894 standard; DNA; 21 BP.  
XX  
AC ABR63894;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #39.  
XX  
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropsychic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN W0200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
DR WPI; 2002-241835/29.  
XX  
PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
PS Example 18; Page 65; 100pp; English.  
XX  
CC The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or

CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, edema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 21 BP; 3 A; 3 C; 7 G; 8 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 836 TGCTGTGATGGCTATGCAT 856  
DB 1 TGCTGTGATGGCTATGCAT 21  
|||||  
RESULT 64  
ABR63875 ID ABR63875 standard; DNA; 21 BP.  
XX  
AC ABR63875;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #20.  
XX  
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN W0200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
DR WPI; 2002-241835/29.  
XX

PT Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

PS Claim 24; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

demyelinating disease; small cell lung cancer; depression;  
 hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 neuro-pathological disorder; stress; antisense; primer; ss.  
 OS Homo sapiens.  
 XX  
 XX WO200213799-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 17-AUG-2001; 2001WO-IB001510.  
 PF  
 XX  
 XX 18-AUG-2000; 2000US-0226066P.  
 PR  
 XX  
 XX (UTWC-) UNIV MCGILL.  
 PA  
 XX  
 XX Henry JL, Cahill CM, Yashpal K;  
 PI  
 XX  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 XX  
 PS Example 18; Page 65; 100pp; English.  
 XX  
 XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (e.g. eczema, psoriasis, allergic contact dermatitis), and/or other  
 CC conditions.

**Homo sapiens.**

PN WO200213799-A2.

PD 21-FEB-2002.

17-AUG-2001; 2001WO-IB001510.

AA  
PR 18-AUG-2000; 2000US-0226086P

AA  
PA  
(UYMC-) UNIV MCGILL.

xx		
PI	Henry JL,	Cahill CM, Yashpal K;

XX  
DR  
WPI: 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

PS Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63306 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP: 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

	Query Match	1.2%	Score 21;	DB 1,	Length 21;
	Best Local Similarity	100.0%;	Pred. No. 37;		
Matches	21;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
Oy	836 TCCTGTCATTGGACTATGCAT	856			
Dd	1 TGCTGTGATTGGCTATGCAT	21			
RESULT 65					
ABK63890//c					
ID	ABK63890	standard; DNA,	21 BP.		
XX	AC	ABK63890;			
XX	DT	18-JUN-2002	(first entry)		
DE	Neworkinin 1 receptor (NK-1) antisense oligonucleotide #35.				
KW	Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; vascular disorder; airway disorder; neuropathic disorder; pain; psychiatric disorder; central nervous system disorder; inflammation; respiratory condition; ophthalmic condition; intestinal condition;				

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred.No. 37;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0



Oy 924 GCAGTCTCTGCCAAGCCAA 944  
Db 21 GCAAGTCTCTGCCAAGCCAA 1

RESULT 66  
ABK63904  
ID ABK63904 standard; DNA, 21 BP.  
XX  
AC ABK63904;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #9.  
XX  
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Example 18; Page 66; 100pp; English.

CC The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include

CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected  
CC reducing side effects of treatment. ABK63851-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

SO Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1567 AGGGAACAATTCATCCTTG 1587  
Db 1 AGGGAACAATTCATCCTTG 21

RESULT 67  
ABK63851  
ID ABK63851 standard; DNA, 21 BP.  
XX  
AC ABK63851;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #2.  
XX  
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Claim 24; Page 20; 100pp; English.

CC The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or

CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention

XX Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGAATGATGTCGTGGTGTCA 976

DB 1 TGAATGATGTCGTGGTGTCA 21

RESULT 68

ABK63885

ID ABK63885 standard; DNA; 21 BP.

XX ABK63885;

DT 18-JUN-2002 (first entry)

DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #30.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
XX immune disorder; autoimmune disorder; cardiovascular disorder;  
XX vascular disorder; airway disorder; neuropathic disorder; pain;  
XX psychiatric disorder; central nervous system disorder; inflammation;  
XX respiratory condition; ophthalmic condition; intestinal condition;  
XX demyelinating disease; small cell lung cancer; depression;  
XX hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
XX neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
XX neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

XX WO200213799-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.  
XX 18-AUG-2000; 2000US-0226086P.  
XX (UYMC-) UNIV MCGILL.  
XX Henry JL, Cahill CM, Yashpal K;  
XX WPI; 2002-241835/29.  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
XX pain or inflammation, by administering oligonucleotide or a non-  
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
XX pathway.

XX Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
XX receptor, especially treating, attenuating or preventing pain or  
XX inflammatory condition. The method comprises administering to a mammal, a  
XX compound chosen from an oligonucleotide, its analogue, and a disruptor  
XX which interferes with function or production of NK-1 receptors. The  
XX method is useful for treating a pathological condition characterised by  
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
XX cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
XX psychiatric and central nervous system disorders (e.g. anxiety,  
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or  
XX peripheral aspects of chronic or acute pain, and for treating,  
XX attenuating or preventing pain or inflammation, neuropathic pain, inflammation or  
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or  
XX pain relating to psychiatric disorders and central nervous system  
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
XX in a mammal, in particular human. NK-1 receptor related disorders,  
XX diseases, or pathological conditions treatable by this method include  
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
XX Crohn's disease), cardiovascular conditions (stroke), chronic  
XX gastrointestinal tract inflammation, and inflammatory diseases such as  
XX inflammatory bowel diseases. Other disorders and diseases include  
XX cardiovascular pathologies including stroke, chronic inflammatory  
XX diseases such as rheumatoid arthritis, demyelinating diseases such as  
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
XX disorders such as allergies and poison ivy, vasospastic diseases such as  
XX angina, addiction disorders such as alcoholism, neurodegenerative  
XX disorders such as acquired immune deficiency syndrome (AIDS) related  
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
XX disorders such as peripheral neuropathy, oedema, stress related and  
XX somatic disorders, and osteoarthritis. Antisense oligonucleotides  
XX effectively treat chronic conditions and other pathological states  
XX without the co-administration of substance P, and reduce the number of  
XX activated receptors while not reducing the number of quiescent NK-1  
XX receptors. Receptors not chronically stimulated are less affected,  
XX reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
XX receptor coding sequences and oligonucleotides of the invention

XX Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 21; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGAAACATTCATCCTTG 1587

DB 1 AGGAAACATTCATCCTTG 21

RESULT 69

ABK63889/C

ID ABK63889 standard; DNA; 21 BP.

XX



AC	ABK63889;
AD	
DT	18-JUN-2002 (first entry)
XX	
DE	Neurokinin 1 receptor (NK-1) antisense oligonucleotide #34.
XX	
KM	Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM	immune disorder; autoimmune disorder; cardiovascular disorder;
KM	vascular disorder; airway disorder; neuropathic disorder; pain;
KM	psychiatric disorder; central nervous system disorder; inflammation;
KM	respiratory condition; ophthalmic condition; intestinal condition;
KM	demylinating disease; small cell lung cancer; depression;
KM	hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM	neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM	neuro-pathological disorder; acquired immune deficiency syndrome; ss.
OS	Homo sapiens.
XX	
PN	WO200213799-A2.
XX	
PD	21-FEB-2002.
XX	
PF	17-AUG-2001; 2001WO-1B001510.
XX	
PR	18-AUG-2000; 2000US-0226086P.
XX	
PA	(UWMC-) UNIV MCGILL.
XX	
PI	Henry JL, Cahill CM, Yashpal K;
DR	WPI; 2002-241835/29.
XX	
PT	Treating pathological condition involving neurokinin receptor-1, e.g.
PT	pain or inflammation, by administering oligonucleotide or a non-
PT	nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT	pathway.
XX	
PS	Example 18; Page 65; 100pp; English.
XX	
CC	The invention relates to a method of treating a pathological condition
CC	characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC	receptor, especially treating, attenuating or preventing pain or
CC	inflammatory condition. The method comprises administering to a mammal, a
CC	compound chosen from an oligonucleotide, its analogue, and a disruptor
CC	which interferes with function or production of NK-1 receptors. The
CC	method is useful for treating a pathological condition characterised by
CC	involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC	cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC	psychiatric and central nervous system disorders (e.g. anxiety,
CC	psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC	peripheral aspects of chronic or acute pain, and for treating,
CC	attenuating or preventing pain or inflammation such as peripheral,
CC	chronic, acute pain or inflammation, neuropathic pain, inflammation or
CC	pain relating to psychiatric disorders and central nervous system
CC	disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia
CC	in a mammal, in particular human. NK-1 receptor related disorders,
CC	diseases, or pathological conditions treatable by this method include
CC	respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic
CC	conditions (e.g. conjunctivitis), cutaneous/dermatological conditions
CC	(allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and
CC	Crohn's disease), cardiovascular conditions (stroke), chronic
CC	gastrointestinal tract inflammation, and inflammatory diseases such as
CC	inflammatory bowel diseases. Other disorders and diseases include
CC	cardiovascular pathologies including stroke, chronic inflammatory
CC	diseases such as Rheumatoid arthritis, demyelinating diseases such as
CC	multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC	disorders such as allergies and poison ivy, vasospastic diseases such as
CC	angina, addiction disorders such as alcoholism, neurodegenerative
CC	disorders such as acquired immune deficiency syndrome (AIDS) related
CC	dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC	disorders such as peripheral neuropathy, oedema, stress related and
CC	somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC	effectively treat chronic conditions and other pathological states

	without the co-administration of substance P, and reduce the number of
CC	activated receptors while not reducing the number of quiescent NK-1
CC	receptors. Receptors not chronically stimulated are less affected,
CC	reducing side effects of treatment. ABK63874-ABK63906 represent NK-1
CC	receptor coding sequences and oligonucleotides of the invention
XX	
SQ	Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
	Query Match                  1.2%; Score 21; DB 1; Length 21;
	Best Local Similarity    100.0%; Pred. No. 37;
	Matches     21; Conservative     0; Mismatches       0; Indels       0; Gaps       0;
OY	956 TGATGATTGTCTGGTGCGCA 976       Db            21 TGATGATTGTCTGGTGCGCA 1
RESULT 70	
ID	ABK63870/c
AC	ABK63870 standard; DNA; 21 BP.
XX	
XX	ABK63870;
DT	
DT	18-JUN-2002 (first entry)
DE	
XX	Neurokinin 1 receptor (NK-1) antisense oligonucleotide #15.
KW	
KM	Human; neurokinin receptor-1; NK-1; dermatological disorder;
KM	immune disorder; autoimmune disorder; cardiovascular disorder;
KM	vascular disorder; airway disorder; neuropathic disorder; pain;
KM	psychiatric disorder; central nervous system disorder; inflammation;
KM	respiratory condition; ophthalmic condition; intestinal condition;
KM	dysmetastatic disease; small cell lung cancer; depression;
KM	hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KM	hyperdegenerative disorder; acquired immune deficiency syndrome; AIDS;
KM	neuro-pathological disorder; stress; amnesia; primer; ss.
OS	Homo sapiens.
PN	WO200213799-A2.
XX	
PD	21-FEB-2002.
XX	
PF	17-AUG-2001; 2001WO-IB001S10.
XX	
PR	18-AUG-2000; 2000US-0226086P.
PA	(UWMC-) UNIV MCGILL.
PI	
PI	Henry JL, Cahill CM, Yaehpal K;
DR	WPI; 2002-241835/29.
PT	Treating pathological condition involving neurokinin receptor-1, e.g.
PT	pain or inflammation, by administering oligonucleotide or a non-
PT	nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
PT	pathway.
PS	
PS	Claim 24; Page 65; 100pp; English.
XX	
CC	The invention relates to a method of treating a pathological condition
CC	characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC	receptor, especially treating, attenuating or preventing pain or
CC	inflammatory condition. The method comprises administering to a mammal, a
CC	compound chosen from an oligonucleotide, its analogue, and a disruptor
CC	which interferes with function or production of NK-1 receptors. The
CC	method is useful for treating a pathological condition characterised by
CC	involvement of NK-1 receptor such as dermatological, immune, autoimmune,
CC	cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,
CC	psoriasis, central nervous system disorders (e.g. anxiety,
CC	psychosis, schizophrenia), gut inflammation, arthritis, and central or
CC	peripheral aspects of chronic or acute pain, and for treating,
CC	attenuating or preventing pain or inflammation such as peripheral,

CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions and inflammatory diseases such as  
CC gastrointestinal tract inflammation, and inflammatory diseases include  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected.  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGTGATGTCGTGTCGTCGA 976  
21 TGTGATGTCGTGTCGTCGA 1

RESULT 71  
ABK63878  
ID ABK63878 strand; DNA; 21 BP.

AC ABK63878;

DT 18-JUN-2002 (first entry)

XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #23.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW Immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.  
XX  
XX  
XX WO200213799-A2.

PD 21-FEB-2002.

PF 17-AUG-2001; 2001WO-1B001510.

PR 18-AUG-2000; 2000US-0226086P.

XX (UWMC-) UNIV MCGILL.

XX Henry JL, Cahill CM, Yashpal K;

XX WI, 2002-241835/29.

XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.

PS Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
XX receptor, especially treating, attenuating or preventing pain or  
XX inflammatory condition. The method comprises administering to a mammal, a  
XX compound chosen from an oligonucleotide, its analogue, and a disruptor  
XX which interferes with function or production of NK-1 receptors. The  
XX method is useful for treating a pathological condition characterised by  
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
XX psychiatric and central nervous system disorders (e.g. anxiety,  
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or  
XX peripheral aspects of chronic or acute pain, and for treating,  
XX attenuating or preventing pain or inflammation such as peripheral,  
XX chronic, acute pain or inflammatory disorders and central nervous system  
XX pain relating to psychiatric disorders and central nervous system  
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
XX in a mammal, in particular human. NK-1 receptor related disorders,  
XX diseases, or pathological conditions treatable by this method include  
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
XX Crohn's disease), cardiovascular conditions and inflammatory diseases such as  
XX gastrointestinal tract inflammation, and inflammatory diseases include  
XX inflammatory bowel diseases. Other disorders and diseases include  
XX cardiovascular pathologies including stroke, chronic inflammatory  
XX diseases such as rheumatoid arthritis, demyelinating diseases such as  
XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
XX disorders such as allergies and poison ivy, vasospastic diseases such as  
XX angina, addiction disorders such as alcoholism, neurodegenerative  
XX disorders such as acquired immune deficiency syndrome (AIDS) related  
XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
XX disorders such as peripheral neuropathy, oedema, stress related and  
XX somatic disorders, and osteoarthritis. Antisense oligonucleotides  
XX effectively treat chronic conditions and other pathological states  
XX without the co-administration of substance P, and reduce the number of  
XX activated receptors while not reducing the number of quiescent NK-1  
XX receptors. Receptors not chronically stimulated are less affected.  
XX reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
XX receptor coding sequences and oligonucleotides of the invention  
XX

Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

559 TTGCGCAGTATCTACTTCATG 579  
1 TTGCGCAGTATCTACTTCATG 21

RESULT 72  
ABK63866/c  
ID ABK63866 strand; DNA; 21 BP.

AC ABK63866;

DT 18-JUN-2002 (first entry)

XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #17.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW Immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;

KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 OS Homo sapiens.  
 XX MO200213799-A2.  
 PN 21-FEB-2002.  
 PD 17-AUG-2001; 2001WO-IB001510.  
 PF 18-AUG-2000; 2000US-0226086P.  
 PR (UVMC-) UNIV MCGILL.  
 PA Henry JL, Cahill CM, Yaeshpal K;  
 PI WPI; 2002-241835/29.  
 DR  
 XX  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS  
 PS  
 XX Claim 24; Page 20; 100pp; English.  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addition disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 XX  
 SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1567 AGGAAAAACATTCATCCTTG 1587  
 Db 21 AGGAAAAACATTCATCCTTG 1  
 RESULT 73  
 ABK63880  
 ID ABK63880 standard; DNA, 21 BP.  
 XX  
 AC ABK63880;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #25.  
 XX  
 KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 OS Homo sapiens.  
 OS  
 XX  
 XX  
 PN MO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UVMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yaeshpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS  
 PS  
 XX Claim 24; Page 65; 100pp; English.  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as

CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, edema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
CC  
XX Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
SQ

Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches	21;	Conservative	0;	Mismatches	0;	Inserts	0;	Deletions	0;
---------	-----	--------------	----	------------	----	---------	----	-----------	----

```

QY      1051 AAGTTATCCAGCAGGCTAC 1071
          |||||
Db      1 AAGTTATCCAGCAGGCTAC 21

```

RESULT 74  
ABK63887/c  
ID ABK63887 standard; DNA; 21 BP.

AC ABK63887;

DT 18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #32.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
XX immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM hypersensitivity disorder; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS  
KM neuro-rathological disorder; stress; anticancer; primer; ss

OS Homo sapiens.

PN WO200213799-A2

PD 21-FEB-2002.

AA  
PF 17-AUG-2001; 2001WO-IB001510.

AA  
PR 18-AUG-2000; 2000US-0226086P.

XX  
PA (UYMC-) UNIV MCGILL.

XX	Cahill CM,	Yashpal K;
PI	Henry JL,	

XX  
DR WPT: 2002-241835/29.

XX  
PT Treating pathological condition involving neurokinin receptor-1, e.g.

PT pain or inflammation, by administering virginicacetic or a non-nucleoside inhibitor compound which modulate NK-1 receptor biosynthesis

PT pathway.

xx The invention relates to a method of treating a pathological condition  
cc characterised partially by involvement of neurokinin receptor-1 (NK-1)  
cc

receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a

compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and for treating, peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralsia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, in a mammal, in particular human, treatable by this method include diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic disease such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

XX  
Sequence 21 BP: 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity	100.0%;	Pred. No. 37;	0;	Indels	0;	Gaps	0;
-----------------------	---------	---------------	----	--------	----	------	----

Matches	21;	Conservative	0;	Mismatches	0;	Inserts	0;	Deletions	0;
---------	-----	--------------	----	------------	----	---------	----	-----------	----

Qy 205 TTCGAATGGATAACGTCCTC 225  
|||||  
Db 21 TTCCAATGGATAACGTCCTC 1

RESULT 75  
ABK63868

AC ABK63868;

AA  
DT 18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) sense oligonucleotide #19.

XX Human, neurokinin receptor-1, NK-1, dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS  
 KW neuro-rheumatological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

AA WO200213799-A2  
PN

PD 21-FEB-2002.  
 XX 17-AUG-2001; 2001WO-IB001510.  
 PF 18-AUG-2000; 2000US-0226086P.  
 XX (UWMC-) UNIV MCGILL.  
 PA Henry JL, Cahill CM, Yaeshpal K;  
 PI WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 20; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety, anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 205 TTGGAATGATAGCTCTC 225  
 Db 1 TTGGAATGATAGCTCTC 21  
 RESULT 76  
 ABK63899  
 ID ABK63899 standard; DNA; 21 BP.

XX  
 AC ABK63899;  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #44.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; allergy disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200213799-A2.  
 EN  
 XX 21-FEB-2002.  
 PD  
 PF 17-AUG-2001; 2001WO-IB001510.  
 PF 18-AUG-2000; 2000US-0226086P.  
 PR (UWMC-) UNIV MCGILL.  
 PA Henry JL, Cahill CM, Yaeshpal K;  
 PI WPI; 2002-241835/29.  
 XX  
 DR Treating pathological condition involving neurokinin receptor-1, e.g.  
 XX pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 XX Example 18; Page 65; 100pp; English.  
 XX  
 PS The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety, anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides

effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1051 AAGTTATTCAGCAGGTCTAC 1071  
1 AAGTTATTCAGCAGGTCTAC 21

ABR63897 standard; DNA; 21 BP.

ABR63897;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #42.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; pain; vascular disorder; airway disorder; neuropathic disorder; inflammation; psychiatric disorder; central nervous system disorder; intestinal condition; respiratory condition; small cell lung cancer; depression; demyelinating disease; allergy; vasospastic disease; alcoholism; hypersensitivity disorder; acquired immune deficiency syndrome; AIDS; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.

WO200213799-A2.

21-FEB-2002.

17-AUG-2001; 2001WO-1B001510.

18-AUG-2000; 2000US-0226086P.

(UYMC-) UNIV MCGILL.

Henry JL, Cahill CM, Yashpal K;

WPI; 2002-241835/29.

Treating pathological condition involving neurokinin receptor-1, e.g. pain or inflammation, by administering oligonucleotide or a non-nucleotide disruptor compound which modulate NK-1 receptor biosynthetic pathway.

Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating,

attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABR63834-ABR63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

559 TTGCGCAGTATCTACTCCAG 579  
1 TTGCGCAGTATCTACTCCAG 21

ABR63852 standard; DNA; 21 BP.

ABR63852;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) sense oligonucleotide #3.

Human; neurokinin receptor-1; NK-1; dermatological disorder; immune disorder; autoimmune disorder; cardiovascular disorder; pain; vascular disorder; airway disorder; neuropathic disorder; inflammation; psychiatric disorder; central nervous system disorder; intestinal condition; respiratory condition; ophthalmic condition; intestinal condition; demyelinating disease; small cell lung cancer; depression; hypersensitivity disorder; allergy; vasospastic disease; alcoholism; neurodegenerative disorder; acquired immune deficiency syndrome; AIDS; neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.

WO200213799-A2.

21-FEB-2002.

17-AUG-2001; 2001WO-1B001510.

18-AUG-2000; 2000US-0226086P.

(UYMC-) UNIV MCGILL.

Henry JL, Cahill CM, Yashpal K;



DR WPI; 2002-241835/29.  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX  
PS Claim 24; Page 20; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addition disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
S0 Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 924 GCAAGTCTCTGCCAAGCCGCA 944  
Dn 1 GCAAGTCTCTGCCAAGCCGCA 21  
RESULT 79  
ABK63906/C  
ID ABK63906 standard; DNA; 21 BP.  
AC ABK63906;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX  
DB Neurokinin 1 receptor (NK-1) antisense oligonucleotide #1.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; allergy disorder; neuropathic disorder; pain;

KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001MO-IB001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
PA  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.  
DR  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Example 18; Page 66; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addition disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
S0 Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 TTGGAATGATACGCTC 225  
DB 21 TTGGAATGATACGCTC 1

RESULT 80  
ABK63854/c  
ID ABK63854 standard; DNA; 21 BP.  
XX  
XX  
AC ABK63854;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #5.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immunologic disorder; autoimmune disorder; cardiovascular disorder;  
KW immunologic disorder; autoimmune disorder; cardiovascular disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-1B001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
XX Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.  
XX  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
XX pain or inflammation, by administering oligonucleotide or a non-  
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
XX pathway.  
XX  
XX  
XX Claim 24; Page 20; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
XX receptor, especially treating, attenuating or preventing pain or  
XX inflammatory condition. The method comprises administering to a mammal, a  
XX compound chosen from an oligonucleotide, its analogue, and a disruptor  
XX which interferes with function or production of NK-1 receptors. The  
XX method is useful for treating a pathological condition characterised by  
XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
XX cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
XX psychiatric and central nervous system disorders (e.g. anxiety,  
XX psychosis, schizophrenia), gut inflammation, arthritis, and central or  
XX peripheral aspects of chronic or acute pain, and for treating,  
XX attenuating or preventing pain or inflammation such as peripheral,  
XX chronic, acute pain or inflammation, neuropathic pain, inflammation or  
XX pain relating to psychiatric disorders and central nervous system  
XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
XX in a mammal, in particular human. NK-1 receptor related disorders,  
XX diseases, or pathological conditions treatable by this method include  
XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
XX Crohn's disease), cardiovascular conditions (stroke), chronic

CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
XX Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTCGTGTGTGCA 976  
DB 21 TGATGATTCGTGTGTGCA 1

RESULT 81  
ABK63873  
ID ABK63873 standard; DNA; 21 BP.  
XX  
XX  
AC ABK63873;  
XX  
XX  
DT 18-JUN-2002 (first entry)  
XX  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #18.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immunologic disorder; autoimmune disorder; cardiovascular disorder;  
KW immunologic disorder; autoimmune disorder; cardiovascular disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX  
XX Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-1B001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
XX Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.  
XX  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
XX pain or inflammation, by administering oligonucleotide or a non-  
XX nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
XX pathway.  
XX  
XX  
XX Claim 24; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition



CC characterised partially by involvement of neurokinin receptor-1 (NK-1).  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC cardiovascular diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected.  
 CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention

XX  
 SQ Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

XX  
 Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TGATGATTCGTCGTGCA 976  
 |||||  
 Db 1 TGATGATTCGTCGTGCA 21

RESULT 82  
 ABR63861/c  
 ID ABR63861 standard; DNA; 21 BP.  
 XX  
 AC ABR63861;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #12.  
 XX  
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; 88.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.

XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 XX (UVMC-) UNIV MCGILL.  
 PA  
 XX Henry JL, Cahill CM, Yashpal K;  
 PI  
 DR WPI: 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 20; 100pp; English.

XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected.  
 CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention

XX  
 SQ Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

XX  
 Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGCTAC 1071  
 |||||  
 Db 21 AAGTTATCCAGCAGCTAC 1

RESULT 83  
 ABR63861

ID ABK63881 standard; DNA; 21 BP.  
 AC ABK63881;  
 XX  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #26.  
 DE  
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200213799-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-IB001510.  
 PF  
 XX 18-AUG-2000; 2000US-0226086P.  
 PR  
 XX (UYMC-) UNIV MCGILL.  
 PA  
 XX Henry JL, Cahill CM, Yashpal K;  
 PI  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS  
 XX Claim 24; Page 65; 100pp; English.  
 XX  
 XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC Crohn's disease), cardiovascular, and inflammatory diseases such as  
 CC gastrointestinal tract inflammation, and inflammatory diseases include  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders and alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and

CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 XX  
 XX Sequence 21 BP; 7 A; 8 C; 1 G; 5 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 1.2%; Score 21; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 37;  
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY  
 XX 1105 ATGTACAACCCCATCATCTAC 1125  
 DB 1 ATGTACAACCCCATCATCTAC 21  
 RESULT 84  
 ID ABK63859/c  
 AC ABK63859 standard; DNA; 21 BP.  
 XX  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #10.  
 DE  
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200213799-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-IB001510.  
 PF  
 XX 18-AUG-2000; 2000US-0226086P.  
 PR  
 XX (UYMC-) UNIV MCGILL.  
 PA  
 XX Henry JL, Cahill CM, Yashpal K;  
 PI  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS  
 XX Claim 24; Page 20; 100pp; English.  
 XX  
 XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human, NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

559 TTGGCAGATCTCTCTCATG 579

21 TTGGCAGATCTCTCTCATG 1

RESULT 85

ABR63892 standard; DNA; 21 BP.

ABR63892;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #37.

Human; neurokinin receptor-1; NK-1; dermatological disorder;  
immune disorder; autoimmune disorder; cardiovascular disorder;  
vascular disorder; airway disorder; neuropathic disorder; pain;  
psychiatric disorder; central nervous system disorder; inflammation;  
respiratory condition; ophthalmic condition; intestinal condition;  
demyelinating disease; small cell lung cancer; depression;  
hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
neuro-pathological disorder; stress; antisense; primer; ss.

Homo sapiens.

MO200213799-A2.

21-FEB-2002.

17-AUG-2001; 2001WO-1B001510.

18-AUG-2000; 2000US-0226086P.

(UYMC-) UNIV MCGILL.

Henry JL, Cahill CM, Yaashpal K;

WPI; 2002-241835/29.

Treating pathological condition involving neurokinin receptor-1, e.g.  
pain or inflammation, by administering oligonucleotide or a non-  
nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
pathway.

Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition  
characterised partially by involvement of neurokinin receptor-1 (NK-1)  
receptor, especially treating, attenuating or preventing pain or  
inflammatory condition. The method comprises administering to a mammal, a  
compound chosen from an oligonucleotide, its analogue, and a disruptor  
which interferes with function or production of NK-1 receptors. The  
method is useful for treating a pathological condition characterised by  
involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
psychiatric and central nervous system disorders (e.g. anxiety,  
psychosis, schizophrenia), gut inflammation, arthritis, and central or  
peripheral aspects of chronic or acute pain, and for treating,  
attenuating or preventing pain or inflammation such as peripheral,  
chronic, acute pain or inflammation, neuropathic pain, inflammation or  
pain relating to psychiatric disorders and central nervous system  
disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
in a mammal, in particular human, NK-1 receptor related disorders,  
diseases, or pathological conditions treatable by this method include  
respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
conditions (e.g. conjunctivitis), cutaneous/dermatological conditions and  
CC (allergic dermatitis), intestinal conditions (stroke), chronic  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

Sequence 21 BP; 3 A; 2 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

956 TGATGATTGTCGTGTCGCA 976

1 TGATGATTGTCGTGTCGCA 21

RESULT 86

ABR63900 standard; DNA; 21 BP.

ABR63900;

18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #45.

Human; neurokinin receptor-1; NK-1; dermatological disorder;  
immune disorder; autoimmune disorder; cardiovascular disorder;

KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

XX MO200213799-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001MO-IB001510.

XX 18-AUG-2000; 2000US-0226086P.

XX (UYMC-) UNIV MCGILL.

XX Henry JL, Cahill CM, Yashpal K;

XX MPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

XX Example 18; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
 XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 XX receptor, especially treating, attenuating or preventing pain or  
 XX inflammatory condition. The method comprises administering to a mammal, a  
 XX compound chosen from an oligonucleotide, its analogue, and a disruptor  
 XX which interferes with function or production of NK-1 receptors. The  
 XX method is useful for treating a pathological condition characterised by  
 XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 XX psychiatric and central nervous system disorders (e.g. anxiety,  
 XX psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 XX peripheral aspects of chronic or acute pain, and for treating,  
 XX attenuating or preventing pain or inflammation such as peripheral,  
 XX chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 XX pain relating to psychiatric disorders and central nervous system  
 XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 XX in a mammal, in particular human. NK-1 receptor related disorders,  
 XX diseases, or pathological conditions treatable by this method include  
 XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 XX (allergic dermatitis), intestinal conditions (stroke), chronic  
 XX Crohn's disease), cardiovascular conditions (stroke), chronic  
 XX gastrointestinal tract inflammation, and inflammatory diseases such as  
 XX inflammatory bowel diseases. Other disorders and diseases include  
 XX cardiovascular pathologies including stroke, chronic inflammatory  
 XX diseases such as rheumatoid arthritis, demyelinating diseases such as  
 XX multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 XX disorders such as allergies and poison ivy, vasospastic diseases such as  
 XX angina, addiction disorders such as alcoholism, neurodegenerative  
 XX disorders such as acquired immune deficiency syndrome (AIDS) related  
 XX dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 XX disorders, such as peripheral neuropathy, edema, stress related and  
 XX somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 XX effectively treat chronic conditions and other pathological states  
 XX without the co-administration of substance P, and reduce the number of  
 XX activated receptors while not reducing the number of quiescent NK-1  
 XX receptors. Receptors not chronically stimulated are less affected,  
 XX reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 XX receptor coding sequences and oligonucleotides of the invention  
 XX  
 XX Sequence 21 BP; 7 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACACCCCATCATCTAC 1125  
 DB 1 ATGTACACCCCATCATCTAC 21

RESULT 87

ADU26730  
 ID ADU26730 standard; DNA; 21 BP.

XX ADU26730;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #128.

XX ds; RNA production; protein production; drug development;

XX Knock-down target.

XX Unidentified.

XX WO2004094636-A1.

XX 04-NOV-2004.

XX 24-APR-2003; 2003MO-EP004362.

XX 24-APR-2003; 2003MO-EP004362.

XX 24-APR-2003; 2003MO-EP004362.

XX (GALA-) GALAPAGOS GENOMICS NV.

XX (VSCG/) VAN DER SCHUEREN J.

XX Arts GJF, Lambrecht MJT, Djokic K, Claesen RJ, Mesic E;

XX Griffioen S, Bergs CUL;

XX MPI; 2004-775940/76.

XX New knockdown sequences, useful in lowering the amount of RNA and/or

XX protein production in cells used in drug development processes.

XX Claim 11; SEQ ID NO 131; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The

XX amount of RNA and/or protein production in cells used in drug development

XX process. The present sequence represents a knock-down target sequence.

XX Sequence 21 BP; 7 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

QY 1025 ACATCAACCCAGATCTTACC 1045

DB 1 ACATCAACCCAGATCTTACC 21

ADU26729  
 ID ADU26729 standard; DNA; 21 BP.

XX ADU26729;

XX 27-JAN-2005 (first entry)

XX Knock-down target sequence #127.

XX ds; RNA production; protein production; drug development;

XX Knock-down target.

XX OS Unidentified.  
XX PN WO2004094636-A1.  
XX PD 04-NOV-2004.  
XX PF 24-APR-2003; 2003WO-EP004362.  
XX PR 24-APR-2003; 2003WO-EP004362.  
XX PA (GALA-) GALAPAGOS GENOMICS NV.  
XX PA (VSC/) VAN DER SCHUEREN J.  
XX PI Artb GJF, Lambrecht MJY, Djokic K, Claesen RJ, Mesic E;  
XX PI Griffioen S, Berge CUL;  
XX DR WPI; 2004-775940/76.  
XX PT New knockdown sequences, useful in lowering the amount of RNA and/or  
XX PT protein production in cells used in drug development process.  
XX PS Claim 11, SEQ ID NO 130; 402pp; English.  
XX CC The invention relates to a polynucleotide comprising an RNA sequence. The  
XX CC polynucleotide, vector, libraries, and method are useful in lowering the  
XX CC amount of RNA and/or protein production in cells used in drug development  
XX CC process. The present sequence represents a knock-down target sequence.  
XX SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 21; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 37;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 797 ACCACATCTGTGACTGTGC 817  
DB 1 ACCACATCTGTGACTGTGC 21  
RESULT 89  
AAQ37208  
ID AAQ37208 standard; DNA; 26 BP.  
XX  
XX AAQ37208;  
XX AC  
XX DT 25-MAR-2003 (revised)  
XX DT 17-JUN-1993 (first entry)  
XX  
XX DE PCR primer #1 to amplify substance P receptor coding region.  
XX KW human substance P receptor protein; SP; neurotransmitter; neuromodulator;  
XX KW central nervous system; peripheral nervous system;  
XX KW gastrointestinal disorders; inflammation; immune disease.  
XX OS Synthetic.  
XX PN WO9303137-A1.  
XX PD 18-FEB-1993.  
XX PF 05-AUG-1992; 92MO-US006532.  
XX PR 07-AUG-1991; 91US-00741200.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Krause JE;  
XX WPI; 1993-076495/09.  
XX PT New human substance P receptor protein and DNA encoding it - used e.g.  
XX PT for screening substance P antagonists.

XX PS Example; Page 9; 40pp; English.  
XX CC This PCR primer was used with AAQ37209 to amplify the predicted human  
XX CC substance P receptor coding region from IM-9 cDNA. The amplified fragment  
XX CC was blunt end ligated into SmaI-digested pBS. Transformants were further  
XX CC analysed by restriction mapping and by sequence analysis. One cDNA was  
XX CC isolated after restriction with HindIII and BamHI (present in the pBS  
XX CC polylinker) and made blunt ended with Klenow, as was pM2 after BamHI  
XX CC digestion. The cDNA was ligated to pM2 and used to transform E. coli XL-1  
XX CC Blue cells by electroporation. (Updated on 25-MAR-2003 to correct PN  
XX CC field.)  
XX SQ Sequence 26 BP; 5 A; 10 C; 6 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 21; DB 1; Length 26;  
XX Best Local Similarity 100.0%; Pred. No. 65;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 211 ATGATTAACGTCTCTCCCGTG 231  
DB 6 ATGATTAACGTCTCTCCCGTG 26  
RESULT 90  
AAQ30778/C  
ID AAQ30778 standard; DNA; 24 BP.  
XX  
XX AAQ30778;  
XX AC  
XX DT 25-MAR-2003 (revised)  
XX DT 22-MAR-1993 (first entry)  
XX DE PCR primer rspr7a1h to amplify human NK1R 5' core region.  
XX KW Neurokinin-1 receptor short form; arthritis; Substance P;  
XX KW polymerase chain reaction; rat NK1R; se.  
XX OS Synthetic.  
XX PN EP514207-A2.  
XX PD 19-NOV-1992.  
XX PF 15-MAY-1992; 92EP-00304432.  
XX PR 17-MAY-1991; 91US-00701930.  
XX PR 17-MAY-1991; 91US-00701935.  
XX PR 17-MAY-1991; 91US-00701937.  
XX PA (MERI ) MERCK & CO INC.  
XX PI Strader CD, Fong TM;  
XX DR WPI; 1992-384034/47.  
XX PT New human neurokinin-1 receptor short form protein - useful for  
XX PT identifying and determining substance P antagonists in arthritic  
XX PT patients.  
XX PS Example 1; Page 8; 36pp; English.  
XX CC Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1  
XX CC and U87MG. First strand cDNA was synthesised and used as template with  
XX CC rat primers rspr2s4, rspr2s4h and rspr7a2 (AAQ30774-6) in first round PCR  
XX CC amplification. Secondary PCR was performed on the amplified product using  
XX CC the same 3 primers prior to a third round of amplification, this time  
XX CC using the primers rspr2s4, rspr2s4h, rspr7a1 (AAQ30777) and rspr7a1h  
XX CC (AAQ30778). The tertiary PCR product was sequenced and was found to have  
XX CC 90% identity at the nucleotide level with the central core region of the  
XX CC rat NK1R from amino acid 91 to 280. Primer rspr7a1h is an antisense  
XX CC primer based on the rat NK1R sequence 864-841 (numbering as in  
XX CC J Biol. Chem. 264: 17649-17652, 1989), but designed to incorporate the

CC human codon bias. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 57;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1051 AAGTTATCCAGCAGCTTACTCTG 1074  
 DB 24 AAGTTATCCAGCAGCTTACTCTG 1  
 RESULT 91  
 ABS60911/c  
 ID ABS60911 standard; DNA; 21 BP.  
 XX  
 AC ABS60911;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human genotyping PCR primer #64.  
 XX  
 KW Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 KW Kallikrein 1; KKL1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KW polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KW autoimmune disease; bacterial infection; cancer; wound; genotyping;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 DR WPI; 2002-619265/66.  
 XX  
 DR  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Example 3; Page 899; 977pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysis (MI) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising group above; (4) developing a disorder  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polymucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is a genotyping PCR primer  
 CC for the gene encoding one of the proteins listed above  
 XX  
 SQ Sequence 21 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 20.6; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 43;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1624 CCTCATCTCTGTGACTCTCAA 1644  
 DB 21 CCTCATCTCTGTGACTCTCAA 1  
 RESULT 92  
 AAT18361/c  
 ID AAT18361 standard; DNA; 24 BP.  
 XX  
 AC AAT18361;  
 XX  
 DT 26-AUG-1996 (first entry)  
 XX  
 DE G-protein coupled receptor protein DNA primer TM6-E2.  
 XX  
 KW G-protein coupled receptor protein; G-PCR; agonist; antagonist;  
 KW cystic fibrosis; incontinence; diabetes; diagnosis; gene therapy;  
 KW transgenic animal; polymerase chain reaction; PCR; primer; ss.  
 KW  
 OS Synthetic.  
 XX  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT modified\_base 18  
 FT /\*tag= a  
 FT /mod\_base= i  
 XX  
 PN WO9605302-A1.  
 XX  
 PD 22-FEB-1996.  
 XX  
 PF 10-AUG-1995; 95WO-JP001599.  
 XX  
 PR 11-AUG-1994; 94JP-00189272.  
 PR 11-AUG-1994; 94JP-00189273.  
 PR 11-AUG-1994; 94JP-00189274.  
 PR 30-SEP-1994; 94JP-00236356.  
 PR 30-SEP-1994; 94JP-00236357.  
 PR 02-NOV-1994; 94JP-00270017.  
 PR 28-DEC-1994; 94JP-00326611.

PR	20-JAN-1995;	95JP-00007177.
PR	16-MAR-1995;	95JP-00057186.
PR	19-APR-1995;	95JP-00093989.
XX		
PA	(TAKE ) TAKEDA CHEM IND LTD.	
XX		
PI	Hinuma S, Hosoya M, Fujii R, Ohtaki T, Fukusumi S, Ohgi K;	
DR	WPI; 1996-139698/14.	
XX		
PT	G-protein coupled receptor protein DNA and protein - also methods for	
PT	isolating (ant)agonists for treatment of cystic fibrosis, incontinence	
PT	and diabetes.	
XX		
PS	Claim 1; Page 242; 360pp; English.	
CC	PCR primer TW6-E2 (AAT18361) is complementary to DNA coding for a region	
CC	corresponding to, or near, the sixth transmembrane domain of known G-	
CC	protein coupled receptor proteins (G-PCRs). TW6-E2 and other primers	
CC	(see also AAT18347-60 and AAT18362-65) based on G-PCR transmembrane	
CC	domains are used for the PCR amplification of mammalian DNAs to obtain G-	
CC	PCR-encoding sequences (see also AAT18366-73 and AAT13901-09)	
XX		
SO	Sequence 24 BP; 6 A; 4 C; 7 G; 0 T; 0 U; 7 Other;	
	Query Match	1.2%; Score 20.6; DB 1; Length 24;
	Best Local Similarity	70.8%; Pred. No. 61;
	Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	
Oy	979 TTCCGCATCTGCTGCTGCGCCCTTC 1002	
	:     :     :	
Db	24 TTYGCCNTSTGCTGTMSCCCMWC 1	
	RESULT 93	
1D	AAQ30792 standard; DNA; 20 BP.	
XX		
AC	AAQ30792;	
XX		
DT	25-MAR-2003 (revised)	
DT	22-MAR-1993 (first entry)	
XX		
DE	PCR primer hsp654 to amplify human NK1R sf C-terminal region.	
XX		
KW	Neurokinin-1 receptor short form; arthritis; Substance P;	
KW	anchored polymerase chain reaction; rat NK1R; ss.	
XX		
OS	Synthetic.	
XX		
PN	EP514207-A2.	
XX		
PD	19-NOV-1992.	
XX		
PE	15-MAY-1992; 92EP-00304432.	
XX		
PR	17-MAY-1991; 91US-00701930.	
PR	17-MAY-1991; 91US-00701935.	
PR	17-MAY-1991; 91US-00701937.	
XX		
PA	(MERI ) MERCK & CO INC.	
XX		
PI	Strader CD, Fong TM;	
XX		
DR	WPI; 1992-384034/47.	
XX		
PT	New human neurokinin-1 receptor short form protein - useful for	
PT	identifying and determining substance P antagonists in arthritic	
PT	patients.	
XX		
PS	Example 1; Page 8; 36pp; English.	
XX		
CC	Double-stranded cDNA was prepared from human glioblastoma mRNA and large-	

CC	size cDNA was ligated to EcoRI linkers. linker-ligated cDNA was then
CC	ligated to the calf intestinal phosphatase-treated EcoRI site of the
CC	vector Bluescript SK+. The ligated plasmid DNA was used as template in a
CC	primary PCR amplification with human primers hsp661 and hsp662
CC	(AAQ30789 and AAQ30790) and the vector-specific primer t3 (from
CC	"Stratagene"). The primary PCR product was used as template for secondary
CC	PCR with the human primer hsp663 (AAQ30791) and t3. The product of this
CC	reaction was amplified in a tertiary PCR amplification with hsp664
CC	(AAQ30792) and vector-specific primer SK (also from "Stratagene"). A
CC	400bp DNA fragment was detected which hybridised to human oligoprobe
CC	hsp665 (AAQ30793). This fragment was subcloned and sequenced. It was
CC	found to encode the C-terminal region of human NK1R 6F and also contains
CC	3' UTR. (Updated on 25-MAR-2003 to correct FN field.)
CC	
SO	Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;
XX	
Query Match	1.1%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 47;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1023 CTACATCAACCCAGATCTCT 1042
DB	1 CTACATCAACCCAGATCTCT 20
RESULT 94	
AAQ30788/c	
ID	AAQ30788 standard; DNA; 20 BP.
XX	
AC	AAQ30788;
XX	
DT	25-MAR-2003 (revised)
DT	22-MAR-1993 (first entry)
XX	
DE	PCR primer hsp662 to amplify human NK1R 6F N-terminal region.
XX	
KM	Neurokinin-1 receptor short form; arthritis; Substance P;
KW	polymerase chain reaction; rat NK1R; ss.
XX	
OS	Synthetic.
XX	
FN	EP514207-A2.
XX	
PD	19-NOV-1992.
XX	
PF	15-MAY-1992; 92BP-00304432.
XX	
FR	17-MAY-1991; 91US-00701930.
PR	17-MAY-1991; 91US-00701935.
PR	17-MAY-1991; 91US-00701937.
XX	
PA	(MERI ) MERCK & CO INC.
XX	
P1	Strader CD, Fong TM;
XX	
DR	WPI; 1992-384034/47.
XX	
PT	New human neurokinin-1 receptor short form protein - useful for
PT	identifying and determining substance P antagonists in arthritic
PT	patients.
XX	
PS	
XX	Example 1; Page 8; 36pp; English.
CC	
CC	The core region of human NK1R 6F was isolated by PCR and sequenced (see
CC	AAQ30774-Q30778). The antisense primers hsp635, hsp651, hsp652,
CC	hsp661 and hsp662 (AAQ30784-Q30788) were synthesised based on the human
CC	core sequence. Human glioblastoma mRNA and each of these primers were
CC	used in first strand cDNA synthesis to produce the template for a primary
CC	PCR amplification. Primer hsp635 was used with 2 rat sense primers reprim
CC	and reprimb (AAQ30779 and AAQ30780) for the primary amplification. The PCR
CC	product was then used as template for secondary PCR with the same rat
CC	primers and the human antisense primer hsp634 (AAQ30783). The secondary
CC	PCR product was the template for tertiary PCR amplification. Again using



CC the same rat sense primers but with human antisense primer hsp3a1  
CC (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),  
CC indicating it is not a non-specific by-product. The DNA was sequenced and  
CC found to encode the human NK1R sf N-terminal region and also contains a  
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)  
XX

Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1012 TTCCCTGCGCCCTACATCAA 1031  
Db 20 TTCTCTCTGCGCCCTACATCAA 1

RESULT 95  
AAQ30791  
ID AAQ30791 standard; DNA; 20 BP.

AC AAQ30791;  
XX  
DT 25-MAR-2003 (revised)  
DT 22-MAR-1993 (first entry)

PCR primer hsp663 to amplify human NK1R sf C-terminal region.

Neurokinin-1 receptor short form; arthritis; Substance P;  
anchored polymerase chain reaction; rat NK1R; ss.

Synthetic.

EP514207-A2.

19-NOV-1992.

15-MAY-1992; 92EP-00304432.

17-MAY-1991; 91US-00701930.

17-MAY-1991; 91US-00701935.

17-MAY-1991; 91US-00701937.

(MERI) MERCK & CO INC.

Strader CD, Fong TM;

WPI; 1992-384034/47.

New human neurokinin-1 receptor short form protein - useful for  
identifying and determining substance P antagonists in arthritic  
patients.

Example 1; Page 8; 36pp; English.

XX Double-stranded cDNA was prepared from human glioblastoma mRNA and large-  
XX size cDNA was ligated to EcoRI linkers. linker-ligated cDNA was then  
XX ligated to the calf intestinal phosphatase-treated EcoRI site of the  
XX vector BUESCRIP SK+. The ligated plasmid DNA was used as template in a  
XX primary PCR amplification with human primers hsp661 and hsp662  
XX (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from  
XX "Stratagene"). The primary PCR product was used as template for secondary  
XX PCR with the human primer hsp663 (AAQ30791) and t3. The product of this  
XX reaction was amplified in a tertiary PCR amplification with hsp664  
XX (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A  
XX 400bp DNA fragment was detected which hybridised to human oligoprobe  
XX hsp665 (AAQ30793). This fragment was subcloned and sequenced. It was  
XX found to encode the C-terminal region of human NK1R sf and also contains  
XX 3' UTR. (Updated on 25-MAR-2003 to correct PN field.)  
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query 1000 TTCCACATCTTCTCTCTCT 1019  
Db 1 TTCCACATCTTCTCTCTCT 20

RESULT 96  
AAQ30786/c  
ID AAQ30786 standard; DNA; 20 BP.

AAQ30786;

25-MAR-2003 (revised)

22-MAR-1993 (first entry)

PCR primer hsp5a2 to amplify human NK1R sf N-terminal region.

Neurokinin-1 receptor short form; arthritis; Substance P;  
polymerase chain reaction; rat NK1R; ss.

Synthetic.

EP514207-A2.

19-NOV-1992.

15-MAY-1992; 92EP-00304432.

17-MAY-1991; 91US-00701930.

17-MAY-1991; 91US-00701935.

17-MAY-1991; 91US-00701937.

(MERI) MERCK & CO INC.

Strader CD, Fong TM;

WPI; 1992-384034/47.

New human neurokinin-1 receptor short form protein - useful for  
identifying and determining substance P antagonists in arthritic  
patients.

Example 1; Page 8; 36pp; English.

XX The core region of human NK1R sf was isolated by PCR and sequenced (see  
XX AAQ30774-Q30778). The antisense primers hsp3a5, hsp5a1, hsp5a2,  
XX hsp6a1 and hsp6a2 (AAQ30784-Q30788) were synthesised based on the human  
XX core sequence. Human glioblastoma mRNA and each of these primers were  
XX used in first strand cDNA synthesis to produce the template for a primary  
XX PCR amplification. Primer hsp3a5 was used with 2 rat sense primers rsn  
XX and rsnph (AAQ30779 and AAQ30780) for the primary amplification. The PCR  
XX product was then used as template for secondary PCR with the same rat  
XX primers and the human antisense primer hsp3a4 (AAQ30783). The secondary  
XX PCR product was the template for tertiary PCR amplification, again using  
XX the same rat sense primers but with human antisense primer hsp3a1  
XX (AAQ30782). The amplified DNA fragment hybridised to hsp3a2 (AAQ30781),  
XX indicating it is not a non-specific by-product. The DNA was sequenced and  
XX found to encode the human NK1R sf N-terminal region and also contains a  
XX 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)  
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 862 GTAGTGGGAAATCACTATG 861  
Db 20 GTAGTGGGAAATCACTATG 1





```
XX EP510878-A1.
PN
XX 28-OCT-1992.
PD
XX 16-APR-1992; 92EP-00303457.
PE
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
PA (MERI ) MERCK & CO INC.
XX
XX Fong TM, Strader CD;
PI
XX WPI; 1992-359073/44.
DR
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.
BS
XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 601 TACATGGCCATCATCATCC 620
Db |||||
20 TACATGGCCATCATCATCC 1
RESULT 100
AAQ29675/C
ID AAQ29675 standard; DNA; 20 BP.
XX
XX AAQ29675;
AC
XX 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
DT
XX
XX hsp5a2 primer 793-774.
DE
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX Fong TM, Strader CD;
PI
XX EP510878-A1.
PN
XX 28-OCT-1992.
PD
XX 16-APR-1992; 92EP-00303457.
PE
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
PA (MERI ) MERCK & CO INC.
XX
```

```
XX Fong TM, Strader CD;
PI
XX WPI; 1992-359073/44.
DR
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.
BS
XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC which were used in the isolation of fragments of the human neurokinin-1
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
CC neurotransmitter substance P. The primers were designed using regions of
CC the human NK1R cDNA and also regions of the rat NK1R which were thought
CC to be similar to human regions. Part of the human cDNA sequence was
CC derived by amplification using these primers. The remaining part of human
CC NK1R cDNA was obtained from a human cDNA library utilising portions of
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 862 GTAGTGGGAATCACAATG 881
Db |||||
20 GTAGTGGGAATCACAATG 1
RESULT 101
AAQ29680
ID AAQ29680 standard; DNA; 20 BP.
XX
XX AAQ29680;
AC
XX 25-MAR-2003 (revised)
DT 15-MAR-1993 (first entry)
DT
XX
XX hsp6a3 primer 912-931.
DE
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
KW amplify; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX EP510878-A1.
PN
XX 28-OCT-1992.
PD
XX 16-APR-1992; 92EP-00303457.
PE
XX 25-APR-1991; 91US-00691197.
PR 25-APR-1991; 91US-00691198.
PR 25-APR-1991; 91US-00691200.
PA (MERI ) MERCK & CO INC.
XX
XX Fong TM, Strader CD;
PI
XX WPI; 1992-359073/44.
DR
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
PT substances that bind to substance P receptor, and to determine substance
PT P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.
BS
XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
CC
```

CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilizing portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1000 TTCCACATCTTCTCTCTCT 1019  
1 TTCCACATCTTCTCTCTCT 20  
Db  
RESULT 102  
AAQ29677/c  
ID AAQ29677 standard; DNA; 20 BP.  
XX  
AC AAQ29677;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
DE hsp6a2 primer 943-924.  
XX  
KW Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;  
OS amplify; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP510878-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 16-APR-1992; 92EP-00303457.  
XX  
PR 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Strader CD;  
XX  
DR WPI; 1992-359073/44.  
XX  
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilizing portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1012 TTCTCTGCGCCATCATCAA 1031  
20 TTCTCTGCGCCATCATCAA 1  
Db  
RESULT 103  
AAQ29681  
ID AAQ29681 standard; DNA; 20 BP.  
XX  
AC AAQ29681;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
DE hsp6a4 primer 935-954.  
XX  
KW Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;  
KW neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;  
OS amplify; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP510878-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 16-APR-1992; 92EP-00303457.  
XX  
PR 25-APR-1991; 91US-00691197.  
PR 25-APR-1991; 91US-00691198.  
PR 25-APR-1991; 91US-00691200.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Fong TM, Strader CD;  
XX  
DR WPI; 1992-359073/44.  
XX  
PT New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
PS Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilizing portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1023 CTACATCAACCCAGATCTCT 1042  
1 CTACATCAACCCAGATCTCT 20  
Db  
RESULT 104  
AAQ29673/c  
ID AAQ29673 standard; DNA; 20 BP.

```
XX AAQ29673;
AC 25-MAR-2003 (revised)
XX 15-MAR-1993 (first entry)
DT
XX hepr3a5 primer 568-549.
DE
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;
XX neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;
XX amplify; probe; ss.
XX
XX Homo sapiens.
XX EP510878-A1.
XX 28-OCT-1992.
XX
XX 16-APR-1992; 92EP-00303457.
XX
XX 25-APR-1991; 91US-00691197.
XX 25-APR-1991; 91US-00691198.
XX 25-APR-1991; 91US-00691200.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Fong TM, Strader CD;
XX WPI, 1992-359073/44.
XX
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate
XX substances that bind to substance P receptor, and to determine substance
XX P in body fluid of arthritis patients.
XX
XX Disclosure; Page 8; 35pp; English.
XX
XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers
XX which were used in the isolation of fragments of the human neurokinin-1
XX receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the
XX neurotransmitter substance P. The primers were designed using regions of
XX the human NK1R cDNA and also regions of the rat NK1R which were thought
XX to be similar to human regions. Part of the human cDNA sequence was
XX derived by amplification using these primers. The remaining part of human
XX NK1R cDNA was obtained from a human cDNA library utilising portions of
XX PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred.No.47;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 637 TCAGCCACAGCCACCAAGT 656
XX |||||
XX 20 TCAGCCACAGCCACCAAGT 1
XX
XX RESULT 105
XX AA292287
XX ID AA292287 standard; DNA; 20 BP.
XX
XX AC AA292287;
XX
XX 05-JUN-2000 (first entry)
XX
XX Allele specific primer for NK1R exon 1 polymorphism detection.
XX
XX Neurokinin 1 receptor; NK1R; human; single nucleotide polymorphism; SNP;
XX diagnosis; treatment; asthma; depression; urinary incontinence;
XX inflammatory bowel disease; primer; ss.
XX
XX Homo sapiens.
XX
```

```
XX WO200006768-A1.
XX
XX 10-FEB-2000.
XX
XX 20-JUL-1999; 99WO-GB002340.
XX
XX 25-JUL-1998; 98GB-00016197.
XX 22-AUG-1998; 98GB-00018280.
XX
XX (ZENEC ) ZENEC A LTD.
XX
XX Smith JC, Anand R, Morten JEN;
XX WPI, 2000-183135/16.
XX
XX Novel polymorphisms in the human neurokinin 1 receptor gene used for
XX diagnosis and treatment of NK1R ligand mediated diseases such as asthma.
XX
XX Disclosure; Page 10; 43pp; English.
XX
XX This sequence represents an allele specific primer used to detect the
XX 2361 'T' polymorphism in exon 1 of the human neurokinin 1 receptor gene
XX (see AA292286). The invention relates to single nucleotide polymorphisms
XX (SNPs) in human neurokinin 1 receptor (NK1R). Detection of these
XX polymorphisms is useful for the diagnosis and treatment of NK1R ligand
XX mediated diseases. A method for the diagnosis of one or more SNPs in the
XX NK1R gene in a human, comprises determining the sequence of the nucleic
XX acid at one or more of the polymorphic positions. Diagnostic primers can
XX be used to detect the presence of the polymorphisms. The methods of the
XX invention are used to identify SNPs in the human neurokinin 1 receptor
XX (NK1R) gene. The presence or absence of these polymorphisms can be used
XX in the diagnosis and treatment of NK1R-ligand mediated diseases, such as
XX asthma and depression. A NK1R ligand antagonist drug can also be used to
XX treat pain, migraine, anxiety, depression, urinary incontinence, and
XX inflammatory bowel disease. The methods may also be used for the
XX development of new drug therapies which selectively target one or more
XX allelic variants of the NK1R gene
XX
XX Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred.No.47;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 524 GCAAGTTCACACACTCTTT 543
XX |||||
XX 1 GCAAGTTCACACACTCTTT 20
XX
XX RESULT 106
XX ABS60995
XX ID ABS60995 standard; DNA; 20 BP.
XX
XX AC ABS60995;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human genotyping PCR primer #148.
XX
XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
XX BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
XX kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease; angioedema;
XX aneurysm; embolism; thrombosis; coronary artery disease; sepsis; PCR;
XX arteriosclerosis; atherosclerosis; hyperactivity; sepsis; PCR;
XX autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis.
XX
```

OS Homo sapiens.  
 XX  
 PN W0200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/L/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS  
 PS Example 3; Page 912; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is a genotyping PCR primer  
 CC for the gene encoding one of the proteins listed above  
 XX  
 SQ Sequence 20 BP; 5 A; 10 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

609 CATCATACATCCCTCCAGC 628  
 ||||||||||||||||||

Db 1 CATCATACATCCCTCCAGC 20  
 RESULT 107  
 ABS60996  
 ID ABS60996 standard; DNA; 20 BP.  
 XX  
 AC ABS60996;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human genotyping PCR primer #149.  
 XX  
 KM Human; ser; aminopeptidase P; XPNBP2; bradykinin receptor B1; primer;  
 KM BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;  
 KM kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KM myocardial infarction; ventricular hypertrophy; vascular disease;  
 KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
 KM autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
 KM viral infection; bacterial infection; fungal infection; COPD;  
 KM Chronic obstructive pulmonary disease; enterocolitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/L/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS  
 PS Example 3; Page 912; 977pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angioedema like haemangiomas, tumours, sarcomas, Cronh's  
CC disease, trichomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophotyping of cell lines  
CC and biological samples. The present sequence is a genotyping PCR primer  
CC for the gene encoding one of the proteins listed above  
XX  
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match	1.1%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 47;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 108  
ABK63858/c  
ID ABK63858 standard; DNA; 20 BP.

AC ABK63858;

DT 18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) sense oligonucleotide #9

Human, neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vaccine disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM degranulating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM hypergenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antinease; pimeri; ss.

OS Homo sapiens.

PN WO200213799-A2.

PD 21-FEB-2002.

PF 17-AUG-2001; 2001WO-IB001510.

PR 18-AUG-2000; 2000US-0226086P.

PA (UYMC-) UNIV MCGILL.

PI Henry JL, Cahill CM, Yashpal K;

DR WPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.

PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.

CC The invention relates to a method of treating a pathological condition

characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychosomatic and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and for treating, attenuating or preventing pain or inflammation such as peripheral, central, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders, such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK6384-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match	1.1%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 47;		
Matches 20; Conservative	0;	Mismatches	0;	Gaps 0;

QY           601 TACATGGCCATCATACATCC 620  
            |||||  
Db         20 TACATGGCCATCATACATCC 1

RESULT 109  
ABK63876

AC ABK63876;

DT 18-JUN-2002 (first entry)

Neurokinin 1 receptor (NK-1) antisense oligonucleotide #21.

XX Human; neurokinin receptor-1, NK-1; dermatological disorder;  
KW immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS  
KW neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

PN WO200213799-A2

XX 21-FEB-2002.  
 PD 17-AUG-2001; 2001WO-IB001510.  
 PF 18-AUG-2000; 2000US-0226086P.  
 XX (UYMC-) UNIV MCGILL.  
 PA Henry JL, Cahill CM, Yashpal K;  
 PI WPI; 2002-241835/29.  
 DR  
 XX Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS Claim 24; Page 65; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63857-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 XX Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 637 TCAGCCACGACCAAGT 656  
 Db 1 TCAGCCACGACCAAGT 20  
 RESULT 110  
 ABK63857/c

ID ABK63857 standard; DNA; 20 BP.  
 XX  
 AC ABK63857;  
 AC  
 DT 18-JUN-2002 (first entry)  
 DT  
 XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #8.  
 DE  
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX MO200213799-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-IB001510.  
 PF  
 XX 18-AUG-2000; 2000US-0226086P.  
 PR  
 XX (UYMC-) UNIV MCGILL.  
 PA Henry JL, Cahill CM, Yashpal K;  
 PI WPI; 2002-241835/29.  
 DR  
 XX Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS Claim 24; Page 20; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and



CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected.  
 CC reducing side effects of treatment. ABRK3834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
 QQ  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 637 TCAGCCACAGCCACCAAGT 656  
 Db 20 TCAGCCACAGCCACCAAGT 1  
 RESULT 111  
 ABRK63893  
 ID ABRK63893 standard; DNA; 20 BP.  
 AC  
 XX ABRK63893;  
 XX  
 DT 18-JUN-2002 (first entry)  
 DE  
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #38.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UNWC-) UNIV MCGILL.  
 PI Henry JL, Cahill CM, Yashpal K;  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 PS  
 XX Example 18; Page 65; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or

CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, edema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABRK3834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 CC  
 XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
 QQ  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 862 GTAGTGGGAATTCACACTATG 881  
 Db 1 GTAGTGGGAATTCACACTATG 20  
 RESULT 112  
 ABRK63895  
 ID ABRK63895 standard; DNA; 20 BP.  
 AC  
 XX ABRK63895;  
 XX  
 DT 18-JUN-2002 (first entry)  
 DE  
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #40.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder; pain;  
 KW vascular disorder; airway disorder; neuropathic disorder; inflammation;  
 KW psychiatric disorder; central nervous system disorder; intestinal condition;  
 KW respiratory condition; ophthalmic condition; depression;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UNWC-) UNIV MCGILL.  
 PI Henry JL, Cahill CM, Yashpal K;



XX WPI; 2002-241835/29.  
DR  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX  
PS Example 18; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, vasospastic diseases such as  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addition disorders such as alcoholism, neurodegenerative  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 20 BP; 7 A; 8 C; 3 G; 2 T; 0 U; 0 Other;  
Query March 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 637 TCAGCCACAGCCACCAAGT 656  
Db 1 TCAGCCACAGCCACCAAGT 20  
RESULT 113  
ABK63869/c  
ID ABK63869 standard; DNA; 20 BP.  
XX  
XX ABK63869;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DB Neurokinin 1 receptor (NK-1) antisense oligonucleotide #14.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;

KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W0200213799-A2.  
PN  
XX  
XX 21-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-IB001510.  
PF  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX  
XX (UVMC-) UNIV MCGILL.  
PA  
XX  
XX Henry JL, Cahill CM, Yashpal K;  
PI  
XX  
XX WPI; 2002-241835/29.  
DR  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX  
PS Claim 24; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, vasospastic diseases such as  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addition disorders such as alcoholism, neurodegenerative  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 20 BP; 9 A; 0 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1000 TTCACATCTTCTCTCTCT 1019  
 20 TTCACATCTTCTCTCTCTCT 1

RESULT 114  
 ID ABK63877  
 ABK63877 standard; DNA; 20 BP.

XX  
 AC ABK63877;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #22.

XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

PS Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
 XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 XX receptor, especially treating, attenuating or preventing pain or  
 XX inflammatory condition. The method comprises administering to a mammal, a  
 XX compound chosen from an oligonucleotide, its analogue, and a disruptor  
 XX which interfere with function or production of NK-1 receptors. The  
 XX method is useful for treating a pathological condition characterised by  
 XX involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 XX cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 XX psychiatric and central nervous system disorders (e.g. anxiety, panic  
 XX psychosis, schizophrenia), gut inflammation, arthritis and central or  
 XX peripheral aspects of chronic or acute pain, and for treating  
 XX attenuating or preventing pain or inflammation such as peripheral,  
 XX chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 XX pain relating to psychiatric disorders and central nervous system  
 XX disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 XX in a mammal, in particular human. NK-1 receptor related disorders,  
 XX diseases, or pathological conditions treatable by this method include  
 XX respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 XX conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 XX (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and

CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not chronically stimulating are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention

XX  
 SQ Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 601 TACATGGCCATCATCATCC 620  
 1 TACATGGCCATCATCATCC 20

RESULT 115  
 ID ABK63891  
 ABK63891 standard; DNA; 20 BP.

XX  
 AC ABK63891;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #36.

XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.

XX  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

PS Example 18; Page 65; 100pp; English.

CC The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
CC  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1012 TTCTCTGCTGCTTCATCA 1031  
Db 1 TTCTCTGCTGCTTCATCA 20  
RESULT 116  
ABR63850  
ID ABR63850 standard; DNA; 20 BP.  
XX  
XX ABR63850;  
AC  
XX 18-JUN-2002 (first entry)  
XX  
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #1.  
XX  
KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; allergy disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.

PN WO200213799-A2.  
XX  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-IB001510.  
PF  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX (UTMC-) UNIV MCGILL.  
PA  
XX Henry JL, Cahill CM, Yashpal K;  
PI WPI; 2002-241835/29.  
XX  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Claim 24; Page 20; 100pp; English.  
PS  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
CC  
XX  
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1000 TTCCACATCTTCTTCCTCT 1019  
Db 1 TTCCACATCTTCTTCCTCT 20  
RESULT 117

ABK63888/c  
ID ABK63888 standard; DNA; 20 BP.  
XX  
AC ABK63888;  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #33.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UTWC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
DR WPI; 2002-241835/29.  
XX  
PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
PS Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological

disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 20 BP; 9 A; 0 C; 9 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Dy 1000 TTCCACATCTTCTTCTCTCT 1019  
Db 20 TTCCACATCTTCTTCTCTCT 1

RESULT 118  
ABK63853/c  
ID ABK63853 standard; DNA; 20 BP.  
XX  
AC  
XX ABK63853;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #4.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UTWC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
DR WPI; 2002-241835/29.  
XX  
PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
PS Claim 24; Page 20; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety,

CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human, NK-1 receptor related disorders  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, edema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX

SO Sequence 20 BP; 6 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1012 TTCTCTGCGCCCTACATCAA 1031  
 Db 20 TTCTCTGCGCCCTACATCAA 1

RESULT 119  
 ABK63874  
 ID ABK63874 standard; DNA; 20 BP.

AC ABK63874;

DT 18-JUN-2002 (first entry)

DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #19.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.

OS Homo sapiens.

PN W0200213799-A2.

XX 21-FEB-2002.

PF 17-AUG-2001; 2001WO-IB001510.

XX 18-AUG-2000; 2000US-0226086P.

XX (UYMC-) UNIV MCGILL.

XX

PI Henry JL, Cahill CM, Yashpal K;  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

PS Claim 24; Page 65; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human, NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, edema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX

SO Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 GTATGGAAATCACATATG 881  
 Db 1 GTATGGAAATCACATATG 20

RESULT 120  
 ABK63896

ID ABK63896 standard; DNA; 20 BP.

AC ABK63896;

DT 18-JUN-2002 (first entry)

DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #41.

XX Human; neurokinin receptor-1; NK-1; dermatological disorder;

KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; orbital disease; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antinease; primer; ss.

## OS Homo sapiens.

PN WO200213799-A2.

PD 21-FEB-2002.

PF 17-AUG-2001; 2001WO-IB001510.

PR 18-AUG-2000; 2000US-0226086P.

PA (UYMC-) UNIV MCGILL.

PI Henry JL, Cahill CM, Yashpal K;

DR WPI; 2002-241835/29.

aa Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.

PS Example 18; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders, such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABRK3934-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Query Match	1.1%	Score 20	DB 1	Length 20
Best Local Similarity	100.0%	100	47	0
Matches	20	Conservative	0	Mismatches
			0	Indels
			0	Gaps
			0	0
Q7	601	TACATGGCCATCATCATCC	620	
Db	1	TACATGGCCATCATCATCC	20	
RESULT 121				
ABK63872				
ID	ABK63872	standard; DNA; 20 BP.		
XX	ABK63872;			
AC				
XX				
DT	18-JUN-2002	(first entry)		
XX				
XX				
DE	Neurokinin 1 receptor (NK-1) antisense oligonucleotide #17.			
XX				
KW	Human; neurokinin receptor-1; NK-1; dermatological disorder;			
KW	immune disorder; autoimmune disorder; cardiovascular disorder;			
KW	vascular disorder; airway disorder; neuropathic disorder; pain;			
KW	psychiatric disorder; central nervous system disorder; inflammation;			
KW	respiratory condition; ophthalmic condition; intestinal condition;			
KW	demyelinating disease; small cell lung cancer; depression;			
KW	hypersensitivity disorder; allergy; vasospastic disease; alcoholism;			
KW	neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;			
KW	neuro-pathological disorder; stress; antisense; primer; ss.			
OS	Homo sapiens.			
XX				
XX	MO00213799-A2.			
PN				
PD	21-FEB-2002.			
XX				
PF	17-AUG-2001; 2001WO-IB001510.			
XX				
PR	18-AUG-2000; 2000US-0226086P.			
XX				
PA	(UYMC-) UNIV MCGILL.			
XX				
PI	Henry JL, Cahill CM, Yashpal K;			
XX				
DR	WPI; 2002-241835/29.			
XX				
PT	Treating pathological condition involving neurokinin receptor-1, e.g.			
PT	pain or inflammation, by administering oligonucleotide or a non-			
PT	nucleotide disruptor compound which modulate NK-1 receptor biosynthetic			
PT	pathway.			
XX				
PS	Claim 24; Page 65; 100pp; English.			
XX				
CC	The invention relates to a method of treating a pathological condition			
CC	characterised partially by involvement of neurokinin receptor-1 (NK-1)			
CC	receptor, especially treating, attenuating or preventing pain or			
CC	inflammatory condition. The method comprises administering to a mammal, a			
CC	compound chosen from an oligonucleotide, its analogue, and a disruptor			
CC	which interferes with function or production of NK-1 receptors. The			
CC	method is useful for treating a pathological condition characterised by			
CC	involvement of NK-1 receptor such as dermatological, immune, neuropathic,			
CC	psychiatric and vascular disorders (e.g. migraine), airway, neuropathic,			
CC	psychiatric and central nervous system disorders (e.g. anxiety, and central or			
CC	peripheral aspects of chronic or acute pain, and for treating,			
CC	attenuating or preventing pain or inflammation such as peripheral,			
CC	chronic, acute pain or inflammation, neuropathic pain, inflammation or			
CC	pain relating to psychiatric disorders and central nervous system			
CC	disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia			
CC	in a mammal, in particular human. NK-1 receptor related disorders,			
CC	diseases, or pathological conditions treatable by this method include			
CC	respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic			
CC	conditions (e.g. conjunctivitis), cutaneous/dermatological conditions			



CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1012 TTCTCTCTGCGCTACATCAA 1031  
Db 1 TTCTCTCTGCGCTACATCAA 20

RESULT 122  
ABK63855/c  
ID ABK63855 standard; DNA; 20 BP.

AC ABK63855;  
XX

DT 18-JUN-2002 (first entry)  
XX

DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #6.  
XX

KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX

OS Homo sapiens.  
XX

PN WO200213799-A2.  
XX

PD 21-FEB-2002.  
XX

PF 17-AUG-2001; 2001WO-IB001510.  
XX

PR 18-AUG-2000; 2000US-0226086P.  
XX

PA (UVMC-) UNIV MCGILL.  
XX

PI Henry JL, Cahill CM, Yashpal K;  
XX

DR WPI; 2002-241835/29.  
XX

PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX

PS Claim 24; Page 20; 100pp; English.

XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX

SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 862 GTAGTGGGAATCACACTATG 881  
Db 20 GTAGTGGGAATCACACTATG 1

RESULT 123  
ABT16453/c  
ID ABT16453 standard; DNA; 20 BP.

AC ABT16453;  
XX

DT 20-MAR-2003 (first entry)  
XX

DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 34.  
XX

KM Cytostatic; antineoplastic; antiinflammatory; cardiant; polymorphic site;  
KM human neurokinin 1 receptor; TACRI; disease phenotype; forensics;  
KM TACRI ligand mediated disease; asthma; paternity testing; cancer;  
KM inflammation; heart disease; central nervous system; infection; PCR;  
KM primer; ss.  
XX

OS Unidentified.  
XX

PN EPI262565-A2.  
XX

PD 04-DEC-2002.

XX 23-MAY-2002; 2002EP-00253662.  
 PF 25-MAY-2001; 2001US-0293425P.  
 PR (PFIZ ) PFIZER PROD INC.  
 XX  
 PA Affourtit JP, Nelson DL, Seymour AB, Webb SM;  
 XX WPI; 2003-150228/15.  
 DR  
 XX Novel nucleic acid segment from human neurokinin 1 receptor, including  
 PT polymorphic sites for diagnosing and treating asthma, and in forensics,  
 PT paternity testing, and genetic mapping of the traits.  
 XX  
 PS Example; Page 12; 27pp; English.  
 XX  
 CC The invention relates to a nucleic acid segment from the human neurokinin  
 CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment  
 CC having a polymorphic site or a complement of the fragment. The TACR1  
 CC segment is useful for analysing a nucleic acid, by obtaining the nucleic  
 CC acid from an individual, and determining the base occupying any one of  
 CC the polymorphic sites in the segment. The nucleic acid is obtained from  
 CC several individuals, and the base occupying one of the polymorphic sites  
 CC is determined in each of the individuals, and further involves testing  
 CC each of the individuals for the presence of a disease phenotype, and  
 CC correlating the presence with the base. The TACR1 segment is useful for  
 CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.  
 CC The TACR1 segment is also useful in forensics, paternity testing,  
 CC correlating polymorphisms with phenotypic traits, and genetic mapping of  
 CC phenotypic traits. The TACR1 segment is useful in diagnosing and  
 CC monitoring of diseases such as cancer, inflammation, heart disease,  
 CC disorders of central nervous system, and susceptibility to infection to  
 CC microorganisms. The TACR1 segment is also useful in the manufacture of a  
 CC medicament for the treatment of the diseases. This polynucleotide  
 CC sequence represents a PCR primer of the human neurokinin 1 receptor  
 CC (TACR1) gene of the invention  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 355 GGCAACGTGTAGTGTG 374  
 Db 20 GGCAACGTGTAGTGTG 1  
 RESULT 124  
 ABT16465/C  
 ID ABT16465 standard; DNA; 20 BP.  
 XX  
 AC ABT16465;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX  
 DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 46.  
 XX  
 KW Cytostatic; antiasthmatic; antiinflammatory; cardiac; polymorphic site;  
 KW human neurokinin 1 receptor; TACR1; disease phenotype; forensics;  
 KW TACR1 ligand mediated disease; asthma; paternity testing; cancer;  
 KW inflammation; heart disease; central nervous system; infection; PCR;  
 KW primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1262565-A2.  
 XX  
 PD 04-DEC-2002.  
 XX  
 PF 23-MAY-2002; 2002EP-00253662.  
 XX

PR 25-MAY-2001; 2001US-0293425P.  
 XX  
 PA (PFIZ ) PFIZER PROD INC.  
 XX  
 PI Affourtit JP, Nelson DL, Seymour AB, Webb SM;  
 XX WPI; 2003-150228/15.  
 DR  
 XX Novel nucleic acid segment from human neurokinin 1 receptor, including  
 PT polymorphic sites for diagnosing and treating asthma, and in forensics,  
 PT paternity testing, and genetic mapping of the traits.  
 XX  
 PS Example; Page 12; 27pp; English.  
 XX  
 CC The invention relates to a nucleic acid segment from the human neurokinin  
 CC 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment  
 CC having a polymorphic site or a complement of the fragment. The TACR1  
 CC segment is useful for analysing a nucleic acid, by obtaining the nucleic  
 CC acid from an individual, and determining the base occupying any one of  
 CC the polymorphic sites in the segment. The nucleic acid is obtained from  
 CC several individuals, and the base occupying one of the polymorphic sites  
 CC is determined in each of the individuals, and further involves testing  
 CC each of the individuals for the presence of a disease phenotype, and  
 CC correlating the presence with the base. The TACR1 segment is useful for  
 CC diagnosing and treating TACR1 ligand mediated diseases, such as asthma.  
 CC The TACR1 segment is also useful in forensics, paternity testing,  
 CC correlating polymorphisms with phenotypic traits, and genetic mapping of  
 CC phenotypic traits. The TACR1 segment is useful in diagnosing and  
 CC monitoring of diseases such as cancer, inflammation, heart disease,  
 CC disorders of central nervous system, and susceptibility to infection to  
 CC microorganisms. The TACR1 segment is also useful in the manufacture of a  
 CC medicament for the treatment of the diseases. This polynucleotide  
 CC sequence represents a PCR primer of the human neurokinin 1 receptor  
 CC (TACR1) gene of the invention  
 CC  
 SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1483 CCCTTCATGCATGGAATTC 1502  
 Db 20 CCCTTCATGCATGGAATTC 1  
 RESULT 125  
 ABT16467/C  
 ID ABT16467 standard; DNA; 20 BP.  
 XX  
 AC ABT16467;  
 XX  
 DT 20-MAR-2003 (first entry)  
 XX  
 DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 48.  
 XX  
 KW Cytostatic; antiasthmatic; antiinflammatory; cardiac; polymorphic site;  
 KW human neurokinin 1 receptor; TACR1; disease phenotype; forensics;  
 KW TACR1 ligand mediated disease; asthma; paternity testing; cancer;  
 KW inflammation; heart disease; central nervous system; infection; PCR;  
 KW primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1262565-A2.  
 XX  
 PD 04-DEC-2002.  
 XX  
 PF 23-MAY-2002; 2002EP-00253662.  
 XX  
 PR 25-MAY-2001; 2001US-0293425P.  
 XX  
 PA (PFIZ ) PFIZER PROD INC.



XX Affourtit JP, Nelson DL, Seymour AB, Webb SM;  
PI WPI; 2003-150228/15.  
XX Novel nucleic acid segment from human neurokinin 1 receptor, including  
PT polymorphic sites for diagnosing and treating asthma, and in forensics,  
PI paternity testing, and genetic mapping of the traits.  
XX Example; Page 12; 27pp; English.  
XX The invention relates to a nucleic acid segment from the human neurokinin  
CC 1 receptor (TRACR1) gene of 10-100 nucleotides comprising a fragment  
CC having a polymorphic site or a complement of the fragment. The TRACR1  
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic  
CC acid from an individual, and determining the base occupying any one of  
CC the polymorphic sites in the segment. The nucleic acid is obtained from  
CC several individuals, and the base occupying one of the polymorphic sites  
CC is determined in each of the individuals, and further involves testing  
CC each of the individuals for the presence of a disease phenotype, and  
CC correlating the presence with the base. The TRACR1 segment is useful for  
CC diagnosing and treating TRACR1 ligand mediated diseases, such as asthma.  
CC The TRACR1 segment is also useful in forensics, paternity testing,  
CC correlating polymorphisms with phenotypic traits, and genetic mapping of  
CC phenotypic traits. The TRACR1 segment is useful in diagnosing and  
CC monitoring of diseases such as cancer, inflammation, heart disease,  
CC diseases of central nervous system, and susceptibility to infection of a  
CC microorganisms. The TRACR1 segment is also useful in the manufacture of a  
CC medicament for the treatment of the diseases. This polynucleotide  
CC sequence represents a PCR primer of the human neurokinin 1 receptor  
CC (TRACR1) gene of the invention  
XX  
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1746 GCGAGTGCTCATTTTCAGGAT 1765  
DB 20 GCGAGTGCTCATTTTCAGGAT 1  
RESULT 126  
ABT16466  
ID ABT16466 standard; DNA; 20 BP.  
XX  
AC ABT16466;  
XX  
DT 20-MAR-2003 (first entry)  
XX  
DE Human neurokinin 1 receptor gene related PCR primer SEQ ID No 47.  
XX  
KW Cytostatic; antiasthmatic; antiinflammatory; cardiac; polymorphic site;  
KW human neurokinin 1 receptor; TRACR1; disease phenotype; forensics;  
KW TRACR1 ligand mediated disease; asthma; paternity testing; cancer;  
KW inflammation; heart disease; central nervous system; infection; PCR;  
KW primer; ss.  
XX  
OS Undifferentiated.  
XX  
PN EPI262565-A2.  
XX  
PD 04-DEC-2002.  
XX  
PE 23-MAY-2002; 2002EP-00253662.  
XX  
PR 25-MAY-2001; 2001US-0293425P.  
XX  
PA (PFI2 ) PRIZER PROD INC.  
PI Affourtit JP, Nelson DL, Seymour AB, Webb SM;

DR WPI; 2003-150228/15.  
XX  
XX Novel nucleic acid segment from human neurokinin 1 receptor, including  
PT polymorphic sites for diagnosing and treating asthma, and in forensics,  
PI paternity testing, and genetic mapping of the traits.  
XX Example; Page 12; 27pp; English.  
XX The invention relates to a nucleic acid segment from the human neurokinin  
CC 1 receptor (TRACR1) gene of 10-100 nucleotides comprising a fragment  
CC having a polymorphic site or a complement of the fragment. The TRACR1  
CC segment is useful for analysing a nucleic acid, by obtaining the nucleic  
CC acid from an individual, and determining the base occupying any one of  
CC the polymorphic sites in the segment. The nucleic acid is obtained from  
CC several individuals, and the base occupying one of the polymorphic sites  
CC is determined in each of the individuals, and further involves testing  
CC each of the individuals for the presence of a disease phenotype, and  
CC correlating the presence with the base. The TRACR1 segment is useful for  
CC diagnosing and treating TRACR1 ligand mediated diseases, such as asthma.  
CC The TRACR1 segment is also useful in forensics, paternity testing,  
CC correlating polymorphisms with phenotypic traits, and genetic mapping of  
CC phenotypic traits. The TRACR1 segment is useful in diagnosing and  
CC monitoring of diseases such as cancer, inflammation, heart disease,  
CC diseases of central nervous system, and susceptibility to infection of a  
CC microorganisms. The TRACR1 segment is also useful in the manufacture of a  
CC medicament for the treatment of the diseases. This polynucleotide  
CC sequence represents a PCR primer of the human neurokinin 1 receptor  
CC (TRACR1) gene of the invention  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1417 TCCAGTGTGCTCTTCAGGC 1436  
DB 1 TCCAGTGTGCTCTTCAGGC 20  
RESULT 127  
ABD51262  
ID ABD51262 standard; DNA; 20 BP.  
XX  
AC ABD51262;  
XX  
DT 29-DEC-2005 (first entry)  
XX  
DE Human tachykinin receptor 1 (TRACR1) cDNA forward PCR primer.  
XX  
KW Screening; diagnosis; tachykinin receptor 1; TRACR1;  
KW cardiovascular disease; infection; dermatological disease;  
KW gastrointestinal disease; cancer; neoplasm; inflammation;  
KW metabolic disorder; hematological disease; respiratory disease;  
KW musculoskeletal disease; neurological disease; gynecological disorder;  
KW gynecology and obstetrics; genitourinary disease; cardiovascular-gen;  
KW cardiac; hypotensive; antimicrobial; antibacterial; fungicide; virucide;  
KW dermatological; immunosuppressive; gastrointestinal-gen.; antiinflammatory;  
KW cyostatic; immunosuppressive; anorectic; antidiabetic; antiamebic;  
KW respiratory-gen.; antiasthmatic; muscular-gen.; osteopathic;  
KW arthritic; neuroprotective; nootropic; antiparkinsonian;  
KW gynecological; antifertility; nephrotropic; metabolic; uropathic; PCR;  
KW ss; primer.  
XX  
OS Homo sapiens.  
XX  
PN W02005100986-A1.  
XX  
PD 27-OCT-2005.  
XX  
PE 02-APR-2005; 2005MO-EP003465.  
XX  
PR 15-APR-2004; 2004EP-00008923.



PT P in body fluid of arthritis patients.  
XX  
XX Disclosure; Page 8; 35pp; English.  
XX  
CC The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
CC which were used in the isolation of fragments of the human neurokinin-1  
CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
CC neurotransmitter substance P. The primers were designed using regions of  
CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
CC to be similar to human regions. Part of the human cDNA sequence was  
CC derived by amplification using these primers. The remaining part of human  
CC NK1R cDNA was obtained from a human cDNA library utilising portions of  
CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 21 BP; 7 A; 2 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 523 TGCAGTTCCACCACTTCTT 542  
Dn 21 TGCAGTTCCACCACTTCTT 2  
RESULT 130  
ABK63898  
ID ABK63898 standard; DNA; 21 BP.  
XX  
AC ABK63898;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #43.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-IB001510.  
XX  
PR 18-AUG-2000; 2000US-0226086P.  
XX  
PA (UTMC-) UNIV MCGILL.  
XX  
PI Henry JL, Cahill CM, Yashpal K;  
XX  
DR WPI; 2002-241835/29.  
XX  
PT Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
PS Example 18; Page 65; 100pp; English.  
XX  
CC The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a

CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63824-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 21 BP; 5 A; 7 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 523 TGCAGTTCCACCACTTCTT 542  
Dn 1 TGCAGTTCCACCACTTCTT 20  
RESULT 131  
ABK63879  
ID ABK63879 standard; DNA; 21 BP.  
XX  
AC ABK63879;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #24.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200213799-A2.  
XX  
PD 21-FEB-2002.  
XX

PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 65; 100pp; English.  
 PS  
 XX The invention relates to a method of treating a pathological condition  
 XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABE63834-ABE63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX  
 SQ Sequence 21 BP; 5 A; 7 C; 2 G; 7 T; 0 U; 0 Other;  
 XX  
 QY Query Match 1.1%; Score 20; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 54;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Db 523 TGCAGTTCACCACTTCTT 542  
 XX ||||||||||||||||||||  
 XX 1 TGCAGTTCACCACTTCTT 20  
 XX  
 RESULT 132  
 ABE63860/c  
 ID ABE63860 standard; DNA; 21 BP.  
 XX  
 AC ABE63860;

XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #11.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; opthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 20; 100pp; English.  
 PS  
 XX The invention relates to a method of treating a pathological condition  
 XX characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of

CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK6384-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX Sequence 21 BP; 7 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 523 TGCAGTTCACACTCTT 542  
Db 21 TGCAGTTCACACTCTT 2

RESULT 133  
AB081645  
ID AB081645 standard; DNA; 23 BP.

AC AB081645;

DT 12-DEC-2002 (first entry)

DE Oligonucleotide sense-C for the preparation of a modified NK-1 receptor.

XX Techkinin receptor; antiinflammatory; antimigraine; antidepressant;  
XX anorectic; neuroleptic; neuroprotective; tranquilizer;  
XX antianginal; dermatological; antiemetic; protein therapy; gene therapy;  
XX neurotransmission; substance P; SP; neurokinin A; NKA; neurokinin B; NKB;  
XX arthritis; pain; migraine; anxiety; schizophrenia; asthma;  
XX rheumatoid arthritis; gastrointestinal disorder; gastrointestinal tract;  
XX attention deficit disorder; premenstrual syndrome; mania; depression;  
XX inflammation; eating disorder; obesity; cognitive disorder; stress;  
XX movement disorder; schizophrenic disorder; sexual dysfunction;  
XX Alzheimer's disease; angina; multiple sclerosis; scleroderma;  
XX central nervous system disorder; NK-1v; ss.

OS Synthetic.

PN GB2370274-A.

XX 26-JUN-2002.

PF 19-DEC-2000; 2000GB-00031148.

PR 19-DEC-2000; 2000GB-00031148.

PA (WARN ) WARNER LAMBERT CO.

PI Hall MD, McNulty S, Murray JH, Suman-Chauhan N;

DR WPI; 2002-638104/69.

PT Novel modified tachykinin receptors useful for removing or suppressing  
PT substance P in body fluids, and treatment or prophylaxis of a condition  
PT associated with substance P or other tachykinin receptor-binding ligand.

PS Example 1; Page 27; 45pp; English.

XX The invention relates to a mutant tachykinin receptor in which the three  
CC amino acids of the DRV sequence that occurs adjacent to the junction of  
CC the TM3 domain with intracellular loop 2 are replaced with amino acids  
CC whose side chains are neither lipophilic nor contain charged groups.  
CC Mammalian tachykinins include substance P (SP), neurokinin A (NKA) and  
CC neurokinin B (NKB). The mutant receptor of the invention is useful for  
CC treatment or prevention of a condition associated with over-expression or  
CC inappropriate or of an endogenous tachykinin ligand, including protein and  
CC gene therapy. It is useful as a substitute in an assay to identify and/or  
CC evaluate entities that bind to the wild type tachykinin receptor, and in  
CC an assay to determine the concentration of ligand in body fluids in  
CC patients with arthritis, pain, migraine, anxiety, schizophrenia, asthma,  
CC rheumatoid arthritis and in gastrointestinal disorders and diseases of

CC the gastrointestinal tract. Other conditions or disease states that can  
CC be treated, ameliorated or prevented include, attention deficit disorder,  
CC premenstrual syndrome, mania, depression, inflammation, eating disorders,  
CC such as obesity, cognitive disorders, movement disorders, schizophrenic  
CC disorders, sexual dysfunction, stress, Alzheimer's disease, angina,  
CC multiple sclerosis, scleroderma, central nervous system (CNS) disorders  
CC and other conditions where excess tachykinin peptides such as SP are  
CC involved. Tachykinins have an established role in neurotransmission. The  
CC current sequence represents an oligonucleotide designated sense-C, used  
CC in an example from the invention for the preparation of a modified human  
CC NK-1 receptor (NK-1v) by site-directed mutagenesis  
XX

SO Sequence 23 BP; 3 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.8; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 73;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 438 CGCGAGGCTTCATGCTGCAT 460  
Db 1 CGCGAGGCTTCATGCTGCAT 23

RESULT 134

ID ADU41834 standard; DNA; 21 BP.

XX ADU41834;

DT 27-JAN-2005 (first entry)

DE knock-down target sequence #7013.

XX ds; RNA production; protein production; drug development;  
XX knock-down target.

OS Unidentified.

PN W02004094636-A1.

XX 04-NOV-2004.

PF 24-APR-2003; 2003WO-EP004362.

PR 24-APR-2003; 2003WO-EP004362.

PA (GALA-) GALAPAGOS GENOMICS NV.

PA (VSCB/) VAN DER SCHUREN J.

PI Arts GJF, Lambrecht MJY, Djokic K, Claesen RJ, Meaic E;

DR WPI; 2004-775940/76.

PT New knockdown sequences, useful in lowering the amount of RNA and/or  
PT protein production in cells used in drug development process.

PS Claim 11; SEQ ID NO 7062; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The  
CC polynucleotides, vector, libraries, and method are useful in lowering the  
CC amount of RNA and/or protein production in cells used in drug development  
CC process. The present sequence represents a knock-down target sequence.

SO Sequence 21 BP; 3 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 67;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1135 AATGACAGGTTCCGTGCGC 1155  
Db 1 ACTGACAGGTTCCGTGCGC 21

RESULT 135

ADU41833 standard; DNA; 21 BP.

ADU41833;

27-JAN-2005 (first entry)

Knock-down target sequence #7012.

ds; RNA production; protein production; drug development;

knock-down target.

Unidentified.

WO2004094636-A1.

04-NOV-2004.

24-APR-2003; 2003WO-EP004362.

24-APR-2003; 2003WO-EP004362.

(GALA-) GALAPAGOS GENOMICS NV.

(VSCN/) VAN DER SCHUREN J.

Arts GJF, Lambrecht MY, Djokic K, Clasen RJ, Mesic E;

Griffioen S, Bergs CJL;

WPI; 2004-775940/76.

New knockdown sequences, useful in lowering the amount of RNA and/or

protein production in cells used in drug development process.

Claim 11; SEQ ID NO 7061; 402pp; English.

The invention relates to a polynucleotide comprising an RNA sequence. The

amount of RNA and/or protein production in cells used in drug development

process. The present sequence represents a knock-down target sequence.

Sequence 21 BP; 4 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 67;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

526 AAGTTCACAACTTCTTCCC 546

1 ACGTTCACAACTTCTTCCC 21

RESULT 136

AA067148 standard; DNA; 24 BP.

AA067148;

25-MAR-2003 (revised)

21-MAR-1995 (first entry)

Primer for amplifying HTLV envelope coding region.

Immunisation; vaccine; therapy; prophylaxis; defective gene;

non-functional gene; template; antisense; ribozyme; bupivacaine; HTLV;

human T-cell lymphotropic virus; ss.

04-AUG-1994.

26-JAN-1994; 94WO-US000899.

26-JAN-1993; 93US-0008342.

11-MAR-1993; 93US-0009336.

15-JUL-1993; 93US-0009323.

21-SEP-1993; 93US-00124962.

21-SEP-1993; 93US-00125012.

(WEIN/) WEINER D B.

(WILL/) WILLIAMS W V.

(WANG/) WANG B.

(CONE/) CONEY L R.

(MERY/) MERYA M U.

(ZURA/) ZURAWSKI V R.

Weiner DB, Williams WV, Wang B, Coney LR, Merya MU, Zurawski VR;

WPI; 1994-263787/32.

Method for introducing genetic material into cells - utilises

polynucleotide function enhancer and nucleic acid free of retroviral

particles, e.g. HIV immunisation.

Example 22; Page 54; 136pp; English.

Two primers (AA067148, AA067149) were used to amplify a DNA segment

encoding the entire envelope region from HTLV-1/TSP and /ATK isolates.

The genetic material can then be introduced into the cells of an

individual by (a) contacting the individual's cells with a polynucleotide

function enhancer (bupivacaine) and (b) administering to the cells the

nucleic acid molecule free of retroviral particles. Nucleic acid

molecules which are delivered to cells may serve as genetic templates for

proteins that function as prophylactic and/or therapeutic immunising

agents; replacement copies of defective, missing or non-functional genes;

CC genetic templates for therapeutic proteins; genetic templates for

CC antisense molecules or as genetic templates for ribozymes. The HTLV env

CC target protein is useful in the immunisation against and treatment of

CC infection by HTLV and T-cell lymphoma. (Updated on 25-MAR-2003 to correct

CC PN field.)

Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

885 CAGTGAATCCCGGAGACTCTC 908

1 CAGTGAATATCCCGGAGACTCTC 24

RESULT 137

AAT00836 standard; DNA; 24 BP.

AAT00836;

16-MAY-1996 (first entry)

HTLV-1 strains TSP and ATK envelope coding region 5' primer.

Immunisation; disease; pathogen; genetic vaccine facilitator; saponin;

antionic lipid; lectin; oestrogen; alkyl, dimethylsulphoxide; urea; PCR;

retroviral particle; retrovirus; HIV; SIV; epitope; primer; envelope;

amplification; HTLV; lymphoma; ss.

Synthetic.

WO9526718-A1.

12-OCT-1995.

```
XX PF 30-MAR-1995; 95MO-US004071.
XX XX
XX PR 01-APR-1994; 94US-00221579.
XX XX
XX PA (APOL-) APOLLON INC.
XX XX
XX PI Carrano RA;
XX XX
XX DR WPI; 1995-358434/46.
XX XX
XX PT Introducing genetic material into cells of an individual - by contacting
XX PT the cells with a genetic vaccine facilitator and a nucleic acid molecule.
XX XX
XX PS Example 19; Page 50; 114pp; English.
XX XX
XX CC Immunisation of an individual against a disease or pathogen comprises
XX CC introducing genetic material (a genetic vaccine) into the cell of the
XX CC individual by contacting the cell with a genetic vaccine facilitator
XX CC (GVF) selected from anionic lipid, saponins, lectins, oestrogenic cpds.,
XX CC hydroxylated lower alkyls, dimethylsulphoxide (DMSO) or urea, and a
XX CC nucleic acid that is free of retroviral particles. The primers AAT00830-
XX CC 71 are used in the construction of the genetic vaccines based on sequences
XX CC of HIV, SIV or pathogenic bacterial epitopes. The primers AAT00836-7 were
XX CC used to amplify the human T-cell lymphoma virus (HTLV)-1 envelope protein
XX CC gene for construction of the plasmid pCISK/ATK-env. The env protein is
XX CC useful for immunisation against and treatment of HTLV infection and T
XX CC cell lymphoma
XX XX
XX SQ Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 1.1%; Score 19.2; DB 1; Length 24;
XX Best Local Similarity 87.5%; Pred. No. 1e+02;
XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 885 CAGTGAATCCCCGGAGACTCTC 908
DB 1 CAGTGAATCCCCGGAGACTCTC 24
RESULT 138
ABSS5989/c
ID ABSS5989 standard; DNA; 19 BP.
XX AC
XX ABSS5989;
XX DT
XX 05-NOV-2002 (first entry)
XX XX
DE Human DNA representing a single nucleotide polymorphism #49.
XX XX
XX AMinopeptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;
XX KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;
XX KM KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
XX KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
XX KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX KM cardiovascular disease; angina pectoris; hypertension; heart failure;
XX KM myocardial infarction; ventricular hypertrophy; vascular disease;
XX KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
XX KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
XX KM autoimmune disease; inflammatory arthritis; cancer; wound;
XX KM viral infection; bacterial infection; fungal infection; COPD;
XX KM chronic obstructive pulmonary disease; enterocolitis;
XX KM single-nucleotide polymorphism.
XX XX
XX Homo sapiens.
XX OS
XX PN MO200261131-A2.
XX XX
XX PD 08-AUG-2002.
XX XX
XX PF 03-DEC-2001; 2001WO-US047235.
XX XX
XX PR 04-DEC-2000; 2000US-0251015P.
```

```
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PA (TSUC/) TSUCHIHASHI Z.
XX PA (HUI/L/) HUI L.
XX XX
XX PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX PI Swanson BN, Powell JR;
XX XX
XX DR WPI; 2002-619265/66.
XX XX
XX PT New isolated nucleic acid with at least one polymorphic position, useful
XX PT for detecting, diagnosing and treating disorders such as angiodema,
XX PT cancer, viral, bacterial or fungal infection, cardiovascular and
XX PT autoimmune diseases.
XX XX
XX PS Disclosure; Page 653; 977pp; English.
XX XX
XX CC The invention relates to an isolated nucleic acid from a human gene
XX CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
XX CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
XX CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX CC polymorphic position. Also included are (1) a probe that hybridises to a
XX CC polymorphic position as provided in the detailed summary of single
XX CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX CC obtaining the sample from one or more individuals and determining the
XX CC nucleic acid sequence at one or more polymorphic positions in a gene
XX CC encoding a protein selected from the group above; (3) constructing (M2)
XX CC haplotypes using the genes comprising grouping at least two nucleic acids
XX CC ; (4) identifying (M3) an individual at risk of developing a disorder
XX CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
XX CC using the polymorphic data; (5) a library of nucleic acids, each of which
XX CC comprises one or more polymorphic positions within a gene encoding a
XX CC human protein selected from the group above; and (6) genotyping (M4) an
XX CC individual comprising obtaining a nucleic acid sample, determining the
XX CC nucleotide present in at least one polymorphic position, and comparing at
XX CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX CC and compositions are useful for detecting, diagnosing, treating,
XX CC preventing various disorders such as angiodaema and diseases which
XX CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX CC disease, trachomas, and cardiovascular diseases like angina pectoris,
XX CC hypertension, heart failure, myocardial infarction, ventricular
XX CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX CC artery disease, arteriosclerosis and/or atherosclerosis, and
XX CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX CC arthritis, cancer, wounds, viral, bacterial or fungal infection, chronic
XX CC obstructive pulmonary disease (COPD) and enterocolitis (many other
XX CC diseases and disorders are listed in the specification). The
XX CC polymorphisms are also useful for chromosome identification. Antibodies
XX CC against the proteins may be utilised for immunophenotyping of cell lines
XX CC and biological samples. The present sequence represents or contains the
XX CC region surrounding a single-nucleotide polymorphism in one of the genes
XX CC encoding one of the proteins listed above
XX XX
XX SQ Sequence 19 BP; 6 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 59;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1626 TCATGCTGTGTGACTCAA 1644
DB 19 TCATGCTGTGTGACTCAA 1
RESULT 139
ABSS5963/c
ID ABSS5963 standard; DNA; 19 BP.
XX AC
XX ABSS5963;
```



XX 05-NOV-2002 (first entry)

XX Human DNA representing a single nucleotide polymorphism #113.

XX Antinopeptidase P; XPNBP2; bradykinin receptor B1; de; SNP; BDKRB1;

XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;

XX KUK1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis;

XX single-nucleotide polymorphism.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX (TSUC/) TSUCHIHASHI Z.

XX (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

XX for detecting, diagnosing and treating disorders such as angioedema,

XX cancer, viral, bacterial or fungal infection, cardiovascular and

XX autoimmune diseases.

XX Disclosure; Page 663; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene

XX encoding antinopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),

XX tachykinin receptor B1 (TACR1), CI esterase inhibitor (C1NH), kallikrein

XX 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

XX polymorphic position. Also included are (1) a probe that hybridises to a

XX nucleotide position as provided in the detailed summary of single

XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising

XX obtaining the sample from one or more individuals and determining the

XX nucleic acid sequence at one or more polymorphic positions in a gene

XX encoding a protein selected from the group above; (3) constructing (M2)

XX haplotypes using the genes comprising grouping at least two nucleic acids

XX; (4) identifying (M3) an individual at risk of developing a disorder

XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

XX using the polymorphic data; (5) a library of nucleic acids, each of which

XX comprises one or more polymorphic positions within a gene encoding a

XX human protein selected from the group above; and (6) genotyping (M4) an

XX individual comprising obtaining a nucleic acid sample, determining the

XX nucleotide present in at least one polymorphic position, and comparing at

XX least one position with a known data set. The genes, (M1, M2, M3 and M4)

XX and compositions are useful for detecting, diagnosing, treating,

XX preventing various disorders such as angioedema and diseases which

XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

XX disease, trachomas, and cardiovascular diseases like angina pectoris,

XX hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence represents or contains the

CC region surrounding a single-nucleotide polymorphism in one of the genes

CC encoding one of the proteins listed above

XX

XX Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

XX

XX Query Match 1.1%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 59;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX QY 1529 CCTCACACTGGGACTTGA 1547

XX Db 19 CCTCACACTGGGACTTGA 1

XX

XX RESULT 140

XX ABS59895

XX ID ABS59895 standard; DNA; 19 BP.

XX AC ABS59895;

XX AC

XX DT 05-NOV-2002 (first entry)

XX XX

XX Human DNA representing a single nucleotide polymorphism #45.

XX

XX Antinopeptidase P; XPNBP2; bradykinin receptor B1; de; SNP; BDKRB1;

XX tachykinin receptor B1; TACR1; CI esterase inhibitor; C1NH; kallikrein 1;

XX KUK1; bradykinin receptor B2; BDKRB2; gene therapy;

XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

XX cardiovascular disease; angina pectoris; hypertension; heart failure;

XX myocardial infarction; ventricular hypertrophy; vascular disease;

XX aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;

XX autoimmune disease; inflammatory arthritis; cancer; wound;

XX viral infection; bacterial infection; fungal infection; COPD;

XX Chronic obstructive pulmonary disease; enterocolitis;

XX single-nucleotide polymorphism.

XX

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX (TSUC/) TSUCHIHASHI Z.

XX (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

XX Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

XX for detecting, diagnosing and treating disorders such as angioedema,

XX cancer, viral, bacterial or fungal infection, cardiovascular and

XX autoimmune diseases.



PS Disclosure; Page 653; 977bp; English.

XX The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),

CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

CC polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single

CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC / (4) identifying (M3) an individual at risk of developing a disorder

CC upon administration of an ACE inhibitor and/or vasopressin inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)

CC and compositions are useful for detecting, diagnosing, treating, which

CC preventing various disorders such as angioedema and diseases which

CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

CC disease, trachomas, and cardiovascular diseases like angina pectoris,

CC hypertrophy, heart failure, myocardial infarction, ventricular

CC artery disease, arteriosclerosis and/or atherosclerosis, coronary

CC hyperpermeability reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polymorphisms are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence represents or contains the

CC region surrounding a single- nucleotide polymorphism in one of the genes

CC encoding one of the proteins listed above

XX

SQ Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. NO. 59;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

534 CAACCTCTTCCATCGCC 552

1 CAACCTCTTCCATCGCC 19

RESULT 141

ABSS59901/c

ID ABSS59901 standard; DNA; 19 BP.

XX

AC ABSS59901;

XX

XX 05-NOV-2002 (first entry)

XX

DE Human DNA representing a single nucleotide polymorphism #51.

XX

KM Aminopeptidase P, XPNP2; bradykinin receptor B1; de; SNP; BDRB1;

KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; Kallikrein 1;

KM KLK1; bradykinin receptor B2; BDRB2; gene therapy;

KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

KM polymorphisms; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

KM cardiovascular disease; angina pectoris; hypertension; heart failure;

KM myocardial infarction; ventricular hypertrophy; vascular disease;

KM aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

KM arteriosclerosis; atherosclerosis; hyperpermeability; sepsis;

KM autoimmune disease; inflammatory arthritis; cancer; wound;

KM viral infection; bacterial infection; fungal infection; COPD;

KM Chronic obstructive pulmonary disease; enterocolitis;

KM single-nucleotide polymorphism.

XX

OS Homo sapiens.

XX

XX MO200261131-A2.

XX

PD 08-AUG-2002.

XX

XX 03-DEC-2001; 2001MO-US047235.

XX

PP 04-DEC-2000; 2000US-0251015P.

XX

PR 23-JAN-2001; 2001US-0263678P.

PR

PR 02-MAR-2001; 2001US-0273037P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PA

PA (TSCU/) TSUCHIHASHI Z.

PA

PA (HUI/) HUI L.

XX

PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

PI Swanson BN, Powell JR,

XX

XX WPI; 2002-619265/66.

XX

PT New isolated nucleic acid with at least one polymorphic position, useful

PT for detecting, diagnosing and treating disorders such as angioedema,

PT cancer, viral, bacterial or fungal infection, cardiovascular and

PT autoimmune diseases.

XX

PS Disclosure; Page 653; 977bp; English.

XX

CC The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),

CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

CC polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single

CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC / (4) identifying (M3) an individual at risk of developing a disorder

CC upon administration of an ACE inhibitor and/or vasopressin inhibitor.

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)

CC and compositions are useful for detecting, diagnosing, treating, which

CC preventing various disorders such as angioedema and diseases which

CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

CC disease, trachomas, and cardiovascular diseases like angina pectoris,

CC hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hyperpermeability reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polymorphisms are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence represents or contains the

CC region surrounding a single- nucleotide polymorphism in one of the genes

CC encoding one of the proteins listed above

XX

SQ Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. NO. 59;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1335 CACACCTCTGCTGAGAC 1353  
 |||||  
 Db 19 CACACCTCTGCTGAGAC 1

RESULT 142  
 ABR59959/c  
 ID ABR59959 standard; DNA, 19 BP.  
 AC ABR59959;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human DNA representing a single nucleotide polymorphism #109.  
 XX  
 KW Aminopectidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;  
 KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
 KW KUK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW chronic obstructive pulmonary disease; enterocolitis;  
 KW single-nucleotide polymorphism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 XX  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 DR WPI; 2002-619265/66.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 PT  
 PS Disclosure; Page 663; 977pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KUK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases, like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). Antibodies  
 CC polynucleotides are also useful for chromosome identification. Cell lines  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence represents or contains the  
 CC region surrounding a single-nucleotide polymorphism in one of the genes  
 CC encoding one of the proteins listed above

SQ Sequence 19 BP; 7 A; 6 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 663 CTGTGTCATCTGGTCTCTG 681  
 |||||  
 Db 19 CTGTGTCATCTGGTCTCTG 1

RESULT 143  
 ABR63901/c  
 ID ABR63901 standard; DNA, 19 BP.  
 XX  
 AC ABR63901;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #46.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ophthalmic condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 PI Henry UL, Cahill CM, Yashpal K;  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic

PT pathway.  
XX  
XX Example 18; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, vasospastic diseases such as  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 GTGTACGATGTAGGCTT 194  
DB 19 GTGTACGATGTAGGCTT 1  
RESULT 144  
ABK63865/C  
ID ABK63865 standard; DNA; 19 BP.  
AC ABK63865;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #16.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; ophthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;

KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200213799-A2.  
XX  
XX  
XX 21-FEB-2002.  
PD  
XX  
XX 17-AUG-2001; 2001WO-IB001510.  
PF  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX (UMC-) UNIV MCGILL.  
PA  
XX Henry JL, Cahill CM, Yashpal K;  
XX  
XX WPI; 2002-241835/29.  
DR  
XX  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX  
XX Claim 24; Page 20; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, vasospastic diseases such as  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 19 BP; 5 A; 7 C; 1 G; 6 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1548 AAAAGGCTCAGTAGGCTT 1566  
|||||

Db 19 AAAAGGTGATAGGCTT 1

RESULT 145  
ABK63882/c  
ID ABK63882 standard; DNA; 19 BP.  
AC ABK63882;  
XX 18-JUN-2002 (first entry)  
DT  
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #27.  
DE  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW human disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200213799-A2.  
PN  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-1B001510.  
PF  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX (UWMC-) UNIV MCGILL.  
PA  
XX Henry JL, Cahill CM, Yashpal K;  
PI  
XX WPI; 2002-241835/29.  
DR  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
PS Claim 24; Page 65; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine, airway, neuropathic, cardiovascular, nervous system disorders (e.g. anxiety, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia disorders, including hyperalgesia, NK-1 receptor related disorders, in a mammal, in particular conditions treatable by this method include diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastro-intestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity

disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related disorders, epilepsy, Alzheimer's disease, and other neuro-pathological disorders, such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best local Similarity 100.0%; Pred. No. 59;  
Matches 19; Conservative 0; Mismatches 0; Gaps 0;

QY 176 GTGTACAGTATAGGCTT 194  
Db 19 GTGTACAGTATAGGCTT 1

RESULT 146  
ABK63863  
ID ABK63863 standard; DNA; 19 BP.  
AC ABK63863;  
XX 18-JUN-2002 (first entry)  
DT  
XX Neurokinin 1 receptor (NK-1) sense oligonucleotide #14.  
DE  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW human disorder; autoimmune disorder; cardiovascular disorder;  
KW immune disorder; airway disorder; neuropathic disorder; pain;  
KW vascular disorder; central nervous system disorder; inflammation;  
KW psychiatric disorder; ophthalmic condition; intestinal condition;  
KW respiratory condition; small cell lung cancer; depression;  
KW demyelinating disease; allergy; vasospastic disease; alcoholism;  
KW hypersensitivity disorder; acquired immune deficiency syndrome; AIDS;  
KW neurodegenerative disorder; stress; antisense; primer; ss.  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200213799-A2.  
PN  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-1B001510.  
PF  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX (UWMC-) UNIV MCGILL.  
PA  
XX Henry JL, Cahill CM, Yashpal K;  
PI  
XX WPI; 2002-241835/29.  
DR  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
PS Claim 24; Page 20; 100pp; English.

The invention relates to a method of treating a pathological condition characterised partially by involvement of neurokinin receptor-1 (NK-1) receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The

CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention

SO Sequence 19 BP; 5 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACGATGATGAGCTT 194  
 |||||  
 Db 1 GTGTACGATGATGAGCTT 19

RESULT 147  
 ABR63903 standard; DNA; 19 BP.

AC ABR63903;  
 XX  
 XX 18-JUN-2002 (first entry)  
 XX  
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #48.  
 DE  
 XX  
 XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 KM  
 OS Homo sapiens.  
 XX  
 XX  
 XX W0200213799-A2.  
 XX  
 XX 21-FEB-2002.  
 XX  
 XX 17-AUG-2001; 2001WO-IB001510.  
 XX  
 XX

PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 XX (UTMC-) UNIV MCGILL.  
 XX  
 XX Henry JL, Cahill CM, Yaehpal K;  
 XI  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 XX  
 XX Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.

PS Example 18; Page 66; 100pp; English.

XX  
 XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected,  
 CC reducing side effects of treatment. ABR63834-ABR63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention

SO Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGAGCTT 1566  
 |||||  
 Db 1 AAAAGGTCAGTATGAGCTT 19

RESULT 148  
 ABR63884  
 ID ABR63884 standard; DNA; 19 BP.  
 XX  
 XX ABR63884;  
 AC  
 XX 18-JUN-2002 (first entry)  
 DT

DE XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #29.  
 XX  
 XX Human, neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200213799-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2001; 2001WO-IB001510.  
 XX  
 XX 18-AUG-2000; 2000US-0226086P.  
 PR  
 XX (UWMC-) UNIV MCGILL.  
 PA  
 XX Henry JL, Cahill CM, Yashpal K;  
 PI  
 XX WPI; 2002-241835/29.  
 DR  
 XX  
 XX Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 XX Claim 24; Page 65; 100pp; English.  
 PS  
 XX  
 XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (stroke), chronic  
 CC (Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected.

CC reducing side effects of treatment. ABE63834-ABE63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX  
 XX Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 1.1%; Score 19; DB 1; Length 19;  
 XX Best Local Similarity 100.0%; Pred. No. 59;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY  
 XX 1548 AAAAGGTCAGTATGGGTT 1566  
 XX |||||  
 Db 1 AAAAGGTCAGTATGGGTT 19  
 RESULT 149  
 AEB29146  
 ID AEB29146 standard; DNA; 19 BP.  
 XX  
 XX AEB29146;  
 AC  
 XX 22-SEP-2005 (first entry)  
 DT  
 XX  
 XX Human siRNA molecule #52.  
 DE  
 XX Cell differentiation; osteoblast; bone; short interfering RNA; siRNA;  
 KM gene silencing; RNA interference; osteoporosis; hypercalcemia;  
 KM multiple myeloma; hyperparathyroidism; hyperthyroidism; osteopathic;  
 KM endocrine-gen.; antihypertoid; cardiovascular-gen.; CNS-Gen.;  
 KM gastrointestinal-gen.; cytostatic; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO2005063983-A1.  
 PN  
 XX 14-JUL-2005.  
 XX  
 XX 29-DEC-2003; 2003WO-EP014994.  
 XX  
 XX 29-DEC-2003; 2003WO-EP014994.  
 PR  
 XX (GALA-) GALAPAGOS GENOMICS NV.  
 PA  
 XX Van Rompaey LJC, Tonne PPM, Brown RJ;  
 PI  
 XX WPI; 2005-522575/53.  
 DR  
 XX  
 XX Inducing differentiation of undifferentiated mammalian cells into  
 PT osteoblasts, for treating e.g. osteoporosis, by contacting the cell with  
 PT an expression or translation inhibitory agent for a polyribonucleotide  
 PT encoding a polypeptide.  
 XX  
 XX Claim 9; SEQ ID NO 52; 88pp; English.  
 PS  
 XX  
 XX The invention relates to a method of inducing differentiation of  
 CC undifferentiated mammalian cells into osteoblasts comprising inhibiting  
 CC the biological activity of a polypeptide, its fragments and/or  
 CC derivatives, comprising contacting the cell with an expression or  
 CC translation inhibitory agent that inhibits the expression or translation  
 CC in the cell of a polyribonucleotide encoding the polypeptide. The  
 CC invention also relates to a method of identifying a compound that induces  
 CC differentiation of undifferentiated mammalian cells into osteoblasts, a  
 CC vector comprising a nucleotide sequence of the invention, in vitro  
 CC production of bone tissue, osteoblast cells obtainable by the method and  
 CC a method of diagnosing a pathological condition involving a systemic or  
 CC local decrease in mean bone density or a susceptibility to the condition  
 CC in a subject. In the method above, the expression inhibitory agent is  
 CC selected from antisense RNA, a nucleic acid expressing the antisense RNA,  
 CC a ribozyme that cleaves the polyribonucleotide, an antisense  
 CC oligodeoxynucleotide, a small interfering RNA (siRNA) that is  
 CC sufficiently homologous to a portion of the polyribonucleotide such that  
 CC the siRNA is capable of inhibiting the polyribonucleotide that would  
 CC otherwise cause the production of the polypeptide, and an antibody  
 CC reactive to the polypeptide. The osteoblast cells are useful for in vitro



CC production of bone tissue. The polynucleotide or the vector is useful as  
 CC a medicament or for manufacturing a medicament for the treatment of a  
 CC disease involving a systemic or local decrease in mean bone density,  
 CC selected from osteoporosis, hypercalcaemia, multiple myeloma,  
 CC hyperparathyroidism and hyperthyroidism. The method is useful for  
 CC inducing differentiation of undifferentiated mammalian cells into  
 CC osteoblasts. This sequence represents a human siRNA molecule of the  
 CC invention.

XX  
 SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1137 TGACAGGTTCCGTCGTGGGC 1155  
 Db 1 TGACAGGTTCCGTCGTGGGC 19

RESULT 150  
 AEB54827  
 ID AEB54827 standard; DNA, 19 BP.  
 AC AEB54827;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE siRNA targeting human TACR1 gene SEQ ID 53.  
 XX  
 KM Osteoblast; differentiation; bone; gene silencing; RNA interference;  
 KM siRNA; short interfering RNA; ss; osteoporosis; osteopathic;  
 KM muscular-gen.; cytostatic; antiarthritic; antirheumatic;  
 KM antiinflammatory; musculoskeletal disease; Paget's disease; bone disease;  
 KM rheumatoid arthritis; periodontal disease; rickets; osteogenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005063976-A2.  
 XX  
 PD 14-JUL-2005.  
 XX  
 PF 29-DEC-2004; 2004WO-EP014885.  
 XX  
 PR 29-DEC-2003; 2003WO-EP014994.  
 XX  
 XX (GALA-) GALAPAGOS GENOMICS NV.  
 PA Van Rompaey LJC, Tomme PHM, Brown RJ;  
 PI WPI; 2005-541824/55.  
 XX  
 DR WPI; 2005-541824/55.  
 XX  
 PT Inducing differentiation of undifferentiated mammalian cells into  
 PT osteoblasts, comprises contacting undifferentiated cells with inhibitors  
 PT of polypeptides of isolated knock-down constructs and corresponding  
 PT target gene sequences.

XX  
 PS Claim 8; SEQ ID NO 53; 98bp; English.  
 XX  
 XX The invention relates to inducing differentiation of undifferentiated  
 CC mammalian cells into osteoblasts, comprising contacting the  
 CC undifferentiated cells with an inhibitor of any of the 220 polypeptides  
 CC given in the specification (table 4 for overview of isolated knock-down  
 CC constructs and corresponding target gene sequences), their fragments  
 CC and/or derivatives. Also included are identifying a compound that induces  
 CC differentiation of undifferentiated mammalian cells into osteoblasts  
 CC (comprising contacting one or more compounds with a polypeptide listed in  
 CC table 4 of the specification, encoded by any of the genes listed in table  
 CC 4 of the specification, and/or their fragments and/or derivatives,  
 CC determining the binding affinity of the compound to the polypeptide,  
 CC contacting a population of undifferentiated mammalian cells with the  
 CC compound that exhibits a binding affinity of at least 10 micromolar and  
 CC identifying the compound that induces the differentiation of the

CC undifferentiated mammalian cells), identifying a compound or mixture of  
 CC compounds that induces differentiation of undifferentiated mammalian  
 CC cells into osteoblasts, a polynucleotide comprising a sequence of 17-23  
 CC nucleotides homologous to a nucleotide sequence of the target genes  
 CC listed in table 4 of the specification, a vector comprising a  
 CC polynucleotide comprising a sequence of 17-23 nucleotides, in vitro  
 CC production of bone tissue (comprising applying undifferentiated mammalian  
 CC cells on a substrate to form a cellular substrate, introducing a  
 CC polynucleotide comprising a sequence of 17-23 nucleotides or a vector  
 CC comprising the polynucleotide to differentiate the undifferentiated cells  
 CC into osteoblasts, to produce a continuous bone matrix), diagnosing a  
 CC pathological condition involving a systemic or local decrease in mean  
 CC bone density (or a susceptibility to the condition) in a subject (  
 CC comprising determining the level of expression of a polynucleotide  
 CC encoded by any of the target genes (listed in table 4 of the  
 CC specification) in a biological sample and comparing the level of  
 CC expression with the level of expression of the polynucleotides in a  
 CC sample derived from a healthy subject, and diagnosing a pathological  
 CC condition involving a systemic or local decrease in mean bone density (or  
 CC a susceptibility to the condition) comprising determining the amount of  
 CC polypeptide encoded by the genes. The method is useful for inducing  
 CC differentiation of undifferentiated mammalian cells into osteoblasts. The  
 CC vector comprising the polynucleotide is useful in medicaments for the  
 CC treatment of diseases involving a systemic or local decrease in mean bone  
 CC density. The method is useful for in vitro production of bone tissue and  
 CC osteoblast cells, and for diagnosing a pathological condition involving a  
 CC systemic or local decrease in mean bone density or a susceptibility to  
 CC the condition (e.g. osteoporosis, musculoskeletal disease, Paget's  
 CC disease, bone disease, rheumatoid arthritis, periodontal disease,  
 CC Crohn's syndrome, rickets, opsismodysplasia, pycnodysostosis, Toulouse-  
 CC Lautrec syndrome and osteogenesis). The present sequence is an siRNA  
 CC (short interfering RNA) that targets the mRNA of a gene listed in table 4  
 CC or 5 of the specification (genes which, when their expression is reduced,  
 CC promote differentiation into osteoblasts). NOTE: The present sequence is  
 CC described as an siRNA but appears as a DNA sequence.

XX  
 SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1137 TGACAGGTTCCGTCGTGGGC 1155  
 Db 1 TGACAGGTTCCGTCGTGGGC 19

RESULT 151  
 AED51263/c  
 ID AED51263 standard; DNA, 19 BP.  
 XX  
 AC AED51263;  
 XX  
 DT 29-DEC-2005 (first entry)  
 XX  
 DE Human tachykinin receptor 1 (TACR1) cDNA reverse PCR primer.  
 XX  
 XX Screening; diagnosis; tachykinin receptor 1; TACR1;  
 KM cardiovascular disease; infection; dermatological disease;  
 KM gastrointestinal disease; cancer; neoplasm; inflammation;  
 KM metabolic disorder; hematological disease; respiratory disease;  
 KM musculoskeletal disease; neurological disease; gynecological disorder;  
 KM gynecology and obstetrics; genitourinary disease; cardiovascular-gen.;  
 KM cardiac; hypotensive; antimicrobial; antibacterial; fungicide; virucide;  
 KM dermatological; antiproliferative; gastrointestinal-gen.; antinflammatory;  
 KM cytoskeletal; immunosuppressive; anorectic; antidiabetic; antiamebic;  
 KM respiratory-gen.; antiaschemic; muscular-gen.; osteopathic;  
 KM antiarthritic; neuoprotective; nocotropic; antiparkinsonian;  
 KM gynecological; antifertility; nephrotropic; metabolic; uropathic; PCR;  
 KM ss; primer.  
 XX  
 OS Homo sapiens.  
 XX

PN WO2005100986-A1.  
 XX  
 XX 27-OCT-2005.  
 PD  
 XX  
 PF 02-APR-2005; 2005WO-EP003465.  
 XX  
 XX 15-APR-2004; 2004EP-00008923.  
 PR  
 XX (PARB ) BAYER HEALTHCARE AG.  
 XX  
 PI Golz S, Brueggemeier U, Geerts A;  
 DR WPI; 2005-758663/77.  
 XX  
 XX Screening for therapeutic agents, useful for treating a disease, e.g.  
 PT cardiovascular, infections, dermatological, cancer, inflammation, a  
 PT respiratory, or neurological, comprises contacting a test compound with a  
 PT tachykinin receptor 1.  
 XX  
 XX Example 2; SEQ ID NO 4; 118bp; English.  
 PS  
 XX The invention relates to a method of screening for therapeutic agents  
 CC useful for treating a disease, comprising contacting a test compound with  
 CC a tachykinin receptor 1 (TACRI), polypeptide or polynucleotide, detecting  
 CC binding of the polypeptide or polynucleotide, determining the activity of  
 CC TACRI at a certain concentration of the test compound, in the absence of  
 CC the compound or in the presence of a known regulator of the TACRI  
 CC polypeptide. The invention also relates to a method of diagnosing a  
 CC disease in a mammal comprising determining the amount of a TACRI  
 CC polynucleotide in a sample taken from the mammal and/or diseased mammals, a  
 CC amount of TACRI polynucleotide in healthy and/or diseased mammals, a  
 CC pharmaceutical composition for treating diseases in a mammal comprising a  
 CC TACRI polynucleotide or polypeptide or a therapeutic agent which binds to  
 CC or regulates the activity of a TACRI polypeptide, and preparing a  
 CC pharmaceutical composition useful for treating diseases in a mammal. The  
 CC disease is chosen from cardiovascular diseases, infections, cancer, inflammation,  
 CC dermatological diseases, gastrointestinal diseases, cancer, inflammation,  
 CC metabolic disorders, hematological diseases, respiratory diseases,  
 CC musculoskeletal diseases, neurological diseases, gynecological disorders  
 CC and genitourinary diseases. This sequence represents a PCR primer used in  
 CC expression profiling of the human TACRI cDNA of the invention.  
 CC  
 XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 322 GCCTACACGGTCATTGTGG 340  
 DB 19 GCCTACACGGTCATTGTGG 1  
 RESULT 152  
 AEE77699 standard; DNA; 20 BP.  
 ID AEE77699;  
 AC AEE77699;  
 XX  
 XX 09-FEB-2006 (first entry)  
 DT  
 XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1320.  
 DE  
 XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2005118843-A1.  
 PN  
 XX 15-DEC-2005.  
 PD  
 XX 01-JUN-2005; 2005WO-AU000775.  
 PF

XX  
 XX 01-JUN-2004; 2004AU-00902919.  
 PR  
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
 XX  
 XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
 PI WPI; 2006-047555/05.  
 DR  
 XX Identifying genetic profile associated with a neurological, psychiatric,  
 PT or psychological condition, comprises screening individuals for a  
 PT polymorphism in a genetic locus comprising the dopamine receptor D2  
 PT (DRD2) gene.  
 PT  
 XX Claim 31; SEQ ID NO 1320; 634bp; English.  
 PS  
 XX The invention relates to a method of identifying a genetic profile  
 CC associated with a neurological, psychiatric or psychological condition,  
 CC phenotype or state including a sub-threshold neurological, psychiatric or  
 CC psychological condition, phenotype or state in an individual, comprising  
 CC screening individuals for a polymorphism in a genetic locus comprising  
 CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
 CC genetic mutation providing a genetic marker for a neurological,  
 CC psychiatric, or psychological condition, state or phenotype in an  
 CC individual, where the presence of a 957C polymorphism is indicative of a  
 CC predisposition to developing a neurological, psychiatric or psychological  
 CC condition, phenotype or state. The compositions and methods are useful  
 CC for identifying a genetic profile associated with a neurological,  
 CC psychiatric or psychological condition. The method enables clinicians to  
 CC make a genetic-based diagnosis of a neurological, psychiatric or  
 CC psychological condition and can thereby implement treatment or  
 CC preventative or symptom-ameliorating protocols to reduce the adverse  
 CC consequences of the condition. This sequence represents a human dopamine  
 CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
 CC invention.  
 CC  
 XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 984 CATCTGCTGGCTGCCCTTC 1002  
 DB 2 CATCTGCTGGCTGCCCTTC 20  
 RESULT 153  
 AEE77700 standard; DNA; 20 BP.  
 ID AEE77700;  
 AC AEE77700;  
 XX  
 XX 09-FEB-2006 (first entry)  
 DT  
 XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1321.  
 DE  
 XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
 KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2005118843-A1.  
 PN  
 XX 15-DEC-2005.  
 PD  
 XX 01-JUN-2005; 2005WO-AU000775.  
 PF  
 XX 01-JUN-2004; 2004AU-00902919.  
 PR  
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
 PA  
 XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
 PI



XX WPI; 2006-047555/05.  
DR  
XX  
PT Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
XX  
PS Claim 31; SEQ ID NO 1321; 634pp; English.  
XX  
CC The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 984 CATCTGCTGCTGCCCTTC 1002  
Db 1 CATCTGCTGCTGCCCTTC 19  
XX  
RESULT 154  
AAQ47254  
ID AAQ47254 standard; DNA; 20 BP.  
XX  
AC AAQ47254;  
XX  
DT 25-MAR-2003 (revised)  
DT 25-JAN-1994 (first entry)  
XX  
DE PCR primer for amplifying tachykinin receptor specific mRNA from human  
DE leukocytes.  
XX  
KM Polynucleotide; synthesis; solid support; ss.  
XX  
OS Synthetic.  
XX  
PN WO9315228-A1.  
XX  
PD 05-AUG-1993.  
XX  
PF 29-JAN-1993; 93WO-US001040.  
XX  
PR 29-JAN-1992; 92US-00827975.  
XX  
PA (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
XX  
PI Keller C, Mitsuhashi M, Akitaya T;  
XX  
DR WPI; 1993-258700/32.  
XX  
PT Prodn. of double stranded cDNA immobilised support - by binding

PT polynucleotide with sequence complementary to poly-adenylic acid tail of  
PT mRNA to insol. support.  
XX  
PS Example 3; Page 26; 54pp; English.  
XX  
CC A polynucleotide is immobilised on an insoluble solid support and used to  
CC synthesise de-cDNA, ss-cDNA and both sense and antisense mRNA. The  
CC advantage of this system is that RNA bound to the solid support need not  
CC be precipitated when changing solutions. Two primers were used to amplify  
CC tachykinin receptor specific mRNA after its synthesis using the above  
CC method (AAQ47254, AAQ47255). (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 1.0%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 84;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 562 GCCAGTCTTACTTCATGAC 581  
Db 1 GCCAGCATCTACTTCATGAC 20  
XX  
RESULT 155  
AAQ55048  
ID AAQ55048 standard; DNA; 20 BP.  
XX  
AC AAQ55048;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-JUL-1994 (first entry)  
XX  
DE Sequence of PCR primer no.11, which binds to transmembrane domain 6 of  
DE peptide ligand receptors.  
XX  
KM PCR; oligo; primer; peptide ligand receptor; ss.  
XX  
OS Synthetic.  
XX  
PN EP578962-A2.  
XX  
PD 19-JAN-1994.  
XX  
PF 04-JUN-1993; 93EP-00108984.  
XX  
PR 17-JUL-1992; 92US-00915966.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Hadcock JR, Ozenberger BA, Pausch MH;  
XX  
DR WPI; 1994-017562/03.  
XX  
PT Isolation and identifying new receptor DNA - pref. G-protein linked  
PT receptors, using PCR with new receptor specific primers.  
XX  
PS Claim 2; Fig 2A; 17pp; English.  
XX  
CC Consensus sequences are identified from nine rat gene receptors. The  
CC receptors are for somatostatin, substance K, substance P, neuromedin K,  
CC thyrotropin, HH/CG and others designated mas, mrg and rta. Four regions  
CC of nucleotide sequence are found to exhibit a degree of conservation  
CC significant enough to design degenerate oligo primers for PCR (see  
CC AAQ55045-49). Five oligos are designed with 4- to 64-fold direct  
CC degeneracy plus 5'-23% inosines. The oligos are designed to anneal  
CC sequences in G protein-linked peptide receptor genes. They are used as  
CC six different primer pairs for PCR using rat genomic DNA as template. All  
CC six reactions produce DNA fragments of the expected size. Nucleotide  
CC sequences of two of these fragments are given in AAQ55054 and AAQ55055.  
XX  
SQ Sequence 20 BP; 1 A; 5 C; 5 G; 6 T; 0 U; 3 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 90;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCGCATCTGCTGCTGCC 998  
 ||:|||||  
 1 TTGCGCATCTGCTGCTGCC 20

## RESULT 156

AAQ30793  
 ID AAQ30793 standard; DNA; 18 BP.

XX AAQ30793;  
 AC 25-MAR-2003 (revised)  
 DT 22-MAR-1993 (first entry)

XX Oligo probe hsp65 to human NKIR sf C-terminal region.

XX Neurokinin-1 receptor short form; arthritis; Substance P;  
 anchored polymerase chain reaction; rat NKIR; ss.

OS Synthetic.

XX EP514207-A2.

XX 19-NOV-1992.

PD 15-MAY-1992; 92EP-00304432.

XX 17-MAY-1991; 91US-00701930.

PR 17-MAY-1991; 91US-00701935.

PR 17-MAY-1991; 91US-00701937.

XX (MERI ) MERCK & CO INC.

XX Strader CD, Fong TM;

DR WPI; 1992-384034/47.

XX New human neurokinin-1 receptor short form protein - useful for  
 PT identifying and determining substance P antagonists in arthritic  
 PT patients.

XX Example 1; Page 8; 36pp; English.

XX Double-stranded cDNA was prepared from human glioblastoma mRNA and large-  
 CC size cDNA was ligated to EcoRI linkers. Linker-ligated cDNA was then  
 CC ligated to the calf intestinal phosphatase-treated EcoRI site of the  
 CC vector Bluescript SK+. The ligated plasmid DNA was used as template in a  
 CC primary PCR amplification with human primers hsp651 and hsp652

CC (AAQ30789 and AAQ30790) and the vector-specific primer t3 (from  
 CC "Stratagene"). The primary PCR product was used as template for secondary  
 CC PCR with the human primer hsp653 (AAQ30791) and t3. The product of this  
 CC reaction was amplified in a tertiary PCR amplification with hsp654  
 CC (AAQ30792) and vector-specific primer SK (also from "Stratagene"). A  
 CC 400bp DNA fragment was detected which hybridised to human oligoprobe  
 CC hsp655 (AAQ30793). This fragment was subcloned and sequenced. It was  
 CC found to encode the C-terminal region of human NKIR sf and also contains  
 CC 3'UTR. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 1.0%; Score 18; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTCTGAAGAAGTT 1055  
 |||||  
 1 TCTTACTCTGAAGAAGTT 18

## RESULT 157

AAQ29682  
 ID AAQ29682 standard; DNA; 18 BP.

XX AAQ29682;

XX 25-MAR-2003 (revised)  
 DT 15-MAR-1993 (first entry)

XX hsp655 primer 950-967.

XX Human; neurokinin-1 receptor; NKIR; membrane receptor; substance P;  
 KW neurotransmitter; polymerase chain reaction; PCR; rat NKIR; primer;  
 KW amplify; probe; ss.

OS Homo sapiens.

XX EP510878-A1.

XX 28-OCT-1992.

XX 16-APR-1992; 92EP-00303457.

XX 25-APR-1991; 91US-00691197.

PR 25-APR-1991; 91US-00691198.

PR 25-APR-1991; 91US-00691200.

XX (MERI ) MERCK & CO INC.

XX Fong TM, Strader CD;

XX WPI; 1992-359073/44.

XX New recombinant human neurokinin-1 receptor - used to detect and evaluate  
 PT substances that bind to substance P receptor, and to determine substance  
 PT P in body fluid of arthritis patients.

XX Disclosure; Page 8; 35pp; English.

XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
 CC which were used in the isolation of fragments of the human neurokinin-1  
 CC receptor (NKIR) cDNA. Human NKIR is a membrane receptor for the  
 CC neurotransmitter substance P. The primers were designed using regions of  
 CC the human NKIR cDNA and also regions of the rat NKIR which were thought  
 CC to be similar to human regions. Part of the human cDNA sequence was  
 CC derived by amplification using these primers. The remaining part of human  
 CC NKIR cDNA was obtained from a human cDNA library utilising portions of  
 CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 1.0%; Score 18; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTCTGAAGAAGTT 1055  
 |||||  
 1 TCTTACTCTGAAGAAGTT 18

## RESULT 158

AAT76448/C  
 ID AAT76448 standard; DNA; 18 BP.

XX AAT76448;

XX 16-SEP-1997 (first entry)

XX Substance P receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;

KM chronic obstructive pulmonary disease; bronchitis; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640162-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009306.  
XX  
PR 07-JUN-1995; 95US-00474497.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW, Metzger WJ;  
XX  
DR WPI; 1997-051871/05.  
XX  
PT Treatment of airway diseases such as asthma - by topically applying  
PT adenosine-free antisense oligonucleotide to airway epithelium of  
PT subject.  
XX  
PS Example 5; Page 40; 71pp; English.  
XX  
CC A method for treating airway disease in a subject has been produced,  
CC which involves the topical administration of an essentially adenosine  
CC free antisense oligonucleotide (ON) to the airway epithelium of the  
CC subject. The present sequence is an antisense oligonucleotide specific  
CC for the substance P receptor. The method can be used to treat airway  
CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary  
CC disease, bronchitis and other airway diseases characterised by an  
CC inflammatory response. By eliminating adenosine from the antisense ON,  
CC the liberation upon antisense degradation is prevented, thereby  
CC preventing adenosine-induced bronchoconstriction in patients with hyper-  
CC reactive airways  
XX  
SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 638 CAGCCACAGCCACCAAG 655  
DB 18 CAGCCACAGCCACCAAG 1  
XX  
RESULT 159  
AA54239/C  
ID AA54239 standard; DNA; 18 BP.  
XX  
AC AA54239;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Substance P receptor antisense oligonucleotide fragment.  
XX  
KM Antisense oligonucleotide; multiple target; antisense treatment;  
KM impaired respiration; inflammation; lung disease;  
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KM acute asthma; allergy; asthma; impeded respiration;  
KM respiratory distress syndrome; pain; cystic fibrosis;  
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KM prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9913886-A1.  
XX  
PD 25-MAR-1999.

XX  
PF 17-SEP-1998; 98WO-US019419.  
XX  
XX  
PR 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
XX  
DR WPI; 1999-229400/19.  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
XX  
PS Disclosure; Page 59; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AA52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
CC end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AA55272-74. These multiple target oligonucleotides  
CC (specifically AA55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemia, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 638 CAGCCACAGCCACCAAG 655  
DB 18 CAGCCACAGCCACCAAG 1  
XX  
RESULT 160  
AAA33683/C  
ID AAA33683 standard; DNA; 18 BP.  
XX  
AC AAA33683;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:1372.  
XX  
KM Human adenosine receptor; low adenosine antisense oligonucleotide;  
KM phosphorothioate; impaired respiration; inflammation; allergy;  
KM allergic diseases; bronchoconstriction; inhibitor; antiinflammatory;  
KM antiallergic; antisthmatic; cyostatic; analgesic; impaired airway;  
KM lung disease; ischemic condition; pulmonary vasoconstriction; asthma;  
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.  
 XX PF  
 XX 03-AUG-1998; 98US-0095212P.  
 XX PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX PA  
 XX MYCE JW;  
 XX PI  
 XX WPI; 2000-205971/18.  
 XX DR  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 XX PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 XX PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 XX PT cancers.  
 XX PS  
 XX Claim 18; Page 436; 1343pp; English.  
 XX  
 XX The present invention describes a new composition comprising an antisense  
 XX CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 XX CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 XX CC inflammation. The ON can have antiinflammatory, antiallergic,  
 XX CC antiasthmatic, cyostatic and analgesic activities. The compositions are  
 XX CC useful for the treatment of diseases associated with inflammation  
 XX CC impaired airways, including lung disease and diseases whose secondary  
 XX CC effects afflict the lungs of a subject. They can be used for treating  
 XX CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 XX CC e.g. ischemic conditions, respiratory distress syndrome, pain, cystic  
 XX CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 XX CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 XX CC carcinomas, and cancers which may metastasize to the lungs, including  
 XX CC breast and prostate cancer. The reduction of the adenine content of the  
 XX CC ONs reduces side effects. The A-containing ONs break down with the  
 XX CC release of deoxyadenosine which activates adenosine receptors causing the  
 XX CC bronchoconstriction and inflammation. AAA32313 to AAA5312 represent the  
 XX CC nucleotide sequences given in the sequence listing from the present  
 XX CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185  
 XX CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 XX CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 XX CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 XX CC Sequences given in the disclosure of the present invention do not match  
 XX CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 XX CC listing  
 XX  
 XX Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.0%; Score 18; DB 1; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 74;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 638 CAGCCACAGCCACCAAG 655  
 XX ||||||||||||||||||  
 XX DB 18 CAGCCACAGCCACCAAG 1  
 XX  
 XX RESULT 161  
 XX AAF19805/C  
 XX ID AAF19805 standard; DNA; 18 BP.  
 XX AC  
 XX AAF19805;  
 XX  
 XX 14-MAR-2001 (first entry)  
 XX  
 XX Human substance P receptor polynucleotide fragment #1372.  
 XX  
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 XX KW human; airway disorder; bronchoconstriction; lung inflammation;  
 XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 XX KW immunosuppressive; antiasthmatic; hypotensive; cyostatic;  
 XX KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 XX KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 XX KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200062736-A2.  
 XX PN  
 XX 26-OCT-2000.  
 XX PD  
 XX 24-MAR-2000; 2000WO-US008020.  
 XX PF  
 XX 06-APR-1999; 99US-0127958P.  
 XX PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX PA (NYCE/) NYCE J W.  
 XX  
 XX MYCE JW;  
 XX PI  
 XX WPI; 2000-679539/66.  
 XX DR  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 XX PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 XX PT and respiratory obstructions.  
 XX PS  
 XX Claim 14; Page 245; 1592pp; English.  
 XX  
 XX The present invention describes low adenosine (A) content antisense  
 XX CC oligonucleotides and compositions (I) comprising them. In the antisense  
 XX CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 XX CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.  
 XX CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 XX CC expression and/or activity of target polypeptides associated with  
 XX CC lung/respiratory disorders and malignancies, such as stimulating and  
 XX CC activating peptide factors and antibodies, antibody receptors, cytokines and  
 XX CC immunoglobulins and antipodides, produced specific and non-specific enzymes,  
 XX CC chemokines, endogenously produced specific and non-specific enzymes,  
 XX CC and binding proteins, adhesion molecules and their receptors, cytokine and  
 XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 XX CC nervous system (CNS) and peripheral nervous and non-nervous system  
 XX CC receptors, CNS and peripheral nervous and non-nervous system  
 XX CC transmitters, defensins, growth factors, vasodilator receptors, central  
 XX CC receptors, binding proteins and malignancy associated proteins. The  
 XX CC antisense oligonucleotides may be used in this way to treat disorders  
 XX CC including respiratory obstruction (especially pulmonary obstruction  
 XX CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or  
 XX CC surfactant hypoproduction which are associated with a disease or  
 XX CC condition selected from pulmonary vasoconstriction, inflammation,  
 XX CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 XX CC (RDS), pain, cystic fibrosis (Cf), allergic rhinitis (AR), pulmonary  
 XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 XX CC fragments and antisense oligonucleotides used in the exemplification of  
 XX CC the present invention  
 XX  
 XX Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.0%; Score 18; DB 1; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 74;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 638 CAGCCACAGCCACCAAG 655  
 XX ||||||||||||||||||  
 XX DB 18 CAGCCACAGCCACCAAG 1  
 XX  
 XX RESULT 162  
 XX ABS61000  
 XX ID ABS61000 standard; DNA; 18 BP.  
 XX AC  
 XX ABS61000;  
 XX  
 XX





DT 18-JUN-2002 (first entry)  
 XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #50.  
 XX  
 KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KW immune disorder; autoimmune disorder; cardiovascular disorder;  
 KW vascular disorder; airway disorder; neuropathic disorder; pain;  
 KW psychiatric disorder; central nervous system disorder; inflammation;  
 KW respiratory condition; ocular condition; intestinal condition;  
 KW demyelinating disease; small cell lung cancer; depression;  
 KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KW neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200213799-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PE 17-AUG-2001; 2001WO-1B001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yaeshpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Example 18; Page 66; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ocular  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, oedema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1

CC receptors. Receptors not chronically stimulated are less affected.  
 CC reducing side effects of treatment. ABK63867-ABK63906 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX  
 SQ Sequence 18 BP; 6 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1.0%; Score 18; DB 1; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 74;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1038 TCTTACCTGAGAGATT 1055  
 CC  
 CC Db 18 TCTTACCTGAGAGATT 1  
 CC  
 CC  
 CC RESULT 166  
 CC ABK63867  
 CC ID ABK63867 standard; DNA; 18 BP.  
 CC  
 CC AC ABK63867;  
 CC  
 CC XX 18-JUN-2002 (first entry)  
 CC  
 CC DE Neurokinin 1 receptor (NK-1) sense oligonucleotide #18.  
 CC  
 CC KW Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 CC immune disorder; autoimmune disorder; cardiovascular disorder;  
 CC vascular disorder; airway disorder; neuropathic disorder; pain;  
 CC psychiatric disorder; central nervous system disorder; inflammation;  
 CC respiratory condition; ocular condition; intestinal condition;  
 CC demyelinating disease; small cell lung cancer; depression;  
 CC hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 CC neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 CC neuro-pathological disorder; stress; antisense; primer; ss.  
 CC  
 CC OS Homo sapiens.  
 CC  
 CC PN MO200213799-A2.  
 CC  
 CC PD 21-FEB-2002.  
 CC  
 CC PE 17-AUG-2001; 2001WO-1B001510.  
 CC  
 CC PR 18-AUG-2000; 2000US-0226086P.  
 CC  
 CC PA (UYMC-) UNIV MCGILL.  
 CC  
 CC PI Henry JL, Cahill CM, Yaeshpal K;  
 CC  
 CC DR WPI; 2002-241835/29.  
 CC  
 CC PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 CC pain or inflammation, by administering oligonucleotide or a non-  
 CC nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 CC pathway.  
 CC  
 CC PS Claim 24; Page 20; 100pp; English.  
 CC  
 CC XX The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychiatric and central nervous system disorders (e.g. anxiety,  
 CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system



disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrintestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addiction disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, oedema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected. CC reducing side effects of treatment. ABK6384-ABK63906 represent NK-1 CC receptor coding sequences and oligonucleotides of the invention CC

Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTTACTGAGAGAGTT 1055  
DB 1 TCTTACTGAGAGAGTT 18

RESULT 167  
ABT16451/c  
ID ABT16451 standard; DNA; 18 BP.  
AC ABT16451;  
XX 20-MAR-2003 (first entry)  
DT Human neurokinin 1 receptor gene related PCR primer SEQ ID NO 32.  
XX  
DE Human neurokinin 1 receptor gene related PCR primer SEQ ID NO 32.  
XX  
KW Cytostatic; antispasmodic; antiinflammatory; cardiant; polymorphic site;  
KW human neurokinin 1 receptor; TACR1; disease phenotype; forensics;  
KW TACR1 ligand mediated disease; asthma; paternity testing; cancer;  
KW inflammation; heart disease; central nervous system; infection; PCR;  
KW primer; ss.  
XX  
OS Unidentified.  
XX  
PN BP1262565-A2.  
XX 04-DEC-2002.  
PD  
XX 23-MAY-2002; 2002EP-00253662.  
PF  
XX 25-MAY-2001; 2001US-0293425P.  
PR  
XX (PFIZ ) PFIZER PROD INC.  
PA  
XX Affourtit JP, Nelson DL, Seymour AB, Webb SM,  
PI  
XX WPI; 2003-150228/15.  
DR  
XX Novel nucleic acid segment from human neurokinin 1 receptor, including  
PT polymorphic sites for diagnosing and treating asthma, and in forensics,  
PT paternity testing, and genetic mapping of the trates.  
XX  
PS Example; Page 12; 27pp; English.

The invention relates to a nucleic acid segment from the human neurokinin 1 receptor (TACR1) gene of 10-100 nucleotides comprising a fragment having a polymorphic site or a complement of the fragment. The TACR1 segment is useful for analysing a nucleic acid, by obtaining any one of acid from an individual, and determining the base occupying any one of the polymorphic sites in the segment. The nucleic acid is obtained from several individuals, and the base occupying one of the polymorphic sites is determined in each of the individuals, and further involves testing each of the individuals for the presence of a disease phenotype, and correlating the presence with the base. The TACR1 segment is useful for diagnosing and treating TACR1 ligand mediated diseases, such as asthma. The TACR1 segment is also useful in forensics, paternity testing, correlating polymorphisms with phenotypic traits, and genetic mapping of phenotypic traits. The TACR1 segment is useful in diagnosing and monitoring of diseases such as cancer, inflammation, heart disease, diseases of central nervous system, and susceptibility to infection to microorganisms. The TACR1 segment is also useful in the manufacture of a medicament for the treatment of the diseases. This polynucleotide (TACR1) gene of the invention

Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 CGCCAGTTGAGCTTTCGA 75  
DB 18 CGCCAGTTGAGCTTTCGA 1

RESULT 168  
ABZ95499/c  
ID ABZ95499 standard; DNA; 18 BP.  
AC ABZ95499;  
XX 17-OCT-2003 (first entry)  
DT Human substance P receptor antisense fragment no.1363.  
XX  
DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antispasmodic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
DR  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 10741; 872pp; English.



XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to, adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequences  
XX

Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 638 CAGCCACAGCCACCAAG 655  
18 CAGCCACAGCCACCAAG 1

RESULT 169  
ABD19638/C  
ID ABD19638 standard; DNA; 18 BP.

AC ABD19638;

DT 29-JUN-2004 (first entry)

XX Human substance P receptor DNA fragment 1363.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KM pulmonary transplantation rejection; ds.

XX Homo sapiens.

OS W020285309-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013143.

PR 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Myce JM, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 10741; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, allergies and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hyperplasia, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX

Sequence 18 BP; 0 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 638 CAGCCACAGCCACCAAG 655  
18 CAGCCACAGCCACCAAG 1

RESULT 170  
AEE77698

ID AEE77698 standard; DNA; 20 BP.

AC AEE77698;

DT 09-FEB-2006 (first entry)

XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1319.

XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.

XX Homo sapiens.

PN W0200511843-A1.

PD 15-DEC-2005.

PF 01-JUN-2005; 2005WO-AU000775.

PR 01-JUN-2004; 2004AU-00902919.

XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;

XX WPI; 2006-047555/05.

PT Identifying genetic profile associated with a neurological, psychiatric,  
 PT or psychological condition, comprises screening individuals for a  
 PT polymorphism in a genetic locus comprising the dopamine receptor D2  
 PT (DRD2) gene.  
 XX  
 XX Claim 31; SEQ ID NO 1319; 634bp; English.  
 PS  
 CC The invention relates to a method of identifying a genetic profile  
 CC associated with a neurological, psychiatric or psychological condition,  
 CC phenotype or state including a sub-threshold neurological, psychiatric or  
 CC psychological condition, phenotype or state in an individual, comprising  
 CC screening individuals for a polymorphism in a genetic locus comprising  
 CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
 CC genetic mutation providing a genetic marker for a neurological,  
 CC psychiatric, or psychological condition, state or phenotype in an  
 CC individual, where the presence of a 957c polymorphism is indicative of a  
 CC predisposition to developing a neurological, psychiatric or psychological  
 CC condition, phenotype or state. The compositions and methods are useful  
 CC for identifying a genetic profile associated with a neurological,  
 CC psychiatric or psychological condition. The method enables clinicians to  
 CC make a genetic-based diagnosis of a neurological, psychiatric or  
 CC psychological condition and can thereby implement treatment or  
 CC preventative or symptom-ameliorating protocols to reduce the adverse  
 CC consequences of the condition. This sequence represents a human dopamine  
 CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
 CC invention.  
 XX  
 XX Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;  
 SO  
 Query Match 1.0%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 984 CATCTGCTGCGTGCCTT 1001  
 ||||||||||||||||  
 Db 3 CATCTGCTGCGTGCCTT 20  
 RESULT 171  
 AEE77701  
 ID AEE77701 standard; DNA; 20 BP.  
 XX  
 AC AEE77701;  
 XX  
 DT 09-FEB-2006 (first entry)  
 XX  
 DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1322.  
 XX  
 KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
 KW neuropsychological disorder; dopamine receptor D2; DRD2; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO2005118843-A1.  
 XX  
 PD 15-DEC-2005.  
 XX  
 PF 01-JUN-2005; 2005WO-AU000775.  
 XX  
 PR 01-JUN-2004; 2004AU-00902919.  
 XX  
 PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.  
 XX  
 PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
 DR WPI; 2006-047555/05.  
 XX  
 PT Identifying genetic profile associated with a neurological, psychiatric,  
 PT or psychological condition, comprises screening individuals for a  
 PT polymorphism in a genetic locus comprising the dopamine receptor D2  
 PT (DRD2) gene.  
 XX

PS Claim 31; SEQ ID NO 1322; 634pp; English.

XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotypic or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
CC

SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 985 ATCTGCTGGCTGCCTTC 1002  
|||||  
1 ATCTGCTGACTGCCCTTC 18

RESULT 172  
ABS61085  
ID ABS61085 standard; DNA; 22 BP.  
XX  
AC ABS61085;  
DT 05-NOV-2002 (first entry)  
XX  
DE Human automated genomic bit analysis (GBA) PCR primer #62.

Human; S6; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;  
KW BKBRB1; tachykinin receptor B1; TAARL1; Cl esterase inhibitor; CLNH;  
KW Kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
KW polycystic kidney disease; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
KW myocardial infarction; ventricular hypertrophy; vascular disease;  
KW myocardial embolism; thrombosis; coronary artery disease; angioedema;  
KW aneurysm; arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;  
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;  
KW viral infection; bacterial infection; fungal infection; COPD; GBA;  
KW Chronic obstructive pulmonary disease; enterocolitis;  
KW automated genetic bit analysis.

OS Homo sapiens.  
XX  
PM WO200261131-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 03-DEC-2001; 2001WO-US047235.  
XX  
PR 04-DEC-2000; 2000US-0251015P.  
PR 23-JAN-2001; 2001US-026378P.  
PR 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSTUC/) TSUCHIHASHI Z.  
HU L. (HUTL/)

PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR;  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angioedema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX Example 3; Page 931; 977pp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),  
CC tachykinin receptor B1 (TRCR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC ; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angioedema and diseases which  
CC involve angiotensin like haemangiomatosis, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antibodies  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is a genotyping PCR primer  
CC for the gene encoding one of the proteins listed above, using the method  
CC of automated genetic bit analysis, GBA  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 4 G; 5 T; 0 U; 1 Other;  
Query Match 1.0%; Score 18; DB 1; Length 22;  
Best Local Similarity 94.7%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1681 AGGTGGACACGACTTTTC 1699  
Db 1 AGGTGGACACGACTTTTC 19  
RESULT 173  
ABT40254/C  
ID ABT40254 standard; DNA; 21 BP.  
XX  
XX ABT40254;  
AC  
XX 12-JUN-2003 (first entry)  
DT  
XX Human Chem23 PCR primer SEQ ID No 44.  
DB  
XX Cytostatic; antiinflammatory; immunosuppressive; osteopathic; virucide;  
KW antiparietic; dermatological; antibacterial; antihelminthic; Chem23;

KW gynaecological; G-Protein-Agonist; G-Protein-Antagonist; gene therapy;  
KW orphan G-protein coupled receptor; tazarotene-induced gene 2; TIG2;  
KW modulator; cancer; tumour metastasis; inflammatory disease; inherited;  
KW autoimmune disease; AIDS; osteoporosis; bone healing; bone tissue graft;  
KW graft rejection; psoriasis; eczema; inflammatory infection; bacterial;  
KW trophic diseases; skin; viral; parasitic infection; female infertility;  
KW ovarian; uterine tumour; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200306996-A2.  
XX  
XX 23-JAN-2003.  
XX  
XX 09-JUN-2002; 2002MO-EP007647.  
XX  
XX 09-JUN-2001; 2001US-0303858P.  
PR 13-JUN-2001; 2001US-00905253.  
XX  
XX (EURO-) EUROS GREEN SA.  
XX  
XX Wiltamer V, Communi D, Vandenbogaerde A, Dethaux M, Parmentier M;  
XX WPI; 2003-221782/21.  
XX  
XX Identifying an agent that modulates Chem23 polypeptide using TIG2 gene,  
PT useful for the preparation of a medicament for the treatment of  
PT disorders, such as cancer, inflammatory and autoimmune diseases,  
XX osteoporosis and psoriasis.  
XX  
PS Example 10; Page 60; 99pp; English.  
XX  
XX The invention relates to a novel method for identifying an agent that  
CC modulates the function of an orphan G-protein coupled receptor, Chem23.  
CC The identification comprises contacting a Chem23 polypeptide with a  
CC tazarotene-induced gene 2 (TIG2) polypeptide in the presence and absence  
CC of a candidate modulator to permit the binding of the TIG2 polypeptide to  
CC the Chem23 polypeptide, and measuring the binding of the Chem23 to the  
CC TIG2 polypeptide, where a decrease in the presence of the candidate  
CC modulator, identifies the modulator as an agent that modulates the  
CC function of Chem23. The agent or composition is useful for the  
CC preparation of a medicament for the treatment of a Chem23- or TIG2-  
CC related disease or disorder, such as cancer, tumour metastasis,  
CC inflammatory disease, autoimmune disease, inherited or acquired immune  
CC deficiencies, osteoporosis, bone healing, bone tissue grafts, graft  
CC rejection, psoriasis, eczema, inflammatory infection, trophic diseases of  
CC skin, viral, bacterial and parasitic infections, female infertility and  
CC ovarian and uterine tumours. The truncated or full-length TIG2  
CC polypeptide is useful for the production of a composition of an isolated  
CC Chem23 or TIG2 polypeptide, and/or for the production of a kit for  
CC screening agents that modulate the signalling of Chem23, and/or ligand  
CC for Chem23. This sequence represents a PCR primer used in the  
CC exemplification of the invention  
XX  
SQ Sequence 21 BP; 9 A; 5 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 669 CATCTGGTCTGCTCTCTCT 689  
Db 21 CATCTGGTCTGCTCTCTT 1  
RESULT 174  
ADM43814/C  
ID ADM43814 standard; DNA; 21 BP.  
XX  
XX ADM43814;  
AC  
XX 24-MAR-2005 (first entry)  
DT  
XX

DE Human chemerin RT-PCR primer SEQ ID NO 38.  
 XX gene therapy; diagnosis; cell signaling; gene therapy;  
 KM lymphoproliferative disease; dermatological disease; dermatological;  
 KM hemostatic; inflammation; antinflammatory; hematological disease;  
 KM immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;  
 KM neurological disease; hyperproliferative disorders; cytostatic;  
 KM chemerin; reverse transcriptase PCR; RT-PCR; primer; ss.  
 XX Homo sapiens.  
 XX WO200500875-A2.  
 XX 06-JAN-2005.  
 XX 25-JUN-2004; 2004WO-EP006945.  
 XX 25-JUN-2003; 2003US-00603566.  
 XX (EURO-) EUROSCREEN SA.  
 XX Wiltamer V, Communi D, Detheux M, Parmentier M, Loison C;  
 XX Ooms FDR;  
 XX WPI; 2005-058121/06.  
 XX New Chemerin polypeptides, useful for diagnosing and treating a disease,  
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,  
 PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's  
 PT disease, or histiocytosis.  
 XX  
 XX Example 6; SEQ ID NO 38; 183bp; English.  
 PS The invention describes a polypeptide (I) of up to 50 amino acids where  
 XX the polypeptide binds specifically to a chemerin polypeptide. Also  
 CC described are: a nucleic acid sequence encoding (I); an expression vector  
 CC comprising the coding sequence of the nucleic acid; a transgenic animal  
 CC transfected with the expression vector; a (therapeutic) composition  
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid  
 CC sequence of (I); an antibody that selectively binds to (I); identifying  
 CC an agent that modulates the interaction between a Chemerin polypeptide and  
 CC a Chemerin polypeptide; detecting the presence, in a sample, of an  
 CC agent that modulates the interaction between a Chemerin polypeptide and a  
 CC Chemerin polypeptide; identifying an agent that modulates  
 CC the function of Chemerin polypeptide; detecting the presence, in a  
 CC sample, of an agent that modulates the function of Chemerin polypeptide;  
 CC diagnosing a disease or disorder characterized by dysregulation of  
 CC Chemerin (polypeptide) signaling; a kit, for screening agents that  
 CC modulate the signaling activity of Chemerin polypeptide or for  
 CC diagnosing a disease or disorder characterized by dysregulation of  
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin  
 CC Chemerin polypeptide, (I), an isolated polynucleotide encoding (I), a cell  
 CC transfected with a polynucleotide encoding (I), and its packaging  
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide  
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;  
 CC and an in vitro method of inhibiting cell proliferation. The  
 CC (therapeutic) composition or expression vector is useful for preparing a  
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a  
 CC medicament for inhibiting cell proliferation, where the medicament is  
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,  
 CC lymphoproliferative diseases, disorders, and/or conditions,  
 CC paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's  
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other  
 CC hyperproliferative disease. The polypeptides and polynucleotides and  
 CC methods are useful for diagnosing and treating the cited diseases. This  
 CC sequence represents a reverse transcriptase PCR primer used in an  
 CC analysis of human chemerin receptor (chemerin) expression by quantitative  
 CC RT-PCR.  
 XX  
 XX Sequence 21 BP; 9 A; 5 C; 6 G; 1 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.0%; Score 17.8; DB 1; Length 21;  
 XX Best Local Similarity 90.5%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 669 CATCTGGATCTGGCTTCCT 689  
 Db 21 CATCTGGATCTGGCTTCCT 1  
 RESULT 175  
 AAQ47385  
 ID AAQ47385 standard; cDNA to mRNA; 22 BP.  
 XX  
 AC AAQ47385;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-JAN-1994 (first entry)  
 XX  
 DE Substance P receptor mRNA-specific probe.  
 XX  
 KM Probe; quantification; human; substance P; specific mRNA; detection;  
 KM hybridization; diagnosis; pathophysiology; disease state; hereditary;  
 KM cancer; infectious; neurotransmitter; nerves; pain receptor pathway;  
 KM analgesics; ss.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT modified\_base 1  
 FT /tag= a  
 FT /note= "5' amino group"  
 XX  
 XX W09315221-A1.  
 XX  
 PD 05-AUG-1993.  
 XX  
 XX 29-JAN-1993; 93WO-US000977.  
 XX  
 XX 29-JAN-1992; 92US-00827208.  
 XX 24-MAR-1992; 92US-00857059.  
 PR 12-NOV-1992; 92US-00974409.  
 XX  
 PA (HITB ) HITACHI CHEM CO LTD.  
 PA (HITB ) HITACHI CHEM RES CENT INC.  
 PI Akitaya T, Cooper A, Mitsuhashi M;  
 XX  
 DR WPI; 1993-258695/32.  
 PT Quantitating messenger RNA in sample - using immobilised-polynucleotide  
 PT having sequence complementary to sequence unique to the mRNA.  
 XX  
 XX Claim 12 and 40; Page 56; 177bp; English.  
 XX  
 XX This sequence is a probe which was used in the quantification of human  
 CC substance P receptor mRNA from substance P receptor cDNA-transferred  
 CC cells. This probe was used in the method of the invention, for the  
 CC detection and quantification of mRNA in a sample without the need to  
 CC purify the mRNA from cells. The claimed method comprises identifying a  
 CC polynucleotide sequence unique to the mRNA, and immobilising an oligomer  
 CC complementary to this sequence to an insoluble support. The sample is  
 CC then incubated with the bound oligomer and be immobilised. Non-immobilised  
 CC will hybridise to the bound oligomer and be immobilised. Components are  
 CC components are washed from the support and bound RNA is labelled in such  
 CC a way that the label is incorporated onto the support relative to the  
 CC amount of mRNA on the support. The amount of bound label is then  
 CC determined. This method can be used for the reliable, rapid, simultaneous  
 CC quantification and recognition of patho- physiology of various diseases.  
 CC diagnosing and recognition of patho- physiology of various diseases.  
 CC states, eg. hereditary diseases, cancer, and infectious diseases.  
 CC Substance P is a neurotransmitter. Because the nerves expressing  
 CC substance P are involved in pain receptor pathways, the ability to  
 CC measure the mRNA of substance P would be useful in the development of  
 CC analgesics. See also AAQ47381-666. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

```
XX Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 780 GATTATGAGAAAGTGTACCA 800
Db 2 GACTTATGAGAAAGCTACCA 22

RESULT 176
ABSS9964/C
ID ABSS9964 standard; DNA; 19 BP.
AC ABSS9964;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human DNA representing a single nucleotide polymorphism #114.
XX
XX Aminopeptidase P; XPNBP2; bradykinin receptor B1; ds; SNP; BDKRB1;
XX tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;
XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
XX autoimmune disease; inflammatory arthritis; cancer; wound;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis;
XX single-nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX PF 04-DEC-2000; 2000US-0251015P.
XX PR 23-JAN-2001; 2001US-0263678P.
XX PR 02-MAR-2001; 2001US-0273037P.
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX (TSUC/) TSUCHIHASHI Z.
XX (HUI/L/) HUI L.
XX
XX Teuchshaishi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
XX Swanson BM, Powell JR;
XX
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angiodema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Disclosure; Page 663; 977PD; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),
XX tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein
XX 1 (KKL1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
XX 2 (ACE2), or protease inhibitor 4 (P14), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX polymorphic position as provided in the detailed summary of single
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
```

```
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angiodaema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcoma, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polymorphisms are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence represents or contains the
CC region surrounding a single-nucleotide polymorphism in one of the genes
XX encoding one of the proteins listed above
XX
XX Sequence 19 BP; 3 A; 2 C; 10 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1335 CACACCTCGTCCCTGGAC 1353
Db 19 CACACCTCATCCTGGAC 1

RESULT 177
ABSS9962/C
ID ABSS9962 standard; DNA; 19 BP.
AC ABSS9962;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human DNA representing a single nucleotide polymorphism #112.
XX
XX Aminopeptidase P; XPNBP2; bradykinin receptor B1; ds; SNP; BDKRB1;
XX tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;
XX KKL1; bradykinin receptor B2; BDKRB2; gene therapy;
XX angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
XX polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
XX cardiovascular disease; angina pectoris; hypertension; heart failure;
XX myocardial infarction; ventricular hypertrophy; vascular disease;
XX aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;
XX arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
XX autoimmune disease; inflammatory arthritis; cancer; wound;
XX viral infection; bacterial infection; fungal infection; COPD;
XX Chronic obstructive pulmonary disease; enterocolitis;
XX single-nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX PF 04-DEC-2000; 2000US-0251015P.
XX
```

PR 23-JAN-2001; 2001US-0263678P.  
 XX 02-MAR-2001; 2001US-0273037P.  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 663; 977pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2), or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiotensin like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence represents or contains the  
 CC region surrounding a single-nucleotide polymorphism in one of the genes  
 CC encoding one of the proteins listed above  
 XX  
 SQ Sequence 19 BP; 7 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Match Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1626 TCATGCTGTGACTCAAA 1644  
 DB 19 TCATGCTGTGACTCAAA 1  
 RESULT 178  
 ABS59896/c  
 ID ABS59896 standard; DNA; 19 BP.  
 XX  
 AC ABS59896;

XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human DNA representing a single nucleotide polymorphism #46.  
 XX  
 XX Aminopeptidase P; XPNBP2; bradykinin receptor B1; de; SNP; BDKRB1;  
 KW tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
 KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;  
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; ventricular hypertrophy; vascular disease;  
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;  
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KW autoimmune disease; inflammatory arthritis; cancer; wound;  
 KW viral infection; bacterial infection; fungal infection; COPD;  
 KW Chronic obstructive pulmonary disease; enterocolitis;  
 KW single-nucleotide polymorphism.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200261131-A2.  
 XX  
 XX 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 XX 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX WPI; 2002-619265/66.  
 DR  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 653; 977pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC nucleotide polymorphism comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiotensin like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular

CC hyper trophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hyper sensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence represents or contains the  
 CC region surrounding a single- nucleotide polymorphism in one of the genes  
 CC encoding one of the proteins listed above

XX Sequence 19 BP; 7 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dy 663 CTGTCATCTGGGTCCTG 681  
 |||||  
 19 CTGTCATATGAGTCCCTG 1

RESULT 179  
 ABS59958  
 ID ABS59958 standard; DNA; 19 BP.  
 XX ABS59958;  
 AC  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human DNA representing a single nucleotide polymorphism #108.

XX Amino peptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;  
 KM tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;  
 KM K1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
 KM myocardial infarction; ventricular hypertrophy; vascular disease;  
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KM autoimmune disease; inflammatory arthritis; cancer; wound;  
 KM viral infection; bacterial infection; fungal infection; COPD;  
 KM Chronic obstructive pulmonary disease; enterocolitis;  
 KM single-nucleotide polymorphism.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200261131-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 PR 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (SUC/) TSUCHIHASHI Z.  
 PA (HUI/) HUI L.  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 XX  
 DR WPI; 2002-619265/66.  
 XX  
 PT New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angiodema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX

PS Disclosure; Page 662; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),  
 CC tachykinin receptor B1 (TACR1), Cl esterase inhibitor (C1NH), kallikrein  
 CC 1 (K1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridises to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angiodaema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polynucleotides are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence represents or contains the  
 CC region surrounding a single- nucleotide polymorphism in one of the genes  
 CC encoding one of the proteins listed above

XX Sequence 19 BP; 3 A; 10 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dy 534 CAACTCTTCCATCGCC 552  
 |||||  
 1 CAACTTCTCCATCGCC 19

RESULT 180  
 ABS59900/c  
 ID ABS59900 standard; DNA; 19 BP.  
 XX ABS59900;  
 AC  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human DNA representing a single nucleotide polymorphism #50.

XX Amino peptidase P; XPNP2; bradykinin receptor B1; ds; SNP; BDKRB1;  
 KM tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH; kallikrein 1;  
 KM K1; bradykinin receptor B2; BDKRB2; gene therapy;  
 KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
 KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
 KM myocardial infarction; ventricular hypertrophy; vascular disease;  
 KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
 KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
 KM autoimmune disease; inflammatory arthritis; cancer; wound;  
 KM viral infection; bacterial infection; fungal infection; COPD;  
 KM Chronic obstructive pulmonary disease; enterocolitis;



single-nucleotide polymorphism.  
Homo sapiens.  
W0200261131-A2.  
08-AUG-2002.  
03-DEC-2001; 2001WO-US047235.  
04-DEC-2000; 2000US-0251015P.  
23-JAN-2001; 2001US-0263678P.  
02-MAR-2001; 2001US-0273037P.  
(BRIM) BRISTOL-MYERS SQUIBB CO.  
(TSUC/) TSUCHIHASHI Z.  
(HUI/) HUI L.  
Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
Swanson BN, Powell JR;  
WPI; 2002-619265/66.  
New isolated nucleic acid with at least one polymorphic position, useful  
for detecting, diagnosing and treating disorders such as angioedema,  
cancer, viral, bacterial or fungal infection, cardiovascular and  
autoimmune diseases.  
Disclosure; Page 653; 977pp; English.  
The invention relates to an isolated nucleic acid from a human gene  
encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),  
tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
polymorphic position. Also included are (1) a probe that hybridises to a  
polymorphic position as provided in the detailed summary of single  
nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
obtaining the sample from one or more individuals and determining the  
nucleic acid sequence at one or more polymorphic positions in a gene  
encoding a protein selected from the group above; (3) constructing (M2)  
haplotypes using the genes comprising grouping at least two nucleic acids  
(4) identifying (M3) an individual at risk of developing a disorder  
upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
using the polymorphic data; (5) a library of nucleic acids, each of which  
comprises one or more polymorphic positions within a gene encoding a  
human protein selected from the group above; and (6) genotyping (M4) an  
individual comprising obtaining a nucleic acid sample, determining the  
nucleotide present in at least one polymorphic position, and comparing at  
least one position with a known data set. The genes, (M1, M2, M3 and M4)  
and compositions are useful for detecting, diagnosing, treating,  
preventing various disorders such as angioedema and diseases which  
involve angiotensin II like haemangiomas, tumours, sarcomas, Crohn's  
disease, trachomas, and cardiovascular diseases like angina pectoris,  
hypertension, heart failure, myocardial infarction, ventricular  
hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
artery disease, arteriosclerosis and/or atherosclerosis, and  
hyperensitivity reactions, sepsis, autoimmune diseases, inflammatory  
arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
obstructive pulmonary disease (COPD) and enterocolitis (many other  
diseases and disorders are listed in the specification). The  
polymorphisms are also useful for immunophenotyping of cell lines  
and biological samples. The present sequence represents or contains the  
region surrounding a single-nucleotide polymorphism in one of the genes  
encoding one of the proteins listed above  
Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1529 CCTCACTGAGCTTGCA 1547  
DB 19 CCTCACTGAGCTTGCA 1

RESULT 181  
AEE77697  
ID AEE77697 standard; DNA; 20 BP.  
XX  
AC AEE77697;  
XX  
DT 09-FEB-2006 (first entry)  
XX  
XX Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1318.  
DE  
XX Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
KW neuropsychologic disorder; dopamine receptor D2; DRD2; ss.  
XX  
XX Homo sapiens.  
OS  
XX W02005118843-A1.  
XX  
XX 15-DEC-2005.  
XX  
XX 01-JUN-2005; 2005WO-AU000775.  
XX  
XX 01-JUN-2004; 2004AU-00902919.  
XX  
XX (UYOU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
XX Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
PI WPI; 2006-047555/05.  
XX  
XX Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
XX  
XX Claim 31; SEQ ID NO 1318; 634pp; English.  
XX  
XX The invention relates to a method of identifying a genetic profile  
XX associated with a neurological, psychiatric or psychological condition,  
XX phenotype or state including a sub-threshold neurological, psychiatric or  
XX psychological condition, phenotype or state in an individual, comprising  
XX screening individuals for a polymorphism in a genetic locus comprising  
XX the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
XX genetic mutation providing a genetic marker for a neurological,  
XX psychiatric, or psychological condition, state or phenotype in an  
XX individual, where the presence of a 957C polymorphism is indicative of a  
XX predisposition to developing a neurological, psychiatric or psychological  
XX condition, phenotype or state. The compositions and methods are useful  
XX for identifying a genetic profile associated with a neurological,  
XX psychiatric or psychological condition. The method enables clinicians to  
XX make a genetic-based diagnosis of a neurological, psychiatric or  
XX psychological condition and can thereby implement treatment or  
XX preventative or symptom-ameliorating protocols to reduce the adverse  
XX consequences of the condition. This sequence represents a human dopamine  
XX receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
XX invention.  
SQ Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 984 CATCTGCTGCTGCTGCT 1000  
DB 4 CATCTGCTGCTGCTGCT 20



RESULT_182
AEE77702 ID AEE77702 standard; DNA; 20 BP.
XX AEE77702;
XX DT 09-FEB-2006 (first entry)
XX DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1323.
XX KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;
XX RV neuropsychologic disorder; dopamine receptor D2; DRD2; ss.
XX OS Homo sapiens.
XX PN WO2005118843-A1.
XX PD 15-DEC-2005.
XX PF 01-JUN-2005; 2005WO-AU000775.
XX PR 01-JUN-2004; 2004AU-00902919.
XX PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;
XX DR WPI; 2006-047555/05.
XX PT Identifying genetic profile associated with a neurological, psychiatric,
XX PT or psychological condition, comprises screening individuals for a
XX PT polymorphism in a genetic locus comprising the dopamine receptor D2
XX PT (DRD2) gene.
XX PS Claim 31; SEQ ID NO 1323; 634BP; English.
XX CC The invention relates to a method of identifying a genetic profile
XX CC associated with a neurological, psychiatric or psychological condition,
XX CC phenotype or state including a sub-threshold neurological, psychiatric or
XX CC psychological condition, phenotype or state in an individual, comprising
XX CC screening individuals for a polymorphism in a genetic locus comprising
XX CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a
XX CC genetic mutation providing a genetic marker for a neurological,
XX CC psychiatric, or psychological condition, state or phenotype in an
XX CC individual, where the presence of a 957C polymorphism is indicative of a
XX CC predisposition to developing a neurological, psychiatric or psychological
XX CC condition, phenotype or state. The compositions and methods are useful
XX CC for identifying a genetic profile associated with a neurological,
XX CC psychiatric or psychological condition. The method enables clinicians to
XX CC make a genetic or psychological diagnosis of a neurological, psychiatric or
XX CC psychological condition and can thereby implement treatment or
XX CC preventative or symptom-ameliorating protocols to reduce the adverse
XX CC consequences of the condition. This sequence represents a human dopamine
XX CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the
XX CC invention.
XX SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 986 TCTGCTGGCTGCCCTTC 1002
Ds 1 TCTGCTGGCTGCCCTTC 17
RESULT_183
AAQ36818/C ID AAQ36818 standard; DNA; 21 BP.
XX AAQ36818;
XX

DT	25-MAR-2003	(revised)
DT	22-JUN-1993	(first entry)
XX		
DE	Oligomer SM 82 used in construction of SSP polypeptides.	
XX		
KW	Heptad; plants; custom tailored storage proteins; in vivo; expression;	
KM	ss.	
OS	Synthetic.	
XX		
PN	WO9303160-A1.	
XX		
PD	18-FEB-1993.	
XX		
PF	07-AUG-1992;	92WO-US006412.
XX		
PR	09-AUG-1991;	91US-00743006.
XX		
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Falco SC, Keeler SJ, Rice JA;	
XX		
DR	WP1, 1993-076517/09.	
XX		
PT	Synthetic polypeptide(s) contg. specified heptad units - expressed in	
PT	vivo in plants to serve as custom-tailored storage proteins with	
PT	specified aminoacid content.	
XX		
ES	Disclosure; Page 109; 176pp; English.	
CC		
XX	The sequence represents the DNA sequence encoding a synthetic heptad	
CC	polypeptide. The synthetic polypeptide can be expressed in vivo in plants	
CC	to serve as a synthetic seed storage protein which can be custom-tailored	
CC	for specific end-user requirements. The DNA encoding the heptad may be	
CC	used to transform plants to increase the content of partic. amino acids	
CC	such as lysine or methionine in seeds or leaves. See also AAQ36810-28,	
CC	AAQ37265-301. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;	
Query Match	1.0%; Score 17; DB 1; Length 21;	
Best Local Similarity	100.0%; Freq. No. 1.6e+02;	
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
CY	1404 CTTCAGCTTCCTCTCCA 1420	
DB		
19 CTTCAGCTTCTCTCCA 3		
RESULT 184		
AAQ36820/c		
ID	AAQ36820 standard; DNA; 21 BP.	
XX		
AC	AAQ36820;	
XX		
DT	25-MAR-2003 (revised)	
DT	22-JUN-1993 (first entry)	
XX		
DE	Oligomer SM 86 used in construction of SSP polypeptides.	
XX		
KW	Heptad; plants; custom tailored storage proteins; in vivo; expression;	
KM	ss.	
XX		
OS	Synthetic.	
XX		
PN	WO9303160-A1.	
XX		
PD	18-FEB-1993.	
XX		
PF	07-AUG-1992;	92WO-US006412.
XX		
PR	09-AUG-1991;	91US-00743006.
XX		

PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Falco SC, Keeler SJ, Rice JA;  
 XX  
 DR WPI; 1993-076517/09.  
 XX  
 PT Synthetic polypeptide(s) contg. specified heptad units - expressed in  
 PT vivo in plants to serve as custom-tailored storage proteins with  
 PT specified aminoacid content.  
 XX  
 PS Disclosure; Page 110; 176pp; English.  
 XX  
 CC The sequence represents the DNA sequence encoding a synthetic heptad  
 CC polypeptide. The synthetic polypeptide can be expressed in vivo in plants  
 CC to serve as a synthetic seed storage protein which can be custom-tailored  
 CC for specific end-user requirements. The DNA encoding the heptad may be  
 CC used to transform plants to increase the content of partic. amino acids  
 CC such as lysine or methionine in seeds or leaves. See also AAQ36810-28,  
 CC AAQ37265-301. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1404 CTTGAGCTTCTCCTCCA 1420  
 DB 19 CTTGAGCTTCTCCTCCA 3  
 RESULT 185  
 AAQ36822/C  
 ID AAQ36822 standard; DNA; 21 BP.  
 XX  
 AC AAQ36822;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-JUN-1993 (first entry)  
 XX  
 DE Oligomer SM 88 used in construction of SSP polypeptides.  
 XX  
 KM Heptad; plants; custom tailored storage proteins; in vivo; expression;  
 KM ss.  
 KM  
 KM Synthetic.  
 OS  
 XX  
 PN WO9303160-A1.  
 XX  
 PD 18-FEB-1993.  
 XX  
 PF 07-AUG-1992; 92WO-US006412.  
 XX  
 PR 09-AUG-1991; 91US-00743006.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PI Falco SC, Keeler SJ, Rice JA;  
 PI  
 DR WPI; 1993-076517/09.  
 XX  
 PT Synthetic polypeptide(s) contg. specified heptad units - expressed in  
 PT vivo in plants to serve as custom-tailored storage proteins with  
 PT specified aminoacid content.  
 XX  
 PS Disclosure; Page 111; 176pp; English.  
 XX  
 CC The sequence represents the DNA sequence encoding a synthetic heptad  
 CC polypeptide. The synthetic polypeptide can be expressed in vivo in plants  
 CC to serve as a synthetic seed storage protein which can be custom-tailored  
 CC for specific end-user requirements. The DNA encoding the heptad may be  
 CC used to transform plants to increase the content of partic. amino acids  
 CC such as lysine or methionine in seeds or leaves. See also AAQ36810-28,  
 CC

CC AAQ37265-301. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1404 CTTGAGCTTCTCCTCCA 1420  
 DB 19 CTTGAGCTTCTCCTCCA 3  
 RESULT 186  
 AAQ94986/C  
 ID AAQ94986 standard; DNA; 21 BP.  
 XX  
 AC AAQ94986;  
 XX  
 DT 16-JUL-1996 (first entry)  
 XX  
 DE SSP9 Oligonucleotide SM 88.  
 XX  
 KM Lysine; synthetic storage protein; SSP; vector; pSK6;  
 KM dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;  
 KM Glycine max; transgenic plant; essential amino acid; ss.  
 XX  
 OS Synthetic.  
 XX  
 KM Key Location/Qualifiers  
 KM 1. .21  
 FT misc\_feature /\*tag= a  
 FT 2. .21 /standard\_name= "SM 88"  
 FT CDS /\*tag= b  
 FT  
 XX  
 PN WO9515392-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 21-NOV-1994; 94WO-US013190.  
 XX  
 PR 30-NOV-1993; 93US-00160117.  
 PR 17-JUN-1994; 94US-00261661.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PI Falco SC, Keeler SJ, Rice JA;  
 PI  
 DR WPI; 1995-215272/28.  
 DR P-PSDB; AAR78246.  
 XX  
 PT New chimeric gene providing increased lysine content in plant seeds -  
 PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast  
 PT transport sequence and seed specific promoter; also new plants of  
 PT improved nutritional value.  
 XX  
 PS Example 8; Page 78; 180pp; English.  
 XX  
 CC Oligonucleotide SM88 (AAQ94986) and complementary sequence SM89  
 CC (AAQ94987) code for heptad peptide SSP9 (AAR78246). They were annealed  
 CC and used in the construction a DNA fragment (see also AAQ94995) that was  
 CC inserted into vector pSK6 (see also AAR78236). The DNA fragment codes for  
 CC a synthetic storage protein (SSP) contg. multiple lysine-rich heptad  
 CC repeats (see AAR78252). This can be expressed in the seeds of transformed  
 CC plants, e.g. soybean and corn, to increase lysine content  
 XX  
 SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY      1404 CTTGAGCTTCTCTCCA 1420
Db      19 CTTGAGCTTCTCTCCA 3

RESULT 187
AAQ94984/C
XX      AAQ94984 standard; DNA; 21 BP.
AC
XX      AAQ94984;
XX
XX      16-JUN-1996 (first entry)
XX
XX      SSP8 Oligonucleotide SM 86.
XX
XX      Lysine; synthetic storage protein; SSP; vector; pSK6;
XX      dihydrodipicolinic acid synthase; corn; maize; zea mays; soybean;
XX      Glycine max; transgenic plant; essential amino acid; ss.
XX
XX      Synthetic.
XX
XX      Key
XX      Location/Qualifiers
XX      misc_feature
XX      1..21
XX      /tag= a
XX      /standard_name= "SM 86"
XX      CDS
XX      2..21
XX      /*tag= b

MO9515392-A1.
XX
XX      08-JUN-1995.
XX
XX      21-NOV-1994; 94MO-US013190.
XX
XX      30-NOV-1993; 93US-00160117.
XX      17-JUN-1994; 94US-00261661.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Falco SC, Keeler SJ, Rice JA;
XX
XX      WPI; 1995-215272/28.
XX      P-PSDB; AAR78245.
XX
XX      New chimeric gene providing increased lysine content in plant seeds -
XX      contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX      transport sequence and seed specific promoter, also new plants of
XX      improved nutritional value.
XX
XX      Example 8; Page 78; 180pp; English.
XX
XX      Oligonucleotide SM86 (AAQ94984) and complementary sequence SM87
XX      (AAQ94985) code for heptad peptide SSP8 (AAR78245). They were annealed
XX      and used in the construction a DNA fragment (see also AAQ94994) that was
XX      inserted into vector pSK6 (see also AAR78236). The DNA fragment codes for
XX      a synthetic storage protein (SSP) contg. multiple lysine-rich heptad
XX      repeats (see AAR78251). This can be expressed in the seeds of transformed
XX      plants, e.g. soybean and corn, to increase lysine content
XX
XX      Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

Query March      1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1404 CTTGAGCTTCTCTCCA 1420
Db      19 CTTGAGCTTCTCTCCA 3

RESULT 188
AAQ94976/C
XX      AAQ94976 standard; DNA; 21 BP.
AC
XX      AAQ94976;
XX
XX      16-JUN-1996 (first entry)
XX
XX      SSP7 Oligonucleotide SM 82.
XX
XX      Lysine; synthetic storage protein; SSP; vector; pSK6;
XX      dihydrodipicolinic acid synthase; corn; maize; zea mays; soybean;
XX      Glycine max; transgenic plant; essential amino acid; ss.
XX
XX      Synthetic.
XX
XX      Key
XX      Location/Qualifiers
XX      misc_feature
XX      1..21
XX      /tag= a
XX      /standard_name= "SM 82"
XX      CDS
XX      2..21
XX      /*tag= b

MO9515392-A1.
XX
XX      08-JUN-1995.
XX
XX      21-NOV-1994; 94MO-US013190.
XX
XX      30-NOV-1993; 93US-00160117.
XX      17-JUN-1994; 94US-00261661.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Falco SC, Keeler SJ, Rice JA;
XX
XX      WPI; 1995-215272/28.
XX      P-PSDB; AAR78237.
XX
XX      New chimeric gene providing increased lysine content in plant seeds -
XX      contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX      transport sequence and seed specific promoter, also new plants of
XX      improved nutritional value.
XX
XX      Example 8; Page 76; 180pp; English.
XX
XX      Oligonucleotide SM82 (AAQ94976) and complementary sequence SM83
XX      (AAQ94977) code for heptad peptide SSP7 (AAR78237). They were annealed
XX      and used in the construction DNA fragments (see also AAQ94978-80,
XX      AAQ94992, AAQ95004 and AAQ95006) that were inserted into vector pSK6 (see
XX      also AAR78236). The DNA fragments code for synthetic storage proteins
XX      (SSPs) contg. multiple lysine-rich heptad repeats (see AAR78239-41,
XX      AAR78249, AAR78258 and AAR78260). These can be expressed in the seeds of
XX      transformed plants, e.g. soybean and corn, to improve lysine content
XX
XX      Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;

Query March      1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1404 CTTGAGCTTCTCTCCA 1420
Db      19 CTTGAGCTTCTCTCCA 3

RESULT 189
AAV99519/C
XX      AAV99519 standard; DNA; 21 BP.
AC
XX      AAV99519;
XX
XX      29-MAR-1999 (first entry)
XX
XX      Oligonucleotide SM86 encoding SSP8 heptad repeat.
XX
```

KM	Lysine; transgenic plant; seed storage protein; vector; PSK5; ds.
XX	Synthetic.
OS	
FH	Key Location/Qualifiers
FT	misc_feature 1..3
FT	/tag= a
FT	/note= "5' single stranded overhang"
FT	21
FT	misc_feature
FT	/tag= b
FT	/note= "5' overhang on complementary strand of sequence
FT	5'-ATC-3'"
XX	
PN	W09842831-A2.
XX	
PD	01-OCT-1998.
XX	
PF	27-MAR-1998; 98MO-US006051.
XX	
PR	27-MAR-1997; 97US-00824627.
PA	(DUP) ) DU PONT DE NEMOURS & CO E I.
XX	
PI	Falco SC, Mcdeviltt RE, Epelbaum SU;
XX	
DR	WPI, 1999-045139/04.
XX	
XK	Nucleic acids and chimeric genes for increasing seed lysine content -
PT	comprise sequence encoding all or part of lysine ketoglutarate reductase,
PT	useful to improve nutritional quality of seeds from transformed plants.
PS	
XX	
XX	Example 21; Page 103; 231pp; English.
CC	This synthetic double-stranded oligonucleotide encodes a lysine-rich
CC	heptad repeat peptide. It can be inserted into the unique BstI site in
CC	the 'base gene' (see AAV99509) of vector PSK5 to provide repetitive
CC	heptad coding sequences. Chimeric genes for lysine-rich synthetic seed
CC	storage proteins suitable for expression in the seeds of plants have been
CC	constructed (see AAV9513-18, AAV9527-32, AAV9539-41). The invention
CC	provides methods for improving the nutritional quality of seeds from
CC	transgenic plants by increasing lysine content
SQ	
XX	Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
OY	
Db	Query Match 1.0%; Score 17; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1404 CTTGAGCTTCTCTCCA 1420     19 CTTGAGCTTCTCTCCA 3
RESULT 190	
AAV99509/C	
ID	AAV99509 standard; DNA; 21 BP.
AC	AAV99509;
XX	
DT	29-MAR-1999 (first entry)
XX	
DE	Oligonucleotide SM82 encoding SPB7 heptad repeat.
KX	
KW	Lysine; transgenic plant; seed storage protein; vector; PSK5; ds.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 1..3
FT	/tag= a
FT	/note= "5' single stranded overhang"
FT	21
FT	misc_feature
FT	/tag= b

PT		/note= "5' overhang on complementary strand of sequence
FT		5'-ATC-3'"
XX		
PN	WO9842831-A2.	
XX		
PD	01-OCT-1998.	
XX		
PF	27-MAR-1998;	98WO-US006051.
XX		
FR	27-MAR-1997;	9TUS-00824627.
XX		
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Falco SC, Mcdeviltt RE, Epelbaum SU;	
DR	WPI, 1999-045139/04.	
XX		
PT	Nucleic acids and chimeric genes for increasing seed lysine content -	
PT	comprise sequence encoding all or part of lysine ketoglutarate reductase,	
PT	useful to improve nutritional quality of seeds from transformed plants.	
PS		
XX	Example 21; Page 102; 231pp; English.	
CC	This synthetic double-stranded oligonucleotide encodes a lysine-rich	
CC	heptad repeat peptide. It can be inserted into the unique BstI site in	
CC	the 'base gene' (see AA999505) of vector pSK5 to provide repetitive	
CC	heptad coding sequences. Chimeric genes for lysine-rich synthetic seed	
CC	storage proteins suitable for expression in the seeds of plants have been	
CC	constructed (see AAV99513-18, AAV9547-32, AAV9539-41). The invention	
CC	provides methods for improving the nutritional quality of seeds from	
transgenic plants by increasing lysine content		
SQ	Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;	
OY		
Query Match	1.0%; Score 17; DB 1; Length 21;	
Best Local Similarity	100.0%; Pred. No. 1.6e+02;	
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Db	1404 CTTGAGCTTCCTCCA 1420 19 CTTGAGCTTCCTCCA 3	
RESULT 191		
ID	AAV99521/C	
XX	AAV99521 standard; DNA; 21 BP.	
AC	AAV99521;	
XX		
DT	29-MAR-1999 (first entry)	
XX		
DE	Oligonucleotide SWS6 encoding SSP9 heptad repeat.	
XX		
KM	Lysine; transgenic plant; seed storage protein; vector; pSK5; ds.	
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
PH	misc_feature	1..3
FT	misc_feature	/tag= a
FT	misc_feature	/note= "5' single stranded overhang"
FT	misc_feature	21
XX		
PN	WO9842831-A2.	
XX		
PD	01-OCT-1998.	
XX		
PF	27-MAR-1998;	98WO-US006051.
XX		
XX	27-MAR-1997;	9TUS-00824627.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Falco SC, Mcdeviltt RE, Spelbaum SU;  
XX WPI; 1999-045139/04.  
XX  
XX Nucleic acids and chimeric genes for increasing seed lysine content -  
XX comprise sequence encoding all or part of lysine ketoglutarate reductase,  
XX useful to improve nutritional quality of seeds from transformed plants.  
XX  
XX Example 21; Page 104; 231pp; English.  
XX  
XX This synthetic double-stranded oligonucleotide encodes a lysine-rich  
XX heptad repeat peptide. It can be inserted into the unique *Eari* site in  
XX the 'base gene' (see AAV99505) of vector pSK5 to provide repetitive  
XX heptad coding sequences. Chimeric genes for lysine-rich synthetic seed  
XX storage proteins suitable for expression in the seeds of plants have been  
XX constructed (see AAV99513-18, AAV99527-32, AAV99539-41). The invention  
XX provides methods for improving the nutritional quality of seeds from  
XX transgenic plants by increasing lysine content  
XX  
XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.0%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. NO. 1.6e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1404 CTTGAGCTTCTCTCCCA 1420  
XX 19 CTTGAGCTTCTCTCCCA 3  
XX  
XX RESULT 192  
XX ADA15939/C  
XX ID ADA15939 standard; DNA; 21 BP.  
XX  
XX ADA15939;  
XX  
XX 06-NOV-2003 (first entry)  
XX  
XX Synthetic storage protein oligonucleotide SM88.  
XX  
XX see; lysC; transgenic; lysine accumulation;  
XX dihydrodipicolinic acid synthase; DHDPs; lysine inhibition;  
XX lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;  
XX aspartokinase III; AKIII; synthetic seed storage protein; SSP.  
XX  
XX Synthetic.  
XX  
XX US6459019-B1.  
XX  
XX 01-OCT-2002.  
XX  
XX 24-MAR-1997; 97US-00823771.  
XX  
XX 19-MAR-1992; 92US-00855414.  
XX 06-JUN-1994; 94US-00178212.  
XX 07-JUN-1995; 95US-00474633.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Falco SC, Keeler SJ, Rice JA;  
XX WPI; 2003-028272/02.  
XX P-PSDB; ADA15946.  
XX  
XX Transformed plants that accumulate lysine at higher levels in its seeds  
XX than untransformed plants, has gene fragments encoding lysine-insensitive  
XX dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.  
XX  
XX Example 21; Col 79; 109pp; English.

XX The invention relates to a plant comprising two foreign nucleotide  
XX sequences which cause seeds obtained from the plant to accumulate lysine  
XX at a level of at least 10% higher than seeds of a plant that do not  
XX comprise the nucleotide, where the nucleotide comprises a fragment  
XX encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive  
XX to lysine inhibition, and a fragment encoding a plant lysine  
XX ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment  
XX is operably linked to a plant chloroplast transit sequence (CTS) and the  
XX plant lysine ketoglutarate reductase subfragment is used in antisense  
XX inhibition or cosuppression. Also included are progeny plants from the  
XX above mentioned plant and seeds obtained from the above mentioned plant.  
XX The seeds obtained from the above mentioned plant (e.g., rapeseed,  
XX soybean or corn) comprising the foreign nucleic acid sequences accumulate  
XX lysine at a higher level, preferably at a level of at least 10% higher  
XX than seeds of a plant that do not comprise the foreign nucleic acid  
XX sequences. Chimeric gene comprising DHDPs from *C. glutamicum* and  
XX aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-  
XX insensitive) are also used to generate the above transgenic plants. Also  
XX disclosed are synthetic seed storage proteins (SSP) used as an internal  
XX source of lysine, built up from synthetic peptide monomers based around  
XX an *Eari* site sequence (for generating multimeric proteins). The present  
XX sequence is a strand of an oligonucleotide encoding an SSP monomer.  
XX  
XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.0%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. NO. 1.6e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1404 CTTGAGCTTCTCTCCCA 1420  
XX 19 CTTGAGCTTCTCTCCCA 3  
XX  
XX RESULT 193  
XX ADA15937/C  
XX ID ADA15937 standard; DNA; 21 BP.  
XX  
XX ADA15937;  
XX  
XX 06-NOV-2003 (first entry)  
XX  
XX Synthetic storage protein oligonucleotide SM86.  
XX  
XX see; lysC; transgenic; lysine accumulation;  
XX dihydrodipicolinic acid synthase; DHDPs; lysine inhibition;  
XX lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;  
XX aspartokinase III; AKIII; synthetic seed storage protein; SSP.  
XX  
XX Synthetic.  
XX  
XX US6459019-B1.  
XX  
XX 01-OCT-2002.  
XX  
XX 24-MAR-1997; 97US-00823771.  
XX  
XX 19-MAR-1992; 92US-00855414.  
XX 06-JUN-1994; 94US-00178212.  
XX 07-JUN-1995; 95US-00474633.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Falco SC, Keeler SJ, Rice JA;  
XX WPI; 2003-028272/02.  
XX P-PSDB; ADA15945.  
XX  
XX Transformed plants that accumulate lysine at higher levels in its seeds  
XX than untransformed plants, has gene fragments encoding lysine-insensitive  
XX dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.  
XX  
XX Example 21; Col 79; 109pp; English.

XX The invention relates to a plant comprising two foreign nucleotide  
CC sequences which cause seeds obtained from the plant to accumulate lysine  
CC at a level of at least 10% higher than seeds of a plant that do not  
CC comprise the nucleotide, where the nucleotide comprises a fragment  
CC encoding a dihydrodipicolinic acid synthase (DHDS) that is insensitive  
CC to lysine inhibition, and a fragment encoding a plant lysine  
CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment  
CC is operably linked to a plant chloroplast transit sequence (CTS) and the  
CC plant lysine ketoglutarate reductase subfragment is used in antisense  
CC inhibition or cosuppression. Also included are progeny plants from the  
CC above mentioned plant and seeds obtained from the above mentioned plant.  
CC The seeds obtained from the above mentioned plant (e.g., rapeseed,  
CC soybean or corn) comprising the foreign nucleic acid sequences accumulate  
CC lysine at a higher level, preferably at a level of at least 10% higher  
CC than seeds of a plant that do not comprise the foreign nucleic acid  
CC sequences. Chimeric gene comprising DHDS from *C. glutamicum* and  
CC aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-  
CC insensitive) are also used to generate the above transgenic plants. Also  
CC disclosed are synthetic seed storage proteins (SSP) used as an internal  
CC source of lysine, built up from synthetic peptide monomers based around  
CC an Earl site sequence (for generating multimeric proteins). The present  
CC sequence is a strand of an oligonucleotide encoding an SSP monomer.

Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;

1404 CTTGAGCTTCTCTCCA 1420  
19 CTTGAGCTTCTCTCCA 3

Db 19 CTTGAGCTTCTCTCCA 3

RESULT 194  
ADAI5921/C  
ID ADAI5921 standard; DNA; 21 BP.

AC ADAI5921;

DT 06-NOV-2003 (first entry)

XX Synthetic storage protein oligonucleotide SM82.

XX ss; *lysC*; transgenic; lysine accumulation;

KW dihydrodipicolinic acid synthase; DHDS; lysine inhibition;

KW lysine ketoglutarate reductase; LKR; chloroplast transit sequence; CTS;

KW aspartokinase III; AKIII; synthetic seed storage protein; SSP.

XX Synthetic.

XX US6459019-B1.

PD 01-OCT-2002.

PF 24-MAR-1997; 97US-00823771.

XX 19-MAR-1992; 92US-00855414.

PR 06-JAN-1994; 94US-00178212.

PR 07-JUN-1995; 95US-00474633.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

PA Falco SC, Keeler SJ, Rice JA;

PI WPI; 2003-028272/02.

DR P-PSDB; ADAI5923.

XX Transformed plants that accumulate lysine at higher levels in its seeds  
PT than untransformed plants, has gene fragments encoding lysine-insensitive  
PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.

PS Example 21; Col 78; 109pp; English.

XX The invention relates to a plant comprising two foreign nucleotide  
CC sequences which cause seeds obtained from the plant to accumulate lysine  
CC at a level of at least 10% higher than seeds of a plant that do not  
CC comprise the nucleotide, where the nucleotide comprises a fragment  
CC encoding a dihydrodipicolinic acid synthase (DHDS) that is insensitive  
CC to lysine inhibition, and a fragment encoding a plant lysine  
CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment  
CC is operably linked to a plant chloroplast transit sequence (CTS) and the  
CC plant lysine ketoglutarate reductase subfragment is used in antisense  
CC inhibition or cosuppression. Also included are progeny plants from the  
CC above mentioned plant and seeds obtained from the above mentioned plant.  
CC The seeds obtained from the above mentioned plant (e.g., rapeseed,  
CC soybean or corn) comprising the foreign nucleic acid sequences accumulate  
CC lysine at a higher level, preferably at a level of at least 10% higher  
CC than seeds of a plant that do not comprise the foreign nucleic acid  
CC sequences. Chimeric gene comprising DHDS from *C. glutamicum* and  
CC aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-  
CC insensitive) are also used to generate the above transgenic plants. Also  
CC disclosed are synthetic seed storage proteins (SSP) used as an internal  
CC source of lysine, built up from synthetic peptide monomers based around  
CC an Earl site sequence (for generating multimeric proteins). The present  
CC sequence is a strand of an oligonucleotide encoding an SSP monomer.

Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;

1404 CTTGAGCTTCTCTCCA 1420  
19 CTTGAGCTTCTCTCCA 3

Db 19 CTTGAGCTTCTCTCCA 3

RESULT 195  
ACH03695/C  
ID ACH03695 standard; DNA; 21 BP.

AC ACH03695;

DT 25-SEP-2003 (first entry)

XX Ear I-based lysine-rich heptad repeat oligonucleotide SM88.

XX Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDS;

KW seed lysine content; seed threonine content; seed storage protein; SSP;

KW chloroplast transit sequence; lysine-rich protein;

KW lysine ketoglutarate reductase; LKR; transgenic; ss.

XX Synthetic.

XX US2003056242-A1.

PD 20-MAR-2003.

PF 17-DEC-2001; 2001US-00023066.

XX 19-MAR-1992; 92US-00855414.

PR 18-MAR-1993; 93WO-US002480.

PR 06-JAN-1994; 94US-00178212.

PR 07-JUN-1995; 95US-00474633.

PR 24-MAR-1997; 97US-00823771.

XX (FALC) FALCO S. C.

PA Falco SC;

PI WPI; 2003-521869/49.

DR P-PSDB; ABO44333.

XX New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic

PT acid synthase, useful for increasing threonine or lysine content of seeds  
 PT of plant.  
 XX Example 21; Page 43; 116pp; English.  
 CC The invention relates to an isolated nucleic acid fragment comprising a  
 CC first nucleic acid subfragment encoding aspartokinase (AK) that is  
 CC substantially insensitive to inhibition by lysine, and a second nucleic  
 CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDS) that  
 CC is substantially insensitive to inhibition by lysine. Also included are  
 CC an isolated nucleic acid fragment comprising a nucleic acid subfragment  
 CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where  
 CC the nucleic acid fragment is operably linked to a plant chloroplast  
 CC transit sequence and to a seed-specific regulatory sequence, a plant  
 CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained  
 CC from the plant, increasing threonine or lysine content of the seeds of  
 CC a plant, a plant capable of transmitting the chimeric gene to a progeny of  
 CC plant having the ability to produce levels of free threonine or lysine at  
 CC least two times greater than the free threonine levels of untransformed  
 CC plants, a transformed (soybean) plant comprising seeds that accumulate  
 CC lysine at a level at least ten percent to four-fold higher than the seeds  
 CC of an untransformed plant, a transformed rapeseed comprising seeds that  
 CC accumulate lysine to a level between ten percent and one hundred percent  
 CC higher than that of the seeds of an untransformed plant, a monocot plant  
 CC comprising in its genome the nucleic acid fragment having the monocot-  
 CC embryo specific promoter and a transformed corn plant comprising seeds  
 CC that accumulate lysine to a level between ten percent and one hundred  
 CC thirty percent higher than the seeds of the untransformed plant. Also  
 CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up  
 CC from monomer lysine-rich heptad repeats (encoded by Bari restriction  
 CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed  
 CC plant. The nucleic acid fragments, genes and methods are useful for  
 CC increasing threonine or lysine content of the seeds of the plant. Seeds  
 CC containing increased threonine or lysine content eliminate the need to  
 CC supplement mixed grain feeds with lysine or threonine produced via  
 CC microbial fermentation. The present sequence is one strand of a DNA  
 CC encoding a lysine-rich heptad repeat for use as a monomer unit in a  
 CC synthetic seed storage protein  
 XX  
 SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1404 CTTACGCTTCTCTCCA 1420  
 Db 19 CTTACGCTTCTCTCCA 3  
 RESULT 196  
 ACH03685/c  
 ID ACH03685 standard; DNA; 21 BP.  
 AC ACH03685;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Bar I-based lysine-rich heptad repeat oligonucleotide SM82.  
 XX  
 XX Aspartokinase; AKII; dihydrodipicolinic acid synthase; DHDS;  
 KM seed lysine content; seed threonine content; seed storage protein; SSP;  
 KM chloroplast transit sequence; lysine-rich protein;  
 KM lysine ketoglutarate reductase; LKR; transgenic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US200305642-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 17-DEC-2001; 2001US-00023066.  
 XX

PR 19-MAR-1992; 92US-00855414.  
 PR 18-MAR-1993; 93MO-US002480.  
 PR 06-JUN-1994; 94US-00178212.  
 PR 07-JUN-1995; 95US-00474633.  
 PR 24-MAR-1997; 97US-00823771.  
 XX  
 PA (PALC/) PALCO S. C.  
 XX  
 PT Falco SC;  
 XX  
 DR WPI: 2003-521869/49.  
 P-PSDB; ABO44324.  
 XX  
 PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic  
 PT acid synthase, useful for increasing threonine or lysine content of seeds  
 PT of plant.  
 XX  
 PS Example 21; Page 60; 116pp; English.  
 CC The invention relates to an isolated nucleic acid fragment comprising a  
 CC first nucleic acid subfragment encoding aspartokinase (AK) that is  
 CC substantially insensitive to inhibition by lysine, and a second nucleic  
 CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDS) that  
 CC is substantially insensitive to inhibition by lysine. Also included are  
 CC an isolated nucleic acid fragment comprising a nucleic acid subfragment  
 CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where  
 CC the nucleic acid fragment is operably linked to a plant chloroplast  
 CC transit sequence and to a seed-specific regulatory sequence, a plant  
 CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained  
 CC from the plant, increasing threonine or lysine content of the seeds of  
 CC plant, a plant capable of transmitting the chimeric gene to a progeny of  
 CC plant having the ability to produce levels of free threonine or lysine at  
 CC least two times greater than the free threonine levels of untransformed  
 CC plants, a transformed (soybean) plant comprising seeds that accumulate  
 CC lysine at a level at least ten percent to four-fold higher than the seeds  
 CC of an untransformed plant, a transformed rapeseed comprising seeds that  
 CC accumulate lysine to a level between ten percent and one hundred percent  
 CC higher than that of the seeds of an untransformed plant, a monocot plant  
 CC comprising in its genome the nucleic acid fragment having the monocot-  
 CC embryo specific promoter and a transformed corn plant comprising seeds  
 CC that accumulate lysine to a level between ten percent and one hundred  
 CC thirty percent higher than the seeds of the untransformed plant. Also  
 CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up  
 CC from monomer lysine-rich heptad repeats (encoded by Bari restriction  
 CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed  
 CC plant. The nucleic acid fragments, genes and methods are useful for  
 CC increasing threonine or lysine content of the seeds of the plant. Seeds  
 CC containing increased threonine or lysine content eliminate the need to  
 CC supplement mixed grain feeds with lysine or threonine produced via  
 CC microbial fermentation. The present sequence is one strand of a DNA  
 CC encoding a lysine-rich heptad repeat for use as a monomer unit in a  
 CC synthetic seed storage protein  
 XX  
 SQ Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1404 CTTACGCTTCTCTCCA 1420  
 Db 19 CTTACGCTTCTCTCCA 3  
 RESULT 197  
 ACH03693/c  
 ID ACH03693 standard; DNA; 21 BP.  
 AC ACH03693;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Bar I-based lysine-rich heptad repeat oligonucleotide SM86.  
 XX

XX Aspartokinase; AKII; dihydrodipicolinic acid synthase; DHDPs;  
KW seed lysine content; seed threonine content; seed storage protein; SSP;  
KM chloroplast transit sequence; lysine-rich protein;  
KM lysine ketoglutarate reductase; LKR; transgenic; ss.  
XX Synthetic.  
OS  
PN US200305642-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 17-DEC-2001; 2001US-00023066.  
XX  
PR 19-MAR-1992; 92US-00855414.  
PR 18-MAR-1993; 93WO-US002480.  
PR 06-JAN-1994; 94US-00178212.  
PR 07-JUN-1995; 95US-00474633.  
PR 24-MAR-1997; 97US-00823771.  
XX  
PA (FALC/) FALCO S C.  
XX  
PI Falco SC;  
XX  
DR WPI; 2003-521869/49.  
DR P-PSDB; ABO44332.  
XX  
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic  
PT acid synthase, useful for increasing threonine or lysine content of seeds  
PT of plant.  
XX  
XX Example 21; Page 43; 116pp; English.  
PS  
XX  
XX The invention relates to an isolated nucleic acid fragment comprising a  
CC first nucleic acid subfragment encoding aspartokinase (AK) that is  
CC substantially insensitive to inhibition by lysine, and a second nucleic  
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPs) that  
CC is substantially insensitive to inhibition by lysine. Also included are  
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment  
CC encoding lysine ketoglutarate reductase (LKR), a chimeric gene (where  
CC the nucleic acid fragment is operably linked to a plant chloroplast  
CC transit sequence and to a seed-specific regulatory sequence, a plant  
CC comprising the nucleic acid/chimeric gene in its genome, a seed obtained  
CC from the plant, increasing threonine or lysine content of the seeds of  
CC plant, a plant capable of transmitting the chimeric gene to a progeny of  
CC plant having the ability to produce levels of free threonine or lysine at  
CC least two times greater than the free threonine levels of untransformed  
CC plants, a transformed (soybean) plant comprising seeds that accumulate  
CC lysine at a level at least ten percent to four-fold higher than the seeds  
CC of an untransformed plant, a transformed rapeseed comprising seeds that  
CC accumulate lysine to a level between ten percent and one hundred percent  
CC higher than that of the seeds of an untransformed plant, a monocot plant  
CC comprising in its genome the nucleic acid fragment having the monoco-  
CC embryo specific promoter and a transformed corn plant comprising seeds  
CC that accumulate lysine to a level between ten percent and one hundred  
CC thirty percent higher than the seeds of the untransformed plant. Also  
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up  
CC from monomer lysine-rich heptad repeats (encoded by Bari restriction  
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed  
CC plant. The nucleic acid fragments, genes and methods are useful for  
CC increasing threonine or lysine content of the seeds of the plant. Seeds  
CC containing increased threonine or lysine content eliminate the need to  
CC supplement mixed grain feeds with lysine or threonine produced via  
CC microbial fermentation. The present sequence is one strand of a DNA  
CC encoding a lysine-rich heptad repeat for use as a monomer unit in a  
CC synthetic seed storage protein  
XX  
SO Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
Db 19 CTTGAGCTTCTCTCCA 3  
RESULT 198  
ADW71666/C  
ID ADW71666 standard; DNA; 21 BP.  
XX  
AC ADW71666;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Oligonucleotide SM88 SEQ ID NO:43.  
KW ss; transgenic plant; amino acid production; seed; enzyme engineering.  
XX  
OS Synthetic.  
XX  
PN US2005005330-A1.  
XX  
PD 06-JAN-2005.  
XX  
PF 19-MAR-2004; 2004US-00804678.  
XX  
PR 06-JAN-1994; 94US-00178212.  
PR 07-JUN-1995; 95US-00474633.  
PR 27-MAR-1997; 97US-00824627.  
PR 27-MAR-1998; 98US-00049304.  
XX  
PA (FALC/) FALCO S C.  
PA (MCDE/) MCDEVITT R E.  
PA (EPBL/) EPBLBAUM S U.  
PI Falco SC, Mcdevitt RE, Epelbaum SU;  
XX  
XX WPI; 2005-065280/07.  
DR  
XX  
XX New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase  
PT nucleic acid fragment, useful for increasing levels of lysine in the  
PT seeds of transformed plants.  
XX  
XX Example 21; SEQ ID NO 43; 142pp; English.  
PS  
XX  
XX The invention relates to a novel isolated nucleic acid sequence which is  
CC useful in antisense inhibition or sense suppression of endogenous lysine  
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn  
CC plant or corn plant cell, where the isolated nucleic acid fragment  
CC comprises all or a part of a nucleic acid sequence (ADW71743). The  
CC isolated nucleic acid fragment is useful for increasing levels of lysine  
CC in the seeds of transformed plants. The present sequence represents an  
CC oligonucleotide used to create chimeric genes of the invention.  
XX  
SQ Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1404 CTTGAGCTTCTCTCCA 1420  
Db 19 CTTGAGCTTCTCTCCA 3  
RESULT 199  
ADW71648/C  
ID ADW71648 standard; DNA; 21 BP.  
XX  
AC ADW71648;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Oligonucleotide SM82 SEQ ID NO:25.



XX KM ss; transgenic plant; amino acid production; seed; enzyme engineering.  
XX OS Synthetic.  
XX PN US200505330-A1.  
XX PD 06-JAN-2005.  
XX PF 19-MAR-2004; 2004US-00804678.  
XX PR 06-JAN-1994; 94US-00178212.  
XX PR 07-JUN-1995; 95US-00474633.  
XX PR 27-MAR-1997; 97US-00824627.  
XX PR 27-MAR-1998; 98US-00049304.  
XX PA (FALC/) FALCO S C.  
XX PA (MCDEV/) MCDEVITT R E.  
XX PA (EPEL/) EPELBAUM S U.  
XX PI Falco SC, Mcdevitt RE, Epelbaum SU;  
XX WPI; 2005-065280/07.  
XX PT New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase  
XX PT nucleic acid fragment, useful for increasing levels of lysine in the  
XX PT seeds of transformed plants.  
XX PX Example 21; SEQ ID NO 25; 142pp; English.  
XX CC The invention relates to a novel isolated nucleic acid sequence which is  
XX CC useful in antisense inhibition or sense suppression of endogenous lysine  
XX CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn  
XX CC plant or corn plant cell, where the isolated nucleic acid fragment  
XX CC comprises all or a part of a nucleic acid sequence (ADW71743). The  
XX CC isolated nucleic acid fragment is useful for increasing levels of lysine  
XX CC in the seeds of transformed plants. The present sequence is used in the  
XX CC invention to to insert repeats of the SSP7 heptad in to a base gene  
XX CC construct of the invention.  
XX SQ Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 1.0%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1404 CTTGAGCTTCTCTCCA 1420  
XX Db 19 CTTGAGCTTCTCTCCA 3  
XX  
XX RESULT 200  
XX ADM71664/c  
XX ID ADM71664 standard; DNA; 21 BP.  
XX AC ADM71664;  
XX XX  
XX DT 24-MAR-2005 (first entry)  
XX XX  
XX DE Oligonucleotide SM86 SEQ ID NO:41.  
XX XX  
XX KM ss; transgenic plant; amino acid production; seed; enzyme engineering.  
XX OS Synthetic.  
XX PN US200505330-A1.  
XX PD 06-JAN-2005.  
XX PF 19-MAR-2004; 2004US-00804678.  
XX PR 06-JAN-1994; 94US-00178212.  
XX PR 07-JUN-1995; 95US-00474633.

XX PR 27-MAR-1997; 97US-00824627.  
XX PR 27-MAR-1998; 98US-00049304.  
XX PA (FALC/) FALCO S C.  
XX PA (MCDEV/) MCDEVITT R E.  
XX PA (EPEL/) EPELBAUM S U.  
XX PI Falco SC, Mcdevitt RE, Epelbaum SU;  
XX WPI; 2005-065280/07.  
XX PT New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase  
XX PT nucleic acid fragment, useful for increasing levels of lysine in the  
XX PT seeds of transformed plants.  
XX PS Example 21; SEQ ID NO 41; 142pp; English.  
XX CC The invention relates to a novel isolated nucleic acid sequence which is  
XX CC useful in antisense inhibition or sense suppression of endogenous lysine  
XX CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn  
XX CC plant or corn plant cell, where the isolated nucleic acid fragment  
XX CC comprises all or a part of a nucleic acid sequence (ADW71743). The  
XX CC isolated nucleic acid fragment is useful for increasing levels of lysine  
XX CC in the seeds of transformed plants. The present sequence represents an  
XX CC oligonucleotide used to create chimeric genes of the invention.  
XX SQ Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 1.0%; Score 17; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1404 CTTGAGCTTCTCTCCA 1420  
XX Db 19 CTTGAGCTTCTCTCCA 3  
XX  
XX RESULT 201  
XX ABR44412/c  
XX ID ABR44412 standard; DNA; 20 BP.  
XX AC ABR44412;  
XX XX  
XX DT 06-NOV-2003 (first entry)  
XX DE Chimeric antisense oligonucleotide ISIS 192387 to inhibit human ESRB.  
XX KM Oestrogen receptor beta; ESRB; steroid hormone; female sexual maturation;  
XX KM bone maintenance; cardiovascular system; ER beta; oestrogen receptor 2;  
XX KM ER82; Alzheimer's; uterine leiomyomata; cytostatic; kidney neoplasm; ss;  
XX KM cellular proliferation; cancer; human; antisense; chimeric.  
XX OS Chimeric - Homo sapiens.  
XX PN MO2003050133-A1.  
XX PD 19-JUN-2003.  
XX PF 06-DEC-2002; 2002WO-US039200.  
XX PR 07-DEC-2001; 2001US-00005058.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Dobie KW, Roach MP, Koller E;  
XX WPI; 2003-577284/54.  
XX PT New antisense oligonucleotides for modulating estrogen receptor beta gene  
XX PT expression, particularly useful for treating cancer, specifically  
XX PT leiomyoma, pancreatic cancer, prostate cancer, breast cancer, bone cancer  
XX PT or lymphoma.



CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Oy 979 TTGCGCATCTGCTGCTGCC 998  
Db 1 TTGATCATCTGCTGCTGCC 20  
  
RESULT 204  
AEE77704  
ID AEE77704 standard; DNA; 20 BP.  
XX  
AC AEE77704;  
XX  
DT 09-FEB-2006 (first entry)  
XX  
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1325.  
XX  
KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
XX neuropsychological disorder; dopamine receptor D2; DRD2; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2005118843-A1.  
XX  
PD 15-DEC-2005.  
XX  
PF 01-JUN-2005; 2005WO-AU000775.  
XX  
PR 01-JUN-2004; 2004AU-00902919.  
XX  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
XX  
DR WPI; 2006-047555/05.  
XX  
XX  
XX Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
XX  
XX  
PS Claim 31; SEQ ID NO 1325; 634pp; English.  
XX  
XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

CC Query Match 1.0%; Score 16.8; DB 1; Length 20;  
CC Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
CC Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
Oy 988 TGCTGCTGCCCTTCACAT 1007  
Db 1 TGCTGCTGCCCTTTCAT 20  
  
RESULT 205  
AEE77703  
ID AEE77703 standard; DNA; 20 BP.  
XX  
AC AEE77703;  
XX  
DT 09-FEB-2006 (first entry)  
XX  
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1324.  
XX  
KM Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
XX neuropsychological disorder; dopamine receptor D2; DRD2; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2005118843-A1.  
XX  
PD 15-DEC-2005.  
XX  
PF 01-JUN-2005; 2005WO-AU000775.  
XX  
PR 01-JUN-2004; 2004AU-00902919.  
XX  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
XX  
DR WPI; 2006-047555/05.  
XX  
XX  
XX Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
XX  
XX  
PS Claim 31; SEQ ID NO 1324; 634pp; English.  
XX  
XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Oy 987 CTGCTGCTGCCCTTCACA 1006

Db 1 CTGCTGGCTGGCCCTTCTTCA 20

RESULT 206  
AEE77696  
ID AEE77696 standard; DNA; 20 BP.

AC AEE77696;

DT 09-FEB-2006 (first entry)

Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1317.

AA      Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
KM      neuropsychologic disorder; dopamine receptor D2; DRD2; ss.  
KM

**Homo sapiens.**

PN WO2005118843-A1.

PD 15-DEC-2005.

PF 01-JUN-2005; 2005WO-AU000775.

PR 01-JUN-2004; 2004AU-00902919.

PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;

DR WPI; 2006-047555/05.

AA Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.

PS Claim 31; SEQ ID NO 1317; 634pp; English.

AA The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.

Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match	1.0%	Score 16.8	DB 1	Length 20
Best Local Similarity	90.0%	Pred. No. 1.5e+02		
Matches 18; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY 980 TCGCATCTGCTGGCTGCC 999  
|||  
Db 1 TCATCATCTGCTGGCTGCC 20

RESULT 207  
AEE77705

ID AEE77705 standard; DNA; 20 BP.

AC AEE77705;

DT 09-FEB-2006 (first entry)

AS	DE	Human dopamine receptor D2 (DRD2)	DNA oligonucleotide SEQ ID NO:1326
1	2	3	4

AA Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
 KW neurosychologic disorder; dopamine receptor D2; DRD2; ss.

Homo sapiens.

AA WO2005118843-A1.  
PN

PD 15-DEC-2005

01-JUN-2005; 2005WO-AU000775.

01-JUN-2004; 2004AU-00902919.

(UNIV-) QUEENSLAND TECHNOLOGY.

PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;

DR WPI; 2006-047555/05.

XX Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.

PS Claim 31; SEQ ID NO 1326; 634pp; English.

XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic or genetic diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.

Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

Query Match	1.0%	Score 16.8	DB 1	length 20
Best Local Similarity	90.0%	Pred: No. 1.5e+02		
Matches 18; Conservative	0	Mismatches 2	Indels 0	Gaps 0

```

QY      989 GCTGGCTGCCCTTCACATC 1008
          |||||
Db      1 GCTGGCTGCCCTTCATC 20

```

RESULT 208  
AAZ50619/c  
ID AAZ50619 standard; DNA; 21 BP.

AC AAZ50619;

DT 20-JUN-2000 (first entry)

XX

PR	17-MAY-1991;	91US-00701935-	
PR	17-MAY-1991;	91US-00701937.	
XX			
XX	(MERI ) MERCK & CO INC.		
PA			
XX	Strader CD, Fong TM;		
XX			
DR	WPI, 1992-384034/47.		
XX			
PT	New human neurokinin-1 receptor short form protein - useful for		
PT	identifying and determining substance P antagonists in arthritic		
PT	patients.		
XX			
XX	Example 1; Page 8; 36pp; English.		
XX			
CC	Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1		
CC	and U87MG. First strand cDNA was synthesised and used as template with		
CC	rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR		
CC	amplification. Secondary PCR was performed on the amplified product using		
CC	the same 3 primers prior to a third round of amplification, this time		
CC	using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h		
CC	(AAQ30778). The tertiary PCR product was sequenced and was found to have		
CC	90% identity at the nucleotide level with the central core region of the		
CC	rat NK1R from amino acid 91 to 280. Primer rspr284 is a sense primer		
CC	based on the rat NK1R sequence 238-255 (numbering as in J.Biol.Chem. 264:		
CC	17649-17652, 1989). (Updated on 25-MAR-2003 to correct PN field.)		
XX			
SQ	Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 U; 0 Other;		
Query Match	0.9%; Score 16.4; DB 1; Length 18;		
Best Local Similarity	94.4%; Pred. No. 1.3e+02;		
Matches 17; Conservative	0; Mismatches 1; Indels	0; Gaps	0
QY	448	TCCATGCGTCGATTCAT 465	
DB	1	TGCATGCGTCGATTCAT 18	
RESULT 210			
AAW73459/c			
ID	AAW73459 standard; RNA; 18 BP.		
XX			
AC	AAW73459;		
XX			
DT	28-JUL-1999 (first entry)		
XX			
DE	Mouse flk-1 VEGF receptor hairpin ribozyme substrate #6.		
XX			
KW	Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;		
KW	KDR; hammetthead ribozyme; hairpin ribozyme; cleavage;		
KW	tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;		
KW	fm-1-like cytosine kinase 1; kinase insert domain containing receptor;		
XX	fetal liver kinase 1; ss.		
XX			
OS	Mus sp.		
XX			
PN	MO9715662-A2.		
XX			
PD	01-MAY-1997.		
XX			
PF	25-OCT-1996; 96WO-US017480.		
XX			
PR	26-OCT-1995; 95US-0005974P.		
PR	11-JAN-1996; 96US-00584040.		
XX			
PA	(RIBO-) RIBOZYME PHARM INC.		
PA	(CHIR ) CHIRON CORP.		
XX			
PI	Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;		
XX			
DR	WPI; 1997-259017/23.		
XX			
PT	Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA		

PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
PS Claim 4; Page 150; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAY57275 to AAY5752 represent specific examples  
CC of nucleic acid molecules from the present invention  
CC  
SQ Sequence 18 BP; 2 A; 6 C; 8 G; 0 T; 2 U; 0 Other;  
Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 624 CCAGCCCGGCTGTCAGC 641  
DB 18 CCAGCCCGGCTGTCAGC 1  
RESULT 211  
ADJ47994/C  
ID ADJ47994 standard; DNA; 19 BP.  
XX  
XX ADJ47994;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX  
DE Human OGR-1 probe1, seq id 4.  
XX  
XX Cardiovascular; cytostatic; antiinflammatory; gastrointestinal; CNS;  
XX central nervous system; gene therapy; antagonist; antisense therapy;  
XX haematological disease; cancer; cardiovascular disease;  
XX inflammatory disease; gastrointestinal disease;  
XX ovarian cancer G-protein coupled receptor 1; OGR-1; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004015422-A2.  
XX  
XX 19-FEB-2004.  
PD  
XX  
XX 23-JUL-2003; 2003WO-EP008048.  
PF  
XX  
XX 05-AUG-2002; 2002EP-00016980.  
PR  
XX  
XX (PARB ) BAYER HEALTHCARE AG.  
PA  
XX  
XX Golz S, Brueggemeier U, Summer H;  
PI  
XX  
XX WPI; 2004-191805/18.  
DR  
XX  
XX Screening for therapeutic agents, useful in treating e.g., cancer,  
PT cardiovascular disorders or central nervous system disorder, comprises  
PT contacting a test compound with ovarian cancer G-protein coupled receptor  
PT 1 and determining activity.  
PT  
XX  
XX Example 2; SEQ ID NO 4; 118pp; English.  
PS  
XX  
XX The invention relates to the screening of therapeutic agents useful in  
CC the treatment of haematological diseases, cancer, cardiovascular  
CC diseases, inflammatory diseases, gastrointestinal diseases and disorders  
CC of the peripheral and central nervous system in a mammal. The method  
CC comprises contacting a test compound with an ovarian cancer G-protein  
CC coupled receptor 1 (OGR-1) polypeptide or polynucleotide. The method is  
CC useful in screening for therapeutic agents, and also for the treatment of

CC diseases mentioned above. The regulators of an OGR-1 are useful for  
CC regulating OGR-1 activity or for preparing a pharmaceutical composition  
CC for the treatment of the stated diseases in a mammal. The current  
CC sequence represents a probe used in the expression profiling of human OGR  
CC -1 receptor encoding DNA.  
CC  
XX  
SQ Sequence 19 BP; 7 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 985 ATCTGCTGGCTGCCCTTC 1002  
DB 19 ATCTGCTGGCTGCCCTTC 2  
RESULT 212  
ACCT0594/C  
ID ACCT0594 standard; DNA; 20 BP.  
XX  
XX ACCT0594;  
AC  
XX  
XX 13-AUG-2003 (first entry)  
DT  
XX  
XX Sphingosine-1-phosphate lyase antisense oligonucleotide, SEQ ID 87.  
DE  
XX  
XX Cytostatic; antimicrobial; antiinflammatory; tumour; infection;  
XX sphingosine-1-phosphate lyase; developmental disorder; apoptosis;  
XX inflammation; antisense; phosphorochioate; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "This oligonucleotide has a phosphorochioate  
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'  
FT and 3' ends, which are 5 nucleotides in length. Also all  
FT cytidine residues are 5-methylcytidines"  
XX  
XX  
XX WO2003028637-A2.  
XX  
XX 10-APR-2003.  
PD  
XX  
XX 26-SEP-2002; 2002WO-US030575.  
PF  
XX  
XX 28-SEP-2001; 2001US-00967669.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
XX Bennett FC, Freier SM;  
PI  
XX  
XX WPI; 2003-381581/36.  
DR  
XX  
XX New antisense oligonucleotides for modulating sphingosine-1-phosphate  
PT lyase gene expression, useful for preventing or treating a developmental  
PT disorder or aberrant apoptosis, e.g. infection, inflammation or tumor  
PT formation.  
PT  
XX  
XX Claim 3; Page 74; 118pp; English.  
PS  
XX  
XX The present invention relates to novel antisense oligonucleotides  
CC (ACCT0520-ACCT0597) which are targeted to a sphingosine-1-phosphate lyase  
CC DNA sequence, and specifically hybridizes with the nucleic acid and  
CC inhibits the expression of sphingosine-1-phosphate lyase. The antisense  
CC oligonucleotides are useful for treating an animal having a disease or  
CC condition associated with sphingosine-1-phosphate lyase, particularly a  
CC developmental disorder, or a disease or condition arising from aberrant  
CC apoptosis, e.g. infection, inflammation or tumour formation  
CC  
XX  
SQ Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

[illegible]

RESULT 215  
ID ABR03471 standard; RNA; 17 BP.  
XX ABR03471;  
AC ABR03471;  
XX 12-MAR-2002 (first entry)  
XX  
XX Human CD20 zinzyme #22.  
XX  
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KM cerebroprotective; neuroprotective; antiparkinsonian;  
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KM DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KM inflammatory arthropathy; central nervous system injury;  
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KM Parkinson's disease; ataxia; Huntington's disease;  
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200159103-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
XX PR 28-FEB-2000; 2000US-0185516P.  
XX PR 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSM/) MCSWIGGEN J.  
PA (CHOW/) CHOWMIRA B M.  
XX  
XX Blatt L, Mcswiggen J, Chowmira BM;  
PI  
XX WPI; 2001-607195/69.  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
XX Claim 30; Page 154; 2000P; English.  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
XX expression of a CD20 gene and a nucleic acid molecule which down  
XX regulates expression of a neurite growth inhibitor gene (NOGO). The  
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
XX DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
XX with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
XX of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
XX Furthermore, it may be contacted with a condition associated with the level  
XX of the cell and treat a patient having a condition associated with the level  
XX of CD20. The treatment may further comprise the use of one or more  
XX therapies. In particular, the CD20 targeting nucleic acid may be used to  
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
XX leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
XX presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the

cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a zinzyme molecule of the invention  
XX  
SQ Sequence 17 BP; 2 A; 4 C; 5 G; 0 T; 6 U; 0 Other;  
QY  
QY 801 CATCTGNGTACTGTG 816  
DB 2 CAUCUGUGACUCUG 17  
Query Match 0.9%; Score 16; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
QY 801 CATCTGNGTACTGTG 816  
DB 2 CAUCUGUGACUCUG 17  
RESULT 216  
ID ABL53529 standard; DNA; 20 BP.  
XX ABL53529;  
AC ABL53529;  
XX  
XX 10-JUN-2002 (first entry)  
XX  
XX Mouse SAM1b sense oligonucleotide.  
XX  
XX SAM1b; meliosis activating sterol; MAS; receptor; mouse; oocyte;  
KM signal transduction; fertility; antisense; ss.  
XX Mus musculus.  
XX  
XX Key location/Qualifiers  
XX modified\_base 1..20  
XX /\*tag= a  
XX /note= "phosphorothioate linkage"  
XX  
XX WO200216433-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-DK000558.  
XX  
XX 25-AUG-2000; 2000DK-00001259.  
XX PR 20-AUG-2001; 2001WO-DK000550.  
XX  
XX (NOVO) NOVO NORDISK AS.  
PA (SCHD) SCHERING AG.  
XX  
XX Wahl P, Vissing H, Grondahl C;  
PI  
XX WPI; 2002-257907/30.  
XX  
XX Receptors and signaling proteins of Meiotic Acting Sterols and nucleic  
XX acids, useful in modulating in gamete maturation process induced by beta  
XX -hydroxy-4,4-dimethylcholesterol-8,14,24-triene.  
XX  
XX Example 1; Page 19; 60P; English.  
XX  
XX The present sequence is that of a phosphorothioate sense oligonucleotide  
XX that corresponds to the Kozak sequence of SAM1b mRNA. It was  
XX microinjected into mouse oocytes where, unlike the corresponding  
XX antisense sequence (see ABL53527), it did not selective inhibition of  
XX SAM1b mRNA. SAM1b is a receptor of meiosis activating sterols (MAS) and  
XX is involved in the gamete maturation process induced by beta-hydroxy-4,4  
XX -dimethylcholesterol-8,14,24-triene (PP-MAS), specifically inducing, upon  
XX ligand activation, germinal vesicle breakdown in oocytes. The invention  
XX provides SAM1a polynucleotides (including RNA antisense sequences),



CC	compounds for use in men and women
XX	
SQ	Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
	Query Match                      0.9%; Score 16; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	680 TTGGCTTCCTGCTGGC 695       TTGGCTTCCTGCTGC 1
DB	16 TTGGCTTCCTGCTGC 1
	RESULT 218 ACF79553 ID ACF79553 standard; DNA; 20 BP. XX ACF79553; AC ACF79553; XX DT 18-DEC-2003 (first entry) XX DE Oligonucleotide sense to SAM1b mRNA Kozak sequence. XX KW Mouse; SAM1b, meiotic acting sterol; signal transduction, KM antiinfertility; contraceptive; ss. XX OS Mus sp. XX FH Key Location/Qualifiers FT modified_site 1..20 FT /*tag= a FT /mod Base= OTHER XT /note= "OTHER= phosphorothioate oligonucleotides" XX FN MO2003070766-A2. PD 28-AUG-2003. PF 31-JAN-2003; 2003WO-DK000058. PP 22-FEB-2002; 2002DK-00000277. XX PR (NOVO ) NOVO NORDISK AS. PA PI Grondahl C, Wahl P, Norby PL, Stenmicke VM; P1 WPI; 2003-671806/63. DR XX PT New polynucleotide encoding a transducer of meiotic acting sterols- PT signaling or its regulatory domain, useful for isolating tissue specific PT variants of the transducer which may be used as anti-infertility or PT contraception drugs.
XX	Example 1; Page 18; 55pp; English.
XX	The present sequence is that of a sense oligonucleotide that corresponds
CC	to the Kozak sequence of mouse SAM1b mRNA (see ACF79541). It was used as
CC	a control in experiments with the corresponding antisense oligonucleotide
CC	(see ACF79551). Selective inhibition of the mRNA showed that SAM1b is
CC	crucially involved in meiotic acting sterol (MAS) signalling, since a
CC	functional knockout of de novo protein synthesis partly disrupted MAS
CC	signals in oocytes. SAM1b is a transducer of MAS signalling and is
CC	involved in the gamete maturation process induced by 3beta-hydroxy-4,4-
CC	dimethyl cholesterol-8,14,24-triene (FF-MAS), specifically inducing germinal
CC	vessel breakdown in mouse oocyte cultures in vitro. SAM1b can be used to
CC	screen for agonists or antagonists of FF-MAS activity for use as
CC	antiinfertility or contraceptive drugs
XX	
SQ	Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
	Query Match                      0.9%; Score 16; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGGCTCTCCTGCTGAC 695  
 |||||  
 DB 5 TGGCTCTCCTGCTGAC 20

## RESULT 219

ACF79551/c  
 ID ACF79551 standard; DNA; 20 BP.

ACF79551;

18-DEC-2003 (first entry)

Oligonucleotide antisense to SAM1b mRNA Kozak sequence.

Mouse; SAM1b; meiotic acting sterol; signal transduction;  
 antiinfertility; contraceptive; antisense; ss.

Synthetic.

Key Location/Qualifiers  
 modified\_site 1..20  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "OTHER= phosphorothioate oligonucleotides"

WO2003070766-A2.

28-AUG-2003.

31-JAN-2003; 2003WO-DK000058.

22-FEB-2002; 2002DK-00000277.

(NOVO ) NOVO NORDISK AS.

Grondahl C, Wahl P, Norby PL, Stennicke VM;

WPI; 2003-671806/63.

New polynucleotide encoding a transducer of meiotic acting sterols-  
 signaling or its regulatory domain, useful for isolating tissue specific  
 variants of the transducer which may be used as anti-infertility or  
 contraceptive drugs.

Example 1; Page 18; 55pp; English.

The present sequence is that of an antisense oligonucleotide that is  
 complementary to the Kozak sequence of mouse SAM1b mRNA (see ACF79541).  
 Selective inhibition of the mRNA showed that SAM1b is crucially involved  
 in meiotic acting sterol (MAS) signaling, since a functional knockout of  
 de novo protein synthesis partly disrupted MAS signals in oocytes. SAM1b  
 is a transducer of MAS signaling and is involved in the gamete  
 maturation process induced by 3beta-hydroxy-4,4-dimethyl cholesterol-8,14,24-  
 triene (FF-MAS), specifically inducing germinal vesicle breakdown in  
 mouse oocyte cultures in vitro. SAM1b can be used to screen for agonists  
 or antagonists of FF-MAS activity for use as anti-infertility or  
 contraceptive drugs

Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGGCTCTCCTGCTGAC 695  
 |||||  
 DB 16 TGGCTCTCCTGCTGAC 1

RESULT 220  
 ADH49395/c

ID ADH49395 standard; DNA; 20 BP.

AC ADH49395;

25-MAR-2004 (first entry)

MAS-signalling transducer related SAM1 cDNA primer, SEQ ID 10.

transducer of meiosis activating sterols; MAS; signalling;

antiinfertility; MAS-signalling transducer;

4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol; FF-MAS; tissue;

organ specific; meiosis; infertility; contraception; ss; primer; SAM1.

Unidentified.

US2003219791-A1.

27-NOV-2003.

20-FEB-2003; 2003US-00370860.

(STEN/) STENNICKE V W.

(NORB/) NORBY P L.

(GRON/) GRONDAHL C.

(WAHL/) WAHL P.

Stennicke VM, Norby PL, Grondahl C, Wahl P;

WPI; 2004-060179/06.

Novel transducer of meiosis activating sterols designated SAM1a and SAM1b  
 useful for screening for agonist or antagonist of meiosis activating  
 sterols used to treat infertility or to provide a way of contraception.

Example 2; SEQ ID NO 10; 31pp; English.

The invention relates to a novel isolated transducer of meiosis  
 activating sterols (MAS)-signalling, its peptide fragment or a salt. The  
 isolated MAS-signalling transducer has antiinfertility activity. The MAS-  
 signalling transducer is useful for detecting the presence of a compound  
 or its salt which has affinity for the MAS-signalling transducer. The MAS  
 -signalling transducer is useful for detecting the presence of an  
 antagonist or agonist of the MAS-signalling transducer. The MAS-  
 signalling transducer is useful for detecting the presence of an  
 antagonist of the MAS-signalling transducer. The MAS-signalling  
 transducer is useful for screening for agonist or antagonist activity of  
 4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol (FF-MAS) or MAS. An  
 expression vector containing the nucleic acid which encodes the MAS-  
 signalling transducer is useful for isolation of tissue and/or organ  
 specific variants of the MAS-signalling transducer. The agonist or  
 antagonist of the MAS-signalling transducer identified using the  
 transducer provides a way to control meiosis in order to treat  
 infertility or to achieve a novel principle of contraception. This  
 polynucleotide sequence represents a primer used in the exemplification  
 of the invention.

Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGGCTCTCCTGCTGAC 695  
 |||||  
 DB 16 TGGCTCTCCTGCTGAC 1

RESULT 221  
 ADH49397  
 ID ADH49397 standard; DNA; 20 BP.

XX

AC ADH49397;  
XX  
XX 25-MAR-2004 (first entry)  
DE MAS-signalling transducer related SAM1 cDNA primer, SEQ ID 12.  
XX  
XX transducer of meiosis activating sterol; MAS; signalling;  
XX antifertility; MAS-signalling transducer;  
KM 4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol; FF-MAS; tissue;  
KM organ specific; meiosis; fertility; contraception; ss; primer; SAM1.  
XX  
XX Unidentified.  
OS  
XX US2003219791-A1.  
PN  
XX 27-NOV-2003.  
PD  
XX 20-FEB-2003; 2003US-00370860.  
PF  
XX 20-FEB-2003; 2003US-00370860.  
PR  
XX 20-FEB-2003; 2003US-00370860.  
XX  
XX (STEN/) STENNICK V W.  
PA (NOR/) NORBY P L.  
PA (GRON/) GRONDAHL C.  
PA (WAHL/) WAHL P.  
XX  
XX Stennicke VM, Norby PL, Grondahl C, Wahl P;  
PI  
XX WPI; 2004-060179/06.  
DR  
XX  
XX Novel transducer of meiosis activating sterols designated SAM1a and SAM1b  
PT useful for screening for agonist or antagonist of meiosis activating  
PT sterols used to treat infertility or to provide a way of contraception.  
XX  
XX Example 2; SEQ ID NO 12; 31pp; English.  
XX  
XX The invention relates to a novel isolated transducer of meiosis  
XX activating sterols (MAS)-signalling, its peptide fragment or a salt. The  
XX isolated MAS-signalling transducer has antifertility activity. The MAS-  
XX signalling transducer is useful for detecting the presence of a compound  
XX or its salt which has affinity for the MAS-signalling transducer. The MAS  
XX -signalling transducer is useful for detecting the presence of an  
XX antagonist or agonist of the MAS-signalling transducer. The MAS-  
XX signalling transducer is useful for detecting the presence of an  
XX antagonist or agonist of the MAS-signalling transducer. The MAS-  
XX signalling transducer is useful for detecting the presence of an agonist  
XX or antagonist of the MAS-signalling transducer. The MAS-signalling  
XX transducer is useful for screening for agonist or antagonist activity of  
XX 4,4-dimethyl-5-alpha-cholesta-8,14,24-triene-3-beta-ol (FF-MAS) or MAS. An  
XX expression vector containing the nucleic acid which encodes the MAS-  
XX signalling transducer is useful for isolation of tissue and/or organ  
XX specific variants of the MAS-signalling transducer. The agonist or  
XX antagonist of the MAS-signalling transducer identified using the  
XX transducer provides a way to control meiosis in order to treat  
XX infertility or to achieve a novel principle of contraception. This  
XX polynucleotide sequence represents a primer used in the exemplification  
XX of the invention.  
XX  
XX Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 680 TGGCTCTCCCTGCTGCG 695  
Db 5 TGGCTCTCCCTGCTGCG 20  
RESULT 222  
AAV01172/c  
ID AAV01172 standard; DNA; 19 BP.  
XX AAV01172;  
AC  
XX

DT 23-MAR-1998 (first entry)  
XX  
XX Adrenergic receptor beta 2 PCR primer for universal mammalian STS's.  
DE  
XX PCR primer; polymerase chain reaction; amplification; UM-STS;  
XX universal mammalian sequence tagged site; genomic map; clone; ss.  
XX  
XX Synthetic.  
OS  
XX WO9731012-A1.  
PN  
XX 28-AUG-1997.  
PD  
XX 18-FEB-1997; 97WO-US002403.  
PF  
XX 22-FEB-1996; 96US-0012061P.  
PR  
XX (UNMI ) UNIV MICHIGAN.  
PA (UNMS ) UNIV MICHIGAN STATE.  
XX  
XX Brewer GJ, Venta PJ, Yuzbaevyan-Gurkan V;  
PI  
XX WPI; 1997-435083/40.  
DR  
XX  
XX New oligonucleotide primers amplifying gene regions conserved among  
PT mammals - useful for developing genomic maps, isolating clones and making  
PT cross-species comparisons.  
XX  
XX Claim 1; Page 10; 26pp; English.  
XX  
XX The present sequence represents a specifically claimed oligonucleotide  
XX PCR primer. The oligonucleotide can be used for polymerase chain reaction  
XX (PCR) amplification of DNA, specifically regions of specific genes that  
XX are conserved among mammalian species, i.e. pairs of oligonucleotides  
XX from the present specification represent universal mammalian sequence-  
XX tagged site (UM-STS) primers. The primers are used to develop genomic  
XX maps, to isolate clones from libraries, to make cross-species comparisons  
XX and to develop additional genetic markers. UM-STS allow genomic  
XX comparisons to be made between more species  
XX  
XX Sequence 19 BP; 6 A; 4 C; 8 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.8e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 979 TTCGCATCTGCTGCTGCG 997  
Db 19 TTCACCTCTGCTGCTGCG 1  
RESULT 223  
ADO26346/c  
ID ADO26346 standard; DNA; 19 BP.  
XX  
XX ADO26346;  
AC  
XX 18-NOV-2004 (first entry)  
DT  
XX Haemofiltrate-chondro-osteomodulin protein PCR primer #6.  
DE  
XX osteopathic; antirheumatic; antidiabetic; antiarthritic; immunomodulator;  
KM nephrotropic; dermatological; antipruritic; antiseborrheic; virucide;  
KM antiinflammatory; cytostatic; COM; haemofiltrate-chondro-osteomodulin;  
KM ss; primer; PCR.  
XX  
XX Unidentified.  
OS  
XX WO2004039978-A2.  
PN  
XX 13-MAY-2004.  
PD  
XX 24-OCT-2003; 2003WO-EP011799.  
PF

XX 31-OCT-2002; 2002DE-01051205.  
 PR (IPFP-) IPF PHARM GMBH.  
 PA Meder W, Wendland M, John H, Richter R, Meyer M, Forssmann W;  
 PI WPI; 2004-376193/35.  
 XX New polypeptide hemofiltrate-chondro-osteomodulin, useful for treatment  
 PT and diagnosis of e.g. parathyroid disease and diabetes, also as part of a  
 PT receptor-ligand system for drug screening.  
 XX Claim 13; Page 17; 24pp; German.  
 PS The present invention relates to the polypeptide haemofiltrate (HP) -  
 CC chondro-osteomodulin (COM) and its natural or pharmacologically tolerable  
 CC derivatives, especially amidated, acetylated, phosphorylated or  
 CC glycosylated derivatives, or with N-terminal pyroglutamate. COM and its  
 CC derivatives are useful for treatment of parathyroid disease (especially  
 CC hypoparathyroidism), degenerative bone disease (especially osteoporosis),  
 CC bone fractures, cartilage and connective tissue diseases, rheumatism and  
 CC arthritis, fatty degeneration and diabetes type II, immune system  
 CC disorders, disorders that can be treated by modifying migration of stem  
 CC cells, kidney diseases associated with disrupted electrolyte excretion  
 CC (especially renal insufficiency), also phosphate/calcium excretion, and  
 CC skin diseases, e.g. psoriasis, eczema and acne, also viral, bacterial and  
 CC parasitic infections, female infertility, ovarian and uterine tumours,  
 CC autoimmune diseases and immune defects. They are also useful for  
 CC diagnosis. The present sequence is a PCR primer used to isolate the  
 CC protein of the invention.  
 XX Sequence 19 BP; 9 A; 5 C; 5 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 1.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 671 TCTGGGTCCTGGCTCTCT 689  
 DB 19 TCTGGGTCCTGGCTCTCT 1  
 RESULT 224  
 ADO26348/c  
 ID ADO26348 standard; DNA; 19 BP.  
 XX ADO26348;  
 AC 18-NOV-2004 (first entry)  
 DE Haemofiltrate-chondro-osteomodulin protein PCR primer #8.  
 XX osteopathic; antirheumatic; antidiabetic; antiarthritic; immunomodulator;  
 KW nephrotropic; dermatological; antipsoriatic; antiseborrheic; virucide;  
 KW antiinflammatory; cytostatic; COM; haemofiltrate-chondro-osteomodulin;  
 KW ss; primer; PCR.  
 XX Unidentified.  
 OS WO2004039978-A2.  
 PN 13-MAY-2004.  
 PD 24-OCT-2003; 2003WO-EP011799.  
 PF 31-OCT-2002; 2002DE-01051205.  
 PR (IPFP-) IPF PHARM GMBH.  
 PA Meder W, Wendland M, John H, Richter R, Meyer M, Forssmann W;  
 PI WPI; 2004-376193/35.  
 DR

XX New polypeptide hemofiltrate-chondro-osteomodulin, useful for treatment  
 PT and diagnosis of e.g. parathyroid disease and diabetes, also as part of a  
 PT receptor-ligand system for drug screening.  
 XX Claim 13; Page 17; 24pp; German.  
 PS The present invention relates to the polypeptide haemofiltrate (HP) -  
 CC chondro-osteomodulin (COM) and its natural or pharmacologically tolerable  
 CC derivatives, especially amidated, acetylated, phosphorylated or  
 CC glycosylated derivatives, or with N-terminal pyroglutamate. COM and its  
 CC derivatives are useful for treatment of parathyroid disease (especially  
 CC hypoparathyroidism), degenerative bone disease (especially osteoporosis),  
 CC bone fractures, cartilage and connective tissue diseases, rheumatism and  
 CC arthritis, fatty degeneration and diabetes type II, immune system  
 CC disorders, disorders that can be created by modifying migration of stem  
 CC cells, kidney diseases associated with disrupted electrolyte excretion  
 CC (especially renal insufficiency), also phosphate/calcium excretion, and  
 CC skin diseases, e.g. psoriasis, eczema and acne, also viral, bacterial and  
 CC parasitic infections, female infertility, ovarian and uterine tumours,  
 CC autoimmune diseases and immune defects. They are also useful for  
 CC diagnosis. The present sequence is a PCR primer used to isolate the  
 CC protein of the invention.  
 XX Sequence 19 BP; 9 A; 5 C; 5 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 1.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 671 TCTGGGTCCTGGCTCTCT 689  
 DB 19 TCTGGGTCCTGGCTCTCT 1  
 RESULT 225  
 AEC90914  
 ID AEC90914 standard; RNA; 19 BP.  
 XX AEC90914;  
 AC 17-NOV-2005 (first entry)  
 DE STAT-3 siRNA antisense strand, SEQ ID 512.  
 XX Signal-transducer and activator of transcription-3; RNA interference;  
 KW gene silencing; cyostatic; antipsoriatic; dermatological;  
 KW antiinflammatory; gastrointestinal-gen.; cancer; inflammation; psoriasis;  
 KW eczema; dermatitis; Crohn's disease; inflammatory bowel disease; siRNA;  
 KW short interfering RNA; ss.  
 XX Synthetic.  
 OS US2005196781-A1.  
 PN 08-SEP-2005.  
 PD 15-DEC-2004; 2004US-00014373.  
 PF 18-MAY-2001; 2001US-0292217P.  
 PR 20-JUL-2001; 2001US-0306833P.  
 PR 13-AUG-2001; 2001US-0311865P.  
 PR 20-FEB-2002; 2002US-038580P.  
 PR 06-MAR-2002; 2002US-0362016P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 17-MAY-2002; 2002US-00151116.  
 PR 17-MAY-2002; 2002WO-US015876.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 22-JUL-2002; 2002US-00201394.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0406378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.



RESULT 227  
 AEC73577/C  
 ID AEC73577 standard; RNA; 19 BP.  
 XX  
 AC AEC73577;  
 XX  
 PT 17-NOV-2005 (first entry)  
 XX  
 DE RNAi sense strand, targeting CD83, SEQ ID NO:256.  
 XX  
 KW hypersensitivity; anti-allergic; immunosuppressive; sepsis; antibacterial;  
 KW shock; vasotrophic; burns; vulnery; drug screening; diagnosis;  
 KW allergic rhinitis; antiinflammatory; asthma; antiasthmatic;  
 KW RNA interference; gene silencing; siRNA; short interfering RNA; ss; CD83.  
 XX  
 OS Mus musculus.  
 XX  
 PN MO2005085443-A2.  
 XX  
 PD 15-SEP-2005.  
 XX  
 PF 01-MAR-2005; 2005WO-US006445.  
 XX  
 PR 01-MAR-2004; 2004US-0549070P.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Chen J, Eisen HN, Ge Q;  
 XX  
 DR WPI; 2005-630722/64.  
 XX  
 PT New RNAi agent targeted to a target transcript encoding a protein  
 PT involved in the development, pathogenesis, or symptoms of an IGE-mediated  
 PT disease or condition, useful for treating or preventing, e.g. allergic  
 PT rhinitis or asthma.  
 XX  
 PS Claim 10; SEQ ID NO 256; 133pp; English.  
 XX  
 CC The present invention relates to an RNAi agent targeted to a transcript  
 CC that encodes a protein involved in the development, pathogenesis, or  
 CC symptoms of an IGE-mediated disease or condition. Also claimed are a  
 CC composition comprising an RNAi agent; a method of treating or preventing  
 CC a disease characterized by inappropriate or excessive mast cell activity  
 CC or Th2 helper cell responses, or an IGE-mediated disease or condition  
 CC (e.g. hypersensitivity), or sepsis, shock or a burn-related injury; an  
 CC analog of the siRNA or shRNA; inhibiting expression of a target  
 CC transcript; and identifying an RNAi agent as comprising a sequence  
 CC suitable for treatment of a condition characterized by IGE-mediated  
 CC hypersensitivity or inappropriate or excessive mast cell activity or Th2  
 CC helper cell activity. The transcript encodes a protein selected from  
 CC FcεR1α chain; chain, FcεR1β chain; chain, c-Kit, Lyn, Syk, ICOS,  
 CC CXCR4, CD40, CD80, CD86, RelB, 4-1BB ligand, TLR1, TLR2, TLR3,  
 CC TLR4, TLR5, TLR6, TLR7, TLR9, CD83, SLAM, common gamma chain, and  
 CC COX-2. The RNAi agent is an RNAi vector, siRNA or shRNA. The composition  
 CC and methods are useful for diagnosing, preventing or treating IGE-  
 CC mediated diseases, such as allergic rhinitis, asthma, hypersensitivity,  
 CC sepsis, shock or a burn-related injury. These may also be used in  
 CC screening for agents that may treat or prevent such disease conditions.  
 CC The present sequence is a RNAi sense strand, targeting CD83.  
 XX

RESULT 228  
AEE41027/C

	Query Match	Similarity	Score	DB 1	Length
Best Local	17	Conservative	89.5%	Pred. No. 1.8e+02	19
Matches	17	Conservative	0	Mismatches	2
					Indels
					Gaps
QY	948	GATCAAAATGATGATTGTC	966		
DB	19	GATCAAAATGATGACTGTC	1		

ID ABE41027 standard; cDNA; 19 BP.  
 XX ABE41027;  
 AC  
 XX 09-FEB-2006 (first entry)  
 DT  
 DE Human hairless homolog cDNA 19-mer fragment SEQ ID NO 163.  
 XX  
 XX Human hairless; depilatory; hairless homolog.  
 KM  
 XX  
 OS Homo sapiens.  
 WO2005105157-A2.  
 XX  
 XX 10-NOV-2005.  
 PD  
 XX 22-APR-2005; 2005MO-US013770.  
 PF  
 XX 23-APR-2004; 2004US-0565127P.  
 PR  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 XX  
 XX  
 FI Cristiano AM;  
 PI  
 DR WPI; 2005-769492/78.  
 XX  
 XX Removing human hair comprises applying to a human in an area comprising  
 PT hair follicles a double stranded nucleic acid molecule comprising a  
 PT sequence of at least a portion of human hairless protein mRNA.  
 XX  
 XX Disclosure; SEQ ID NO 163; 216pp; English.  
 PS  
 XX The invention relates to a method of human hair removal which comprises  
 XX applying to a human in an area comprising hair follicles a double  
 CC stranded nucleic acid molecule comprising a sequence of at least a  
 CC portion of human hairless protein mRNA or its complement. In the method  
 CC of human hair removal, inhibition of hair growth in the area persists at  
 CC least one month. The method comprises synchronizing hair growth cycles  
 CC for hair follicles in the area. The method alternatively comprises  
 CC contacting hair follicles in the region with a composition comprising at  
 CC least one double stranded nucleic acid molecule able to inhibit hairless  
 CC mRNA translation. The mammal is a human, mouse, rat, or bovine. The  
 CC method, nucleic acid molecules and compositions useful for removing a  
 CC undesirable hair e.g. hirsutism. The present sequence represents a human  
 CC hairless homolog cDNA 19-mer fragment.  
 XX  
 XX Sequence 19 BP; 3 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

	Query Match	0.9%	Score 15.8	DB 1	Length 19
	Best Local Similarity	89.5%	Pred. No. 1.8e+02		
	Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1234	CTCCAGACCCAGGCGCATGTG	1252		
Dd	19	CTTCAGATCCCCGGCCTGTG	1		

```

RESULT 229
AEE41028
ID AEE41028 standard; cDNA; 19 BP.
XX
XX AEE41028;
AC
XX
XX
DT 09-FEB-2006 (first entry)
XX
XX Human hairless homolog cDNA 19-mer fragment SEQ ID NO 164.
DE
XX
XX ss; hirsutism; depilatory; hairless homolog.
XX
XX Homo sapiens.
OS
XX
XX
PN W02005105157-A2.
XX

```

```
PD 10-NOV-2005.
XX
XX 22-APR-2005, 2005SWO-US013770.
XX
XX 23-APR-2004, 2004US-0565127P.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Christiano AM;
XX
XX WPI, 2005-769492/78.
XX
XX Removing human hair comprises applying to a human in an area comprising
PT hair follicles a double stranded nucleic acid molecule comprising a
PT sequence of at least a portion of human hairless protein mRNA.
XX
XX Disclosure; SEQ ID NO 164; 216bp; English.
XX
XX The invention relates to a method of human hair removal which comprises
CC applying to a human in an area comprising hair follicles a double
CC stranded nucleic acid molecule comprising a sequence of at least a
CC portion of human hairless protein mRNA or its complement. In the method
CC of human hair removal, inhibition of hair growth in the area persists at
CC least one month. The method comprises synchronizing hair growth cycles
CC for hair follicles in the area. The method alternatively comprises
CC contacting hair follicles in the region with a composition comprising at
CC least one double stranded nucleic acid molecule able to inhibit hairless
CC mRNA translation. The mammal is a human, mouse, rat, or bovine. The
CC method, nucleic acid molecules and compositions useful for removing
CC undesirable hair e.g. hirsutism. The present sequence represents a human
CC hairless homolog cDNA 19-mer fragment.
XX
XX Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1234 CTCGAGACCCGAGGCACTG 1252
Db 1 CTCGAGACCCGAGGCGCTGTG 19
RESULT 230
AEF75464/C
ID AEF75464 standard; RNA; 19 BP.
XX
XX AEF75464;
AC
XX
XX 06-APR-2006 (first entry)
DT
XX
XX Human NOGO-A transcript target sequence/siRNA sense strand, SEQ:14.
DE
XX RNA interference; gene silencing; short interfering RNA; siRNA;
XX nervous system injury; spinal cord injury; neuroprotective; vulnerary;
XX cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
XX muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
XX CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;
XX Huntingtons chorea; anticonvulsant; noctropic; dementia;
XX Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0886;
XX reticulon 4; RTN4; 88.
XX
XX Homo sapiens.
OS
XX
XX US2005261212-A1.
XX
XX 24-NOV-2005.
PD
XX
XX 26-JUL-2002, 2002US-00206693.
XX
XX 11-FEB-2000, 2000US-0181797P.
XX
XX 09-FEB-2001, 2001US-00780533.
XX
XX 05-APR-2001, 2001US-00827395.
XX
```

```
PR 20-FEB-2002, 2002US-0358580P.
PR 11-MAR-2002, 2002US-0363124P.
PR 03-APR-2002, 2002WO-US010512.
PR 06-JUN-2002, 2002US-0386782P.
XX
XX (MCSW/) MCSWIGEN J A.
XX
XX Mcswigen JA;
XX
XX WPI, 2006-190836/20.
XX
XX New chemically modified double stranded short interfering nucleic acid
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via
PT RNA interference (RNAi), useful for modulating gene expression.
XX
XX Disclosure; SEQ ID NO 14; 171bp; English.
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of a NOGO receptor gene by
CC RNA interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be,
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising a siRNA targeted to a NOGO receptor mRNA. It
CC further discloses siRNAs targeted to a NOGO receptor gene, siRNAs targeted
CC to a NOGO gene itself, and expression vectors and host cells comprising
CC to a siRNA of the invention. In particular, the invention discloses siRNAs
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-
CC AEF75902) targeted to the human NOGO-A (KIAA0886) gene of DDBJ accession
CC number AB020693. The siRNAs are used to modulate expression of NOGO
CC receptor or NOGO genes in cells, tissue explants or organisms (e.g., by
CC ex vivo gene therapy), or in grafts and transplants for the treatment of
CC a variety of neurodegenerative conditions such as central nervous system
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis
CC (MS), muscular dystrophy, chemotherapy-induced neuropathy, amyotrophic
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntington's
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimer's
CC disease. The siRNAs may also be used in drug screening, diagnosis,
CC therapeutic target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of
CC single nucleotide polymorphisms). The present sequence represents the
CC sense strand of a human NOGO-A-targeted double-stranded siRNA, which is
CC identical to the NOGO-A transcript target sequence.
XX
XX Sequence 19 BP; 9 A; 0 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1001 TCCACATCTCTCCCTCT 1019
Db 19 TCCCTCTCTCTCTCTCT 1
RESULT 231
AEF75690
ID AEF75690 standard; RNA; 19 BP.
XX
XX AEF75690;
AC
XX
XX 06-APR-2006 (first entry)
DT
XX
XX Human NOGO-A siRNA antisense strand, SEQ:240.
DE
XX
XX RNA interference; gene silencing; short interfering RNA; siRNA;
XX nervous system injury; spinal cord injury; neuroprotective; vulnerary;
XX cerebrovascular ischemia; cerebroprotective; multiple sclerosis;
XX muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;
XX
```

KW CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;  
KW Huntingtons chorea; anticonvulsant; noctropic; dementia;  
KW Creutzfeldt Jakob disease; Alzheimers disease; NCOG-A; KIAA0866;  
KW reticulon 4; RTN4; ss.  
XX Homo sapiens.  
XX US2005261212-A1.  
PN  
XX  
XX 24-NOV-2005.  
PD  
XX  
XX 26-JUN-2002; 2002US-00206693.  
PR  
XX 11-FEB-2000; 2000US-0181797P.  
PR 09-FEB-2001; 2001US-00780533.  
PR 05-APR-2001; 2001US-00827395.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 03-APR-2002; 2002MO-US010512.  
PR 06-JUN-2002; 2002US-0366782P.  
PR  
XX (MCSW/) MCSWIGGEN J A.  
PA  
XX  
XX Mcswiggen JA;  
PI  
XX WPI; 2006-190836/20.  
XX  
XX New chemically modified double stranded short interfering nucleic acid  
PT (siRNA) molecule that directs cleavage of a NCOG receptor (NOCOR) RNA via  
PT RNA interference (RNAi), useful for modulating gene expression.  
XX  
XX  
PS Disclosure; SEQ ID NO 240; 171bp; English.  
XX  
XX The invention relates to chemically synthesized short interfering nucleic  
CC acids (siRNAs) which downregulate expression of a NCOG receptor gene by  
CC RNA interference. The siRNAs may or may not comprise ribonucleotides, can  
CC contain deoxyribonucleotides, can be chemically modified and may be  
CC double or single stranded. They further comprise sense and antisense  
CC regions, or alternatively are assembled from a sense oligonucleotide and  
CC an antisense oligonucleotide. Specifically, the siRNAs include short  
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short  
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical  
CC compositions comprising an siRNA targeted to a NCOG receptor mRNA. It  
CC further discloses siRNAs targeted to a NCOG receptor gene, siRNAs targeted  
CC to a NCOG gene itself, and expression vectors and host cells comprising  
CC an siRNA of the invention. In particular, the invention discloses siRNAs  
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NCOG  
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-  
CC AEF75902) targeted to the human NCOG-A (KIAA0866) gene of DDBJ accession  
CC number AB020693. The siRNAs are used to modulate expression of NCOG  
CC receptor or NCOG genes in cells, tissue explants or organisms (e.g., by  
CC ex vivo gene therapy), or in grafts and transplants for the treatment of  
CC a variety of neurodegenerative conditions such as central nervous system  
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis  
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntington's  
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimer's  
CC disease. The siRNAs may also be used in drug screening, diagnosis,  
CC therapeutic target identification and validation, genetic engineering,  
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of  
CC single nucleotide polymorphisms). The present sequence represents the  
CC antisense strand of a human NCOG-A-targeted double-stranded siRNA.  
XX  
SQ Sequence 19 BP; 0 A; 10 C; 0 G; 0 T; 9 U; 0 Other;  
XX  
Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 47.4%; Pred. No. 1.8e+02;  
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;  
OY 1001 TCACATCTTCTCTCTCT 1019  
DB 1 UCUUCUUCUUCUUCUUCU 19

RESULT 232  
AAK72794/C  
ID AAK72794 standard; RNA; 17 BP.  
XX  
XX AAK72794;  
AC  
XX  
XX 28-JUL-1999 (first entry)  
DT  
XX  
XX Mouse ftk-1 VEGF receptor hammerhead ribozyme substrate #227.  
DE  
XX  
XX Vascular endothelial growth factor receptor; VEGF receptor; ftk-1; ftk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
XX Mus sp.  
OS  
XX  
XX W09715662-A2.  
PN  
XX  
XX 01-MAY-1997.  
PD  
XX  
XX 25-OCT-1996; 96WO-US017480.  
PE  
XX  
XX 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR) CHIRON CORP.  
XX  
XX Payco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
PI  
XX WPI; 1997-259017/23.  
XX  
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
XX Claim 4; Page 129; 218bp; English.  
PS  
XX The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAK7275 to AAK75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 1 A; 4 C; 5 G; 0 T; 7 U; 0 Other;  
XX  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 716 CAACCAAGAGACCATG 732  
DB 17 CAACCAAGAGACCATG 1  
XX  
RESULT 233  
ABK01841  
ID ABK01841 standard; RNA; 17 BP.  
XX  
XX ABK01841;  
AC  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX  
XX Human NCOG zinzyme #163.  
XX



KM Human; ss; antisense therapy; cyrostatic; antiinflammatory; haemostatic;  
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammetthead ribozyme;  
KM DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;  
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KM inflammatory arthropathy; central nervous system injury;  
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KM chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KM Parkinson's disease; ataxia; Huntington's disease;  
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN MO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004273.  
XX  
PR 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX  
PI Blatt L, Mcswigen J, Chowrira BM;  
XX  
DR WPI; 2001-607195/69.  
XX  
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
XX  
PS Claim 88; Page 98; 200pp; English.  
XX  
CC The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a zinzyme molecule of the invention

XX  
SQ Sequence 17 BP; 1 A; 11 C; 4 G; 0 T; 1 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.6e+02;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Oy 619 CCCCTCCAGCCCGGCT 635  
Db 1 CCCCGCAGCCCGGCT 17  
RESULT 234  
ADU94309  
ID ADU94309 standard; DNA; 17 BP.  
XX  
AC ADU94309;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human TERT NCH ribozyme substrate sequence #991.  
XX  
XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KM protein-cytosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KM c-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammetthead; HH; halpin; NCH; inozyme; G-cleaver;  
KM amberyze; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KM ds.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 08-NOV-1999; 99US-0156467P.  
PR 06-DEC-1999; 99US-00436430.  
PR 29-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 30-DEC-1999; 99US-0173612P.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA Mcswigen J, Ueman N, Blatt L, Beigelman L, Burgin A;  
PI Kapelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
XX WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
PS Example 1; Page 297; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of

CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
CC aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inosyme), G-cleaver, amberzyme,  
CC zincyme, and/or DNzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.

CC Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 GGACGAGCTTCTCTCA 1702

DB 1 GGCGCAGCTTCTCTCA 17

RESULT 235  
AADS0872/c  
ID AADS0872 standard; DNA; 18 BP.

XX AADS0872;

XX 04-APR-2003 (first entry)

XX Human OGR1 gene specific reverse RT-PCR primer.

KW Human; G-protein coupled receptor; GPCR; breast; ovary; lung; prostate;  
KW colorectal; cancer; GPCR24; GPR4; GPR65; OGR1; gene therapy; cyostatic;  
KW reverse transcription; RT; PCR; primer; ss.

XX Homo sapiens.

XX WO200290925-A2.

XX 14-NOV-2002.

XX 03-MAY-2002; 2002WO-US014164.

XX 07-MAY-2001; 2001US-00850948.

XX (TULA-) TULARIK INC.

XX Yang J, An S;

XX WPI; 2003-103529/09.

PT Detecting breast, ovarian, prostate, colorectal or lung cancer in  
PT mammals, comprises detecting an overexpression of G-protein coupled  
PT receptors (GPCRs), such as GPCR24, GPR4, GPR65 and ORGRI relative to a  
PT control.

XX Example 1; Page 62; 83pp; English.

CC The invention relates to a method for detecting breast, ovarian, lung,  
CC prostate or colorectal cancer in mammals, which involves detecting an  
CC overexpression of G-protein coupled receptors (GPCRs), such as GPCR24,  
CC GPR4, GPR65 and OGR1 relative to a control. The methods, GPCR polypeptide  
CC and inhibitors are useful for treating cancer, e.g. breast, ovarian,  
CC prostate, colorectal or lung cancer. The detection of the polypeptides is

CC useful for monitoring the efficacy of cancer treatment and number or  
CC location of cancer cells in a patient to monitor the progression of  
CC cancer over time. The invention is also used in gene therapy. The present  
CC sequence is a reverse transcription (RT)-PCR primer specific for human  
CC OGR1 gene. This sequence is used to illustrate the method of the  
CC invention

CC Sequence 18 BP; 7 A; 3 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGCTGCTGCTTC 1002

DB 18 TCTGCTGCTGCTGCTTC 2

RESULT 236  
ADRI5253  
ID ADRI5253 standard; DNA; 18 BP.

XX ADRI5253;

XX 21-OCT-2004 (first entry)

XX Human HGRBMV9 PCR primer #1.

KW se; human; G-protein coupled receptor; GPCR; HGRBMV9; analgesic;  
KW antiaddictive; antibacterial; anticonvulsant; antidepressant;  
KW antiinflammatory; antimanic; antiparkinsonian; antiserotonergic;  
KW cardiant; cyostatic; haemostatic; hypnotic; neuroleptic;  
KW neuroprotective; nootropic; tranquiliser; vasotropic; vulnery;  
KW neurodegenerative disease; behavioural disorder; memory disorder;  
KW serotonin; anxiety; parkinson's disease; Huntington's disease;  
KW cognitive disorders; parkinson's disease; Alzheimer's disease;  
KW Tourette's syndrome; meningitis; encephalitis; demyelinating disease;  
KW ischaemia; haemorrhage; schizophrenia; mania; dementia; paranoia; autism;  
KW balance; perception; lung cancer; NFKB expression; primer; PCR.

XX Homo sapiens.

XX US2004147732-A1.

XX 29-JUL-2004.

XX 07-OCT-2003; 2003US-00680402.

XX 27-SEP-2000; 2000US-0235709P.

XX 16-JAN-2001; 2001US-0261775P.

XX 02-AUG-2001; 2001US-0309625P.

XX 26-SEP-2001; 2001US-00964923.

XX (FERDE/) FEDER J N.

XX (MINT/) MINTIER G.

XX (RAMA/) RAMANATHAN C S.

XX (HAWK/) HAWKEN D R.

XX (CACA/) CACACE A M.

XX (BENN/) BENNETT K L.

XX Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace AM;

XX Bennet KL;

XX WPI; 2004-561410/54.

PT New human G-protein coupled receptor, HGRBMV9, expressed highly in brain  
PT and testes, useful in the treatment and diagnosis of conditions such as  
PT neurodegenerative diseases, schizophrenia, lung cancer, and inflammation.

XX Example 11; SEQ ID NO 70; 69pp; English.

CC This invention describes a novel human G-protein coupled receptor (GPCR),  
CC HGRBMV9 which is included in the American Type Culture Collection

CC Deposit No. PTA-2675. The protein of the invention has analgesic,  
CC antiaddictive, antibacterial, anticonvulsant, antidepressant,  
CC antiinflammatory, antianemic, antiparkinsonian, antiserotonergic,  
CC cardiatic, cyostatic, haemostatic, hypnotic, neuroleptic,  
CC neuroprotective, nootropic, tranquiliser, vasotropic and vulnery  
CC activity. The nucleic acid molecule (I), the encoded polypeptide (II),  
CC and the associated reagents and methods are useful for diagnosing,  
CC preventing or treating conditions selected from neurodegenerative disease  
CC states, behavioural disorders, inflammatory conditions, aberrant  
CC behaviour, memory disorders, aberrant cognitive functioning, dorsal raphe  
CC disorders, serotonin expression, serotonin uptake, anxiety, fear,  
CC depression, sleep disorders, pain, locus coeruleus disorder, disorders  
CC associated with a failure to maintain an attentive or alert state,  
CC nucleus accumbens disorders, disorders associated with the expression  
CC and/or release of neurotransmitters such as dopamine, opioid peptides,  
CC serotonin, GABA, and glutamate, addiction, hypothalamus disorders,  
CC disorders affecting ability of the brain to maintain homeostasis,  
CC neuroendocrine functions, hippocampus disorders, long term potentiation  
CC disorders, substantia nigra disorders, disorders affecting dopaminergic  
CC function, Alzheimer's, cognitive disorders, Parkinson's Disease,  
CC Huntington's Disease, Tourette's Syndrome, meningitis, encephalitis,  
CC demyelinating diseases, peripheral neuropathies, neoplasia, trauma,  
CC congenital malformations, spinal cord injuries, ischaemia and infarction,  
CC aneurysms, haemorrhages, schizophrenia, mania, dementia, paranoia,  
CC obsessive compulsive disorder, depression, panic disorder, learning  
CC disabilities, AIDS, psychoses, autism and altered behaviours, including  
CC disorders in feeding, sleep patterns, balance, perception, lung cancer,  
CC proliferative lung disorder, disorders associated with aberrant E-  
CC selectin expression or activity; disorders associated with aberrant NFKB  
CC expression or activity; disorders associated with aberrant IKKalpha  
CC expression or activity; an inflammatory disorder; an inflammatory  
CC disorder associated with aberrant NFKB regulation or regulation of the  
CC NFKB pathway; and proliferative disorders associated with aberrant NFKB  
CC regulation or regulation of the NFKB pathway. This sequence represents a  
CC PCR primer used to amplify the human HGPRTMY9 gene for  
CC immunohistochemistry hybridisation expression profiling.  
XX

SO Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 309 CCTTGGGCGAGCTTCCCT 325

Db 2 CCTTGGGCGAGCTTCCCT 18

RESULT 237

AEF82508

ID AEF82508 standard; DNA, 18 BP.

XX AEF82508;

DT 20-APR-2006 (first entry)

DE Common marmoset 18S ribosome RNA gene RT-PCR primer SEQ ID NO:10.

KM 18S ribosomal RNA; 18S rRNA; RNA detection; DNA detection; expression;  
KM 8S; RT-PCR; primer; reverse transcriptase PCR.

OS Callithrix jacchus.

XX JP2006042804-A.

XX 16-FEB-2006.

PF 04-MAR-2005; 2005JP-00060329.

XX 09-JUL-2004; 2004JP-00202891.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX

PI Yamada T, Oeda K;  
XX  
XX WPI; 2006-150097/16.  
XX  
PT Novel 18S ribosome RNA gene derived from common marmoset, or its partial  
PT fragment, useful as internal standard for measuring difference in  
PT expression level of gene of interest in two or more types of test  
PT samples.  
XX  
XX Disclosure; SEQ ID NO 10; 21bp; Japanese.  
PS

XX The invention relates to a novel 18S ribosome RNA gene (I) derived from a  
CC common marmoset, or its partial fragment (AEF82499). Also claimed is a  
CC composition for detecting DNA or RNA, comprising the 18S rRNA gene. The  
CC 18S rRNA gene is useful as an internal standard or a reference of the  
CC expression level of a gene in the test sample during the measurement of  
CC the difference in the expression level of a gene of interest in two or  
CC more types of test sample, based on the difference in the transcription  
CC product amount of the gene, where the test sample is derived from a  
CC common marmoset. The transcription product amount of the gene of interest  
CC is measured using a DNA array or by quantitative reverse transcriptase-  
CC PCR. The present sequence represents an RT-PCR primer (see also AEF82507)  
CC directed at the 18S rRNA gene.  
XX

SO Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.8e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1245 GGGGAGTGTGTACCAAG 1261

Db 1 GGGGAGTGTGTACCAAG 17

RESULT 238

ID ADF37473 standard; RNA, 19 BP.

XX ADF37473;

DT 12-FEB-2004 (first entry)

DE Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1762.

XX double-stranded short interfering nucleic acid;

KM short interfering nucleic acid; siNA; downregulation;

KM vascular endothelial growth factor receptor; VEGFR; antiangiogenic;

KM cyostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;

KM nephrotropic; gynaecological; angiogenesis-associated condition; cancer;

KM diabetic retinopathy; macular degeneration; neovascular glaucoma;

KM arthritis; psoriasis; endometriosis; angiodioma;

KM polycystic kidney disease; ss.

XX

OS Synthetic.

XX Homo sapiens.

XX WO2003070910-A2.

XX 28-AUG-2003.

XX

PF 20-FEB-2003; 2003WO-US005022.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 29-MAY-2002; 2002WO-US017674.

XX 06-JUN-2002; 2002US-0386782P.

XX 03-JUL-2002; 2002US-0393796P.

XX 29-JUL-2002; 2002US-0399348P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 04-NOV-2002; 2002US-00287949.

PR 27-NOV-2002; 2002US-00306747.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PI Mcswigen J, Beigelman L, Pavco P;  
 DR WPI; 2003-679876/64.  
 XX  
 PT New double-stranded interfering nucleic acid, useful e.g. for treatment  
 PT and diagnosis of cancer, downregulates the vascular endothelial growth  
 PT factor receptor gene.  
 XX  
 XX Example 3; SEQ ID NO 1762; 207pp; English.  
 PS  
 XX The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that downregulates expression of the vascular  
 CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a  
 CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors  
 CC that express siNA; and (5) single-stranded siNA with similar properties.  
 CC The siNAs have antiangiogenic, cytostatic, antidiabetic,  
 CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and  
 CC gynaecological activities. The siNA are useful for modulating  
 CC (downregulating) the expression of VEGFR genes. The siNA are potentially  
 CC useful for treating a wide range of angiogenesis-associated conditions,  
 CC particularly cancers, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiodiroma,  
 CC and polycystic kidney disease. The siNA may also be useful for diagnosis,  
 CC drug screening, target identification and validation, genetic  
 CC engineering, studying gene function, and also for gene mapping (e.g. of  
 CC single-nucleotide polymorphisms). The present sequence is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 139 AGGCGCCAGCCACGAGA 155  
 Db 18 AGGCGCCAGCCACCGA 2  
 RESULT 239  
 ADF37226  
 ID ADF37226 standard; RNA; 19 BP.  
 XX  
 AC ADF37226;  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1515.  
 KM double-stranded short interfering nucleic acid;  
 KM short interfering nucleic acid; siNA; downregulation;  
 KM vascular endothelial growth factor receptor; VEGFR; antiangiogenic;  
 KM cytosstatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;  
 KM nephrotropic; gynaecological; angiogenesis-associated condition; cancer;  
 KM diabetic retinopathy; macular degeneration; neovascular glaucoma;  
 KM arthritis; psoriasis; endometriosis; angiodiroma;  
 KM polycystic kidney disease; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 PV WO2003070910-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005022.  
 XX

PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-036124P.  
 PR 29-MAY-2002; 2002WO-US017674.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 03-JUL-2002; 2002US-0393796P.  
 PR 29-JUL-2002; 2002US-0399348P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 04-NOV-2002; 2002US-00287949.  
 PR 27-NOV-2002; 2002US-00306747.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PI Mcswigen J, Beigelman L, Pavco P;  
 DR WPI; 2003-679876/64.  
 XX  
 PT New double-stranded interfering nucleic acid, useful e.g. for treatment  
 PT and diagnosis of cancer, downregulates the vascular endothelial growth  
 PT factor receptor gene.  
 XX  
 XX Example 3; SEQ ID NO 1515; 207pp; English.  
 PS  
 XX The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that downregulates expression of the vascular  
 CC endothelial growth factor receptor (VEGFR) gene. Also described: (1) a  
 CC siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors  
 CC that express siNA; and (5) single-stranded siNA with similar properties.  
 CC The siNAs have antiangiogenic, cytostatic, antidiabetic,  
 CC ophthalmological, antiarthritic, antipsoriatic, nephrotropic and  
 CC gynaecological activities. The siNA are useful for modulating  
 CC (downregulating) the expression of VEGFR genes. The siNA are potentially  
 CC useful for treating a wide range of angiogenesis-associated conditions,  
 CC particularly cancers, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, arthritis, psoriasis, endometriosis, angiodiroma,  
 CC and polycystic kidney disease. The siNA may also be useful for diagnosis,  
 CC drug screening, target identification and validation, genetic  
 CC engineering, studying gene function, and also for gene mapping (e.g. of  
 CC single-nucleotide polymorphisms). The present sequence is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 139 AGGCGCCAGCCACGAGA 155  
 Db 2 AGGCGCCAGCCACCGA 18  
 RESULT 240  
 ADF37226  
 ID ADF37226 standard; RNA; 19 BP.  
 XX  
 AC ADF37226;  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human TERT siNA lower strand, SEQ ID 449.  
 KM Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;  
 KM neuroprotective; anti-HIV; ophthalmological; antifolcer; antirheumatic;  
 KM antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;  
 KM RNA interference; short interfering nucleic acid; siNA;  
 KM short interfering siRNA; siRNA; double-stranded RNA; micro-RNA; miRNA;  
 KM short hairpin RNA; shRNA; expression modulation; gene therapy;  
 KM drug screening; diagnosis; therapeutic target identification;  
 KM pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.

```
XX OS Homo sapiens.
XX PN WO2003070742-A1.
XX PD 28-AUG-2003.
XX PF 11-FEB-2003; 2003WO-US004088.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0366782P.
XX PR 17-JUL-2002; 2002US-0396600P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcawiggen J, Beigelman L;
XX DR WPI; 2003-689777/65.
XX PT New short interfering nucleic acid downregulates expression of the
XX telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX PS Example 3; SEQ ID NO 449; 145bp; English.
XX CC The invention relates to short interfering nucleic acids (siNA) which
XX CC downregulate expression of the one or more telomerase genes by RNA
XX CC interference. The siNAs may or may not comprise ribonucleotides and may
XX CC be double or single stranded. They further comprise sense and antisense
XX CC regions, or alternatively are assembled from a sense oligonucleotide and
XX CC an antisense oligonucleotide. Specifically, the siNAs include short
XX CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
XX CC can contain deoxyribonucleotides, and can be chemically synthesised,
XX CC expressed from a vector or enzymatically synthesised. The invention also
XX CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
XX CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
XX CC used to modulate expression of the telomerase genes in cells, tissue
XX CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
XX CC transplants for the treatment of a variety of conditions. They may be
XX CC used for treating cancer, restenosis, infectious diseases (specifically
XX CC protozoal), transplant rejection, or autoimmune or age-related diseases,
XX CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
XX CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
XX CC screening, diagnosis, therapeutic target identification and validation,
XX CC genetic engineering, pharmacogenomics, studying gene function, and gene
XX CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
XX CC represents the lower strand of a human TERT-targeted double-stranded
XX CC siNA.
XX SQ Sequence 19 BP; 4 A; 7 C; 2 G; 0 T; 6 U; 0 Other;
OY Query Match 0.9%; Score 15.4; DB 1; Length 19;
Db Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 463 AATACAGTGGTGAACCTT 479
Db 17 AAGACAGTGGTGAACCTT 1
RESULT 241
ADP93468 ID ADF93468 standard; RNA; 19 BP.
XX AC ADF93468;
XX AC ADF93468;
XX DT 26-FEB-2004 (first entry)
XX
```

```
DE Human TERT transcript target sequence/siNA upper strand, SEQ ID 185.
XX CC Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
XX CC neuroprotective; anti-HIV; ophthalmological; antitumor; antineoplastic;
XX CC antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
XX CC RNA interference; short interfering nucleic acid; siNA;
XX CC short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
XX CC short hairpin RNA; shRNA; expression modulation; gene therapy;
XX CC drug screening; diagnosis; therapeutic target identification;
XX CC pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
XX OS Homo sapiens.
XX PN WO2003070742-A1.
XX PD 28-AUG-2003.
XX PF 11-FEB-2003; 2003WO-US004088.
XX PR 20-FEB-2002; 2002US-0358580P.
XX PR 11-MAR-2002; 2002US-0363124P.
XX PR 06-JUN-2002; 2002US-0366782P.
XX PR 17-JUL-2002; 2002US-0396600P.
XX PR 29-AUG-2002; 2002US-0406784P.
XX PR 05-SEP-2002; 2002US-0408378P.
XX PR 09-SEP-2002; 2002US-0409293P.
XX PR 15-JAN-2003; 2003US-0440129P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcawiggen J, Beigelman L;
XX DR WPI; 2003-689777/65.
XX PT New short interfering nucleic acid downregulates expression of the
XX PT telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX PS Example 3; SEQ ID NO 185; 145bp; English.
XX CC The invention relates to short interfering nucleic acids (siNA) which
XX CC downregulate expression of the one or more telomerase genes by RNA
XX CC interference. The siNAs may or may not comprise ribonucleotides and may
XX CC be double or single stranded. They further comprise sense and antisense
XX CC regions, or alternatively are assembled from a sense oligonucleotide and
XX CC an antisense oligonucleotide. Specifically, the siNAs include short
XX CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
XX CC can contain deoxyribonucleotides, and can be chemically synthesised,
XX CC expressed from a vector or enzymatically synthesised. The invention also
XX CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
XX CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
XX CC used to modulate expression of the telomerase genes in cells, tissue
XX CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
XX CC transplants for the treatment of a variety of conditions. They may be
XX CC used for treating cancer, restenosis, infectious diseases (specifically
XX CC protozoal), transplant rejection, or autoimmune or age-related diseases,
XX CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
XX CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
XX CC screening, diagnosis, therapeutic target identification and validation,
XX CC genetic engineering, pharmacogenomics, studying gene function, and gene
XX CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
XX CC represents the upper strand of a human TERT-targeted double-stranded
XX CC siNA, which is identical to the c-fos transcript target sequence.
XX SQ Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
OY Query Match 0.9%; Score 15.4; DB 1; Length 19;
Db Best Local Similarity 70.6%; Pred. No. 2.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 463 AATACAGTGGTGAACCTT 479
Db 3 AAGACAGTGGTGAACCTT 19
```

```

RESULT 242
ADK97381/c
ID ADK97381 standard; DNA; 19 BP.
XX
AC ADK97381;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #3101.
XX
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS Synthetic.
XX
PN JF2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
DR WPI; 2004-093977/10.
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 6410; 2627bp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 19 BP; 0 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 1309 GACGAGCCAGAGGACGG 1325
DB 19 GAAAGACCAAGAGGACGG 3
RESULT 243
AD062492
ID AD062492 standard; RNA; 19 BP.
XX
AC AD062492;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-TERT siRNA SEQ ID NO:2195.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.

```

```

XR      10-SEP-2003; 2003US-0502050P.
XA      (DHAR-) DHARMACON INC.
XX
PI      Anastasia K, Angela R, Devin L, William M, Stephen S;
DR      WPI; 2004-420527/39.
PT      Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT      by selecting a target gene and measuring the functionality of the
PT      nucleotide sequences that are complementary to a stretch of nucleotides
PT      of the target sequence.
XX
PS      Example 12; SEQ ID NO 2195; 199pp; English.
XX
CC      The invention relates to a novel method for selecting siRNA (short
CC      interfering RNA) comprising selecting an siRNA molecule of 19-25
CC      nucleoside bases by selecting a target gene and measuring the
CC      functionality of sequences of 19-25 nucleotides in length that are
CC      substantially complementary to a stretch of nucleotides of the target
CC      sequence, where the functionality is dependent upon non-target specific
CC      criteria. Also claimed are methods for gene-silencing, developing an
CC      siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC      functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC      effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC      siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC      sequence consisting of GGGAGAUGAGUAGAUA; GAAGCAUCUUCUCUACAUU;
CC      GUAGCAACACCGGAGUA; AGAUGAGUAGUAGAUAU; UGAAGAUUCUUCUCUACAUU;
CC      CAUCCGCCUCUUGUAUA; UGCGCCUCUCUGUAGUU; GGAUAGUAGUAGUAGUA;
CC      GGAGAUGAGUAGUAGUAG; and GAAGCUCUCUCUAGUU. The siRNA molecule
CC      comprises a sense strand and an anti-sense strand. The siRNA molecule
CC      comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC      pairs. The kit comprises at least two siRNA, comprising a first optimised
CC      siRNA and a second optimised siRNA. The method is useful in selecting
CC      siRNA for generating a gene silencing reagent. The present sequence is
CC      used in the exemplification of the invention.
SQ      Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
QY      Query Match          0.9%; Score 15.4; DB 1; Length 19;
        Best Local Similarity 70.6%; Pred. No. 2.1e+02;
        Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0.
        463 ATATCATGTCTGAACTT 479
           |||||:::||::|||::|
DB      3 AAAGACAGUGGUGAACCU 19
RESULT 244
ADRO5766/c
ID      ADRO5766 standard; DNA; 19 BP.
XX
AC      ADRO5766;
DT      21-OCT-2004 (first entry)
XX
DE      Ribosome binding site-related oligonucleotide, SEQ ID 3.
KM      Transposase; mariner mobile genetic element; transposon; Mos-1 element;
XX      ribosome binding site; ss.
OS      Synthetic.
PN      FR2850395-A1.
XX
PD      30-JUL-2004.
PF      28-JAN-2003; 2003FR-00000905.
PR      28-JAN-2003; 2003FR-00000905.
XX
PA      (CNRS ) CNRS CENT NAT RECH SCI.
PA      (UYTO-) UNIV TOURS RABELAIS FRANCOIS.

```

XX PI Bigot Y, Auge GC, Hamelin MH, Brilllet B;  
XX DR WPI; 2004-546139/53.  
XX PT New hyperactive mutant of the mariner transposase, useful for targeted  
XX insertion of DNA, particularly for gene therapy, has at least one  
XX phosphorylatable amino residue replaced by non-phosphorylatable residue.  
XX PS Disclosure; SEQ ID NO 3; 62pp; French.  
XX CC The present invention relates to a hyperactive transposase mutant (A)  
XX from a mariner mobile genetic element (BGM). It has at least one mutation  
XX of a phosphorylatable residue (pr), in at least one phosphorylation site,  
XX that renders the site non-phosphorylatable. The BGM is from *Drosophila*  
XX *maritima* and represents the transposon from the Mos-1 element  
XX (AD805764). Unlike the wild-type transposase, (A), when expressed in  
XX eukaryotes, is not subjected to phosphorylation (post-translation  
XX modification), a process that reduces affinity for DNA and limits  
XX conformational activity, resulting in a low capacity for catalysis of  
XX transposition. The non-phosphorylatable mutants are at least 25,  
XX preferably 100, times more active. (A) is useful for in vitro  
XX transposition of transposable DNA of interest into a target DNA,  
XX particularly for use in gene therapy where the transposable DNA is  
XX introduced into a host cell genome. The present sequence was used for  
XX cloning a ribosome binding site for vector construction.  
XX SQ Sequence 19 BP; 5 A; 4 C; 8 G; 2 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 891 GATCCCGGGGACTCTCT 907  
Db 19 GATCCCGGGGACTCTCT 3  
RESULT 245  
ADY88479  
XX ID ADY88479 standard; RNA; 19 BP.  
XX AC ADY88479;  
XX DT 16-JUN-2005 (first entry)  
XX DE VEGFR siRNA SEQ ID NO 1515.  
XX KM ss; siRNA; short interfering RNA; RNA interference; gene silencing;  
XX KW VEGFR; pharmaceutical; cancer; neoplasm; Cytostatic.  
XX OS Synthetic.  
XX PN WO2005028649-A1.  
XX PD 31-MAR-2005.  
XX PF 16-SEP-2004; 2004WO-US030488.  
XX PR 16-SEP-2003; 2003US-00664767.  
XX PR 16-SEP-2003; 2003US-00665255.  
XX PR 23-SEP-2003; 2003US-00670011.  
XX PR 23-OCT-2003; 2003US-00693059.  
XX PR 24-NOV-2003; 2003US-00720448.  
XX PR 03-DEC-2003; 2003US-00727780.  
XX PR 14-JAN-2004; 2004US-00764957.  
XX PR 26-FEB-2004; 2004US-0543480P.  
XX PR 10-FEB-2004; 2004US-00764957.  
XX PR 13-FEB-2004; 2004US-00780447.  
XX PR 16-APR-2004; 2004US-00826966.  
XX PR 23-APR-2004; 2004US-00831620.  
XX PR 30-APR-2004; 2004US-00013456.  
XX PR 11-MAY-2004; 2004US-00844076.

XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;  
XX DR WPI; 2005-254128/26.  
XX XX PT New multifunctional siRNA molecule that directs cleavage of the first and  
XX second VEGF or VEGFR target sequences via RNA interference, useful in  
XX preparing a composition for treating cell proliferative disorders e.g.  
XX cancers.  
XX PS Disclosure; SEQ ID NO 1515; 396pp; English.  
XX CC The invention relates to a multifunctional siRNA molecule comprising a  
XX structure having formula MF-III and which directs cleavage of the first  
XX and second VEGF or VEGFR target sequences via RNA interference. The  
XX multifunctional siRNA molecule is useful in preparing a pharmaceutical  
XX composition for treating cell proliferative disorders, e.g. cancer. The  
XX present sequence represents a VEGFR siRNA.  
XX SQ Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 139 AGGCGCCAGCCACAGGA 155  
Db 2 AGGCGCCAGCCACCGGA 18  
RESULT 246  
ADY88726/C  
XX ID ADY88726 standard; RNA; 19 BP.  
XX AC ADY88726;  
XX DT 16-JUN-2005 (first entry)  
XX DE VEGFR siRNA SEQ ID NO 1762.  
XX KM ss; siRNA; short interfering RNA; RNA interference; gene silencing;  
XX KW VEGFR; pharmaceutical; cancer; neoplasm; Cytostatic.  
XX OS Synthetic.  
XX PN WO2005028649-A1.  
XX PD 31-MAR-2005.  
XX PF 16-SEP-2004; 2004WO-US030488.  
XX PR 16-SEP-2003; 2003US-00664767.  
XX PR 16-SEP-2003; 2003US-00665255.  
XX PR 23-SEP-2003; 2003US-00670011.  
XX PR 23-OCT-2003; 2003US-00693059.  
XX PR 24-NOV-2003; 2003US-00720448.  
XX PR 03-DEC-2003; 2003US-00727780.  
XX PR 14-JAN-2004; 2004US-00757803.  
XX PR 26-FEB-2004; 2004US-00764957.  
XX PR 10-FEB-2004; 2004US-0543480P.  
XX PR 13-FEB-2004; 2004US-00780447.  
XX PR 16-APR-2004; 2004US-00826966.  
XX PR 23-APR-2004; 2004US-00831620.  
XX PR 30-APR-2004; 2004US-00013456.  
XX PR 11-MAY-2004; 2004US-00844076.  
XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX XX Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;  
XX PI WPI; 2005-254128/26.  
XX DR

XX New multifunctional siRNA molecule that directs cleavage of the first and  
PT second VEGF or VEGFR target sequences via RNA interference, useful in  
PT preparing a composition for treating cell proliferative disorders e.g.  
PT cancers.  
XX  
XX Disclosure; SEQ ID NO 1762; 396pp; English.  
XX  
XX The invention relates to a multifunctional siRNA molecule comprising a  
CC structure having Formula MF-II and which directs cleavage of the first  
CC and second VEGF or VEGFR target sequences via RNA interference. The  
CC multifunctional siRNA molecule is useful in preparing a pharmaceutical  
CC composition for treating cell proliferative disorders, e.g. cancer. The  
CC present sequence represents a VEGFR siRNA.  
XX  
XX Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 139 AGGCGCCAGCCACGCA 155  
DB 18 AGGCGCCAGCCACGCA 2  
RESULT 247  
AEA06712/c  
ID AEA06712 standard; DNA; 19 BP.  
XX  
XX AEA06712;  
AC  
XX  
XX 28-JUL-2005 (first entry)  
DT  
XX  
XX G protein-coupled receptor 154 siRNA target SEQ ID NO 149.  
DE  
XX  
XX respiratory-gen.; antiasthmatic; antiinflammatory; RNA interference;  
KM gene expression; diagnosis; respiratory disease; inflammation;  
KM G protein-coupled receptor 154; GPR154; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2005045038-A2.  
PN  
XX  
XX 19-MAY-2005.  
PD  
XX  
XX 20-AUG-2004; 2004WO-US027231.  
PF  
XX  
XX 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 11-MAY-2004; 2004US-0570086P.  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX  
XX Richards I, Polisky B, Mcswigen J;  
PI  
XX  
XX WPI; 2005-366846/37.  
DR  
XX  
XX Novel chemically synthesized double stranded short interfering nucleic  
PT acid molecule useful for cleaving G protein-coupled receptor for asthma  
PT susceptibility RNA or treating respiratory or inflammatory disorders.  
PT  
XX  
XX Example 3; SEQ ID NO 149; 210pp; English.  
PS  
XX  
XX The invention describes a chemically synthesized double stranded short  
CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a G

CC protein-coupled receptor for asthma susceptibility (GPR) RNA through RNA  
CC interference (RNAi), where each strand of (I) has 18-23 nucleotides and  
CC one strand of (I) comprises nucleotide sequence having sufficient  
CC complementarity to the GPR RNA to direct cleavage of the GPR RNA by RNA  
CC interference. Also described is a composition comprising (I) and a siRNA  
CC carrier or diluent; validating GPR; a kit comprising (I); and an siRNA  
CC construct. (I) exhibits improved stability, bioavailability and  
CC activation of cellular responses, thus mediating RNA interference. This  
CC sequence represents the target polynucleotide of a G protein-coupled  
CC receptor 154 (GPR154) specific siRNA used to control GPR gene  
CC expression.  
XX  
XX Sequence 19 BP; 5 A; 0 C; 9 G; 0 T; 5 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1110 CAACCCCTCATCTACT 1126  
DB 17 CAACCCCTCATCTACT 1  
RESULT 248  
AEA06625  
ID AEA06625 standard; DNA; 19 BP.  
XX  
XX AEA06625;  
AC  
XX  
XX 28-JUL-2005 (first entry)  
DT  
XX  
XX G protein-coupled receptor 154 siRNA target SEQ ID NO 62.  
DE  
XX  
XX respiratory-gen.; antiasthmatic; antiinflammatory; RNA interference;  
KM gene expression; diagnosis; respiratory disease; inflammation;  
KM G protein-coupled receptor 154; GPR154; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2005045038-A2.  
PN  
XX  
XX 19-MAY-2005.  
PD  
XX  
XX 20-AUG-2004; 2004WO-US027231.  
PF  
XX  
XX 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 11-MAY-2004; 2004US-0570086P.  
PR 24-MAY-2004; 2004WO-US016390.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX  
XX Richards I, Polisky B, Mcswigen J;  
PI  
XX  
XX WPI; 2005-366846/37.  
DR  
XX  
XX Novel chemically synthesized double stranded short interfering nucleic  
PT acid molecule useful for cleaving G protein-coupled receptor for asthma  
PT susceptibility RNA or treating respiratory or inflammatory disorders.  
PT  
XX  
XX Example 3; SEQ ID NO 62; 210pp; English.  
PS  
XX  
XX The invention describes a chemically synthesized double stranded short  
CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a G  
CC protein-coupled receptor for asthma susceptibility (GPR) RNA through RNA  
CC interference (RNAi), where each strand of (I) has 18-23 nucleotides and  
CC one strand of (I) comprises nucleotide sequence having sufficient



CC complementarity to the GPR RNA to direct cleavage of the GPR RNA by RNA  
CC interference. Also described is a composition comprising (1) and a  
CC carrier or diluent, validating GPR; a kit comprising (1); and an siRNA  
CC construct. (1) exhibits improved stability, bioavailability and  
CC activation of cellular responses, thus mediating RNA interference. This  
CC sequence represents the target polynucleotide of a G protein-coupled  
CC receptor 154 (GPR154) specific siRNA used to control GPR gene  
CC expression.  
XX  
SQ Sequence 19 BP; 5 A; 9 C; 0 G; 0 T; 5 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 70.6%; Pred. No. 2.1e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 1110 CACCCGATCATCTACT 1126  
DB 3 CACCCGATCATCTACT 19  
RESULT 249  
AEA21650/c  
ID AEA21650 standard; RNA; 19 BP.  
XX  
AC AEA21650;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Short interfering RNA (siRNA) molecule #76.  
XX  
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.  
XX  
OS Synthetic.  
XX  
PN WO2005049830-A1.  
XX  
PD 02-JUN-2005.  
XX  
PF 19-NOV-2004; 2004WO-JP017648.  
XX  
PR 20-NOV-2003; 2003JP-00390763.  
PR 01-MAR-2004; 2004JP-00055924.  
XX  
PA (SUZU/) SUZUKI T.  
XX  
PI Suzuki T, Katoh T;  
XX  
WPI; 2005-396112/40.  
XX  
PT Designing siRNA for suppressing expression of target gene having sequence  
PT complementary for target mRNA sequence in target gene, and having bases  
PT constituting double-stranded portion for inhibiting expression of target  
PT gene.  
XX  
PS Example 1; Fig 5B; 39pp; Japanese.  
XX  
CC The invention relates to a method for designing an siRNA molecule having  
CC a sequence complementary to a target mRNA sequence in a target gene and  
CC having 19 bases constituting a double-stranded portion for inhibiting  
CC expression of the target gene. The invention also relates to a method of  
CC searching a base sequence and use of the base sequence as siRNA, and a  
CC method of estimating siRNA activity. The method is useful for designing  
CC siRNA for suppressing the expression of a target gene. This sequence  
CC represents an siRNA molecule used in the method of the invention.  
XX  
SQ Sequence 19 BP; 2 A; 6 C; 7 G; 0 T; 4 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1089 GGCATGAGTCCACCA 1105  
|||||||

DB 18 GGCATGAGTCCACCA 2  
RESULT 250  
AEA21651/c  
ID AEA21651 standard; RNA; 19 BP.  
XX  
AC AEA21651;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Short interfering RNA (siRNA) molecule #77.  
XX  
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.  
XX  
OS Synthetic.  
XX  
PN WO2005049830-A1.  
XX  
PD 02-JUN-2005.  
XX  
PF 19-NOV-2004; 2004WO-JP017648.  
XX  
PR 20-NOV-2003; 2003JP-00390763.  
PR 01-MAR-2004; 2004JP-00055924.  
XX  
PA (SUZU/) SUZUKI T.  
XX  
PI Suzuki T, Katoh T;  
XX  
WPI; 2005-396112/40.  
XX  
PT Designing siRNA for suppressing expression of target gene having sequence  
PT complementary for target mRNA sequence in target gene, and having bases  
PT constituting double-stranded portion for inhibiting expression of target  
PT gene.  
XX  
PS Example 1; Fig 5B; 39pp; Japanese.  
XX  
CC The invention relates to a method for designing an siRNA molecule having  
CC a sequence complementary to a target mRNA sequence in a target gene and  
CC having 19 bases constituting a double-stranded portion for inhibiting  
CC expression of the target gene. The invention also relates to a method of  
CC searching a base sequence and use of the base sequence as siRNA, and a  
CC method of estimating siRNA activity. The method is useful for designing  
CC siRNA for suppressing the expression of a target gene. This sequence  
CC represents an siRNA molecule used in the method of the invention.  
XX  
SQ Sequence 19 BP; 3 A; 6 C; 6 G; 0 T; 4 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1089 GGCATGAGTCCACCA 1105  
|||||||  
DB 17 GGCATGAGTCCACCA 1  
RESULT 251  
AEA21649/c  
ID AEA21649 standard; RNA; 19 BP.  
XX  
AC AEA21649;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Short interfering RNA (siRNA) molecule #75.  
XX  
KM RNA interference; gene silencing; short interfering RNA; siRNA; ss.  
XX  
OS Synthetic.  
XX

```
PN WO2005049830-A1.
XX
PD 02-JUN-2005.
PP 19-NOV-2004; 2004WO-JP017648.
XX
XX 20-NOV-2003; 2003JP-00390763.
PR 01-MAR-2004; 2004JP-00055924.
XX
XX (SUZU/) SUZUKI T.
PA
PI Suzuki T, Katoh T;
XX
XX WPI; 2005-396112/40.
DR
XX
XX Designing siRNA for suppressing expression of target gene having sequence
PT complementary for target mRNA sequence in target gene, and having bases
PT constituting double-stranded portion for inhibiting expression of target
PT gene.
XX
XX Example 1; Fig 5B; 39pp; Japanese.
PS
XX The invention relates to a method for designing an siRNA molecule having
XX a sequence complementary to a target mRNA sequence in a target gene and
XX having 19 bases constituting a double-stranded portion for inhibiting
XX expression of the target gene. The invention also relates to a method of
XX searching a base sequence and use of the base sequence as siRNA, and a
XX method of estimating siRNA activity. The method is useful for designing
XX siRNA for suppressing the expression of a target gene. This sequence
XX represents an siRNA molecule used in the method of the invention.
SQ
XX
XX Sequence 19 BP; 2 A; 5 C; 8 G; 0 T; 4 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1089 GGCCATGAGCTCCACCA 1105
DB 19 GGCCATGAGCTCCACCA 3
RESULT 252
AEB15725
ID AEB15725 standard; RNA; 19 BP.
XX
XX AEB15725;
AC
XX
XX 22-SEP-2005 (first entry)
DT
XX
XX Human telomerase-targeted siRNA strand SeqID216.
DE
XX RNA interference; gene silencing; short interfering RNA; siRNA;
XX cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
XX restenosis; transplant rejection; autoimmune disease; hyperproliferation;
XX aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
XX telomerase.
XX
XX Homo sapiens.
OS
XX
XX US2005153916-A1.
PN
XX
XX 14-JUL-2005.
PD
XX
XX 20-AUG-2004; 2004US-00923330.
XX
XX
XX 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
```

```
PR 06-JUN-2002; 2002US-0386782P.
PR 17-JUL-2002; 2002US-0396600P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 11-FEB-2003; 2003WO-US004088.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX
XX Mcswigen J, Belgelman L;
PI
XX
XX WPI; 2005-496858/50.
DR
XX
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of telomerase RNA by RNA interference,
PT useful for treating cancer and restenosis.
PT
XX
XX Claim 33; SEQ ID NO 216; 304pp; English.
PS
XX
XX The invention relates to chemically synthesized short interfering nucleic
XX acids (siRNAs) which downregulate expression of telomerase genes by RNA
XX interference. The siRNAs may or may not comprise ribonucleotides, can
XX contain deoxyribonucleotides, can be chemically modified and may be
XX double or single stranded. They further comprise sense and antisense
XX regions, or alternatively are assembled from a sense oligonucleotide and
XX an antisense oligonucleotide. Specifically, the siRNAs include short
XX interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
XX hairpin RNA (shRNA). The invention also relates to pharmaceutical
XX compositions comprising an siRNA targeted to the human telomerase mRNA
XX which may have a cytosolic, immunosuppressive, vasotropic or
XX antimicrobial activity. The invention further discloses expression
XX vectors and host cells comprising an siRNA of the invention. The siRNAs are
XX used to modulate expression of the telomerase gene in cells, tissue
XX explants or organisms (for example by ex vivo gene therapy), or in grafts
XX and transplants for the treatment of a variety of conditions. They may be
XX used in the treatment of cancer, restenosis, infectious, and age-related
XX rejection, and/or autoimmune, proliferative, and age-related
XX diseases, disorders or conditions. The siRNAs may also be used in drug
XX screening, diagnosis, therapeutic target identification and validation,
XX genetic engineering, pharmacogenomics, studying gene function, and gene
XX mapping (for example of single nucleotide polymorphisms). The present
XX sequence represents the sense strand of a human telomerase-targeted
XX double-stranded siRNA, which is identical to the telomerase transcript
XX target sequence.
XX
XX Sequence 19 BP; 6 A; 2 C; 7 G; 0 T; 4 U; 0 Other;
SQ
XX
XX Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 463 AATACAGTGTGAACCTT 479
DB 3 AAGACAGUGUGAACCUU 19
RESULT 253
AEB15948/c
ID AEB15948 standard; RNA; 19 BP.
```

XX AC AEB15948;  
XX DT 22-SEP-2005 (first entry)  
XX DE Human telomerase-targeted siRNA strand SeqID439.  
XX RNA interference; gene silencing; short interfering RNA; siRNA;  
XX cytoskeletal; immunosuppressive; vasotropic; antimicrobial; cancer;  
XX restenosis; transplant rejection; autoimmune disease; hyperproliferation;  
XX aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;  
XX telomerase.  
XX OS Homo sapiens.  
XX PN US2005153916-A1.  
XX PD 14-JUL-2005.  
XX PF 20-AUG-2004; 2004US-00923330.  
XX PR 18-MAY-2001; 2001US-0292217P.  
XX PR 20-JUL-2001; 2001US-0306883P.  
XX PR 13-AUG-2001; 2001US-0311865P.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 06-MAR-2002; 2002US-0362016P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 20-MAY-2002; 2002WO-US015876.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 17-JUL-2002; 2002US-0396600P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409293P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PR 11-FEB-2003; 2003WO-US004088.  
XX PR 20-FEB-2003; 2003WO-US005028.  
XX PR 20-FEB-2003; 2003WO-US005346.  
XX PR 30-APR-2003; 2003US-00427160.  
XX PR 23-MAY-2003; 2003US-00444853.  
XX PR 23-OCT-2003; 2003US-00693059.  
XX PR 24-NOV-2003; 2003US-00720448.  
XX PR 03-DEC-2003; 2003US-00727780.  
XX PR 14-JAN-2004; 2004US-00757803.  
XX PR 10-FEB-2004; 2004US-0543489P.  
XX PR 13-FEB-2004; 2004US-00780447.  
XX PR 16-APR-2004; 2004US-00826966.  
XX PR 30-APR-2004; 2004WO-US013456.  
XX PR 24-MAY-2004; 2004WO-US016390.  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX Mcewlggen J, Belgelman L;  
XX WPI; 2005-496858/50.  
XX PT Novel chemically synthesized double-stranded short interfering nucleic  
XX acid molecule directing cleavage of telomerase RNA by RNA interference,  
XX useful for treating cancer and restenosis.  
XX PS Claim 33; SEQ ID NO 439; 304pp; English.  
XX CC The invention relates to chemically synthesized short interfering nucleic  
XX acids (siRNAs) which downregulate expression of telomerase genes by RNA  
XX interference. The siRNAs may or may not comprise ribonucleotides, can  
XX contain deoxyribonucleotides, can be chemically modified and may be  
XX double or single stranded. They further comprise sense and antisense  
XX regions, or alternatively are assembled from a sense oligonucleotide and  
XX an antisense oligonucleotide. Specifically, the siRNAs include short  
XX interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short  
XX hairpin RNA (shRNA). The invention also relates to pharmaceutical  
XX compositions comprising an siRNA targeted to the human telomerase mRNA  
XX which may have a cytoskeletal, immunosuppressive, vasotropic or  
XX antimicrobial activity. The invention further discloses expression

CC vectors and host cells comprising an siRNA of the invention. The siRNAs are  
CC used to modulate expression of the telomerase gene in cells, tissue  
CC explants or organisms (for example by ex vivo gene therapy), or in grafts  
CC and transplants for the treatment of a variety of conditions. They may be  
CC used in the treatment of cancer, restenosis, transplant and/or tissue  
CC rejection, and/or autoimmune, proliferative, infectious, and age-related  
CC diseases, disorders or conditions. The siRNAs may also be used in drug  
CC screening, diagnosis, therapeutic target identification and validation,  
CC genetic engineering, pharmacogenomics, studying gene function, and gene  
CC mapping (for example of single nucleotide polymorphisms). The present  
CC sequence represents the antisense strand of a human telomerase-targeted  
CC double-stranded siRNA.  
XX  
XX SQ Sequence 19 BP; 4 A; 7 C; 2 G; 0 T; 6 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DY 463 AATACAGTGTGAACCTT 479  
DB 17 AAGACAGTGTGAACCTT 1  
RESULT 254  
AED37961/C  
ID AED37961 standard; RNA, 19 BP.  
XX AC AED37961;  
XX DT 15-DEC-2005 (first entry)  
XX DE VEGF or VEGFR-specific siRNA sequence - SEQ ID 1762.  
XX KW vascular endothelial growth factor;  
XX KW vascular endothelial growth factor receptor; respiratory disease;  
XX KW respiratory gen.; asthma; antiasthmatic; allergic rhinitis; anti-allergic;  
XX KW chronic obstructive pulmonary disease; allergic rhinitis; anti-allergic;  
XX KW anti-inflammatory; RNA interference; gene silencing; siRNA;  
XX short interfering RNA; ss.  
XX OS Unidentified.  
XX PN US2005222066-A1.  
XX PD 06-OCT-2005.  
XX PF 12-OCT-2004; 2004US-00962898.  
XX PR 18-MAY-2001; 2001US-0292217P.  
XX PR 20-JUL-2001; 2001US-0306883P.  
XX PR 13-AUG-2001; 2001US-0311865P.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 06-MAR-2002; 2002US-0362016P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 17-MAY-2002; 2002WO-US015876.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 03-JUL-2002; 2002US-0393796P.  
XX PR 29-JUL-2002; 2002US-0399348P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409493P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PR 14-FEB-2003; 2003WO-US004566.  
XX PR 20-FEB-2003; 2003WO-US005022.  
XX PR 20-FEB-2003; 2003WO-US005028.  
XX PR 20-FEB-2003; 2003WO-US005346.  
XX PR 30-APR-2003; 2003US-00427160.  
XX PR 23-MAY-2003; 2003US-00444853.  
XX PR 16-SEP-2003; 2003US-00664767.  
XX PR 16-SEP-2003; 2003US-00665255.  
XX PR 23-SEP-2003; 2003US-00670011.  
XX PR 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00722780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 26-JAN-2004; 2004US-00764957.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 23-APR-2004; 2004US-00831620.  
PR 30-APR-2004; 2004US-05013456.  
PR 11-MAY-2004; 2004US-00844076.  
PR 24-MAY-2004; 2004US-05016390.  
PR 09-JUN-2004; 2004US-00863973.  
PR 20-AUG-2004; 2004US-00922675.  
PR 16-SEP-2004; 2004US-00944611.  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Richards I, Mcswiggen J;  
XX WPI; 2005-664178/68.  
XX  
XX  
XX New multifunctional siNA molecule comprising a structure having Formula  
XX MF-III, useful for creating a respiratory disease selected from asthma,  
XX COPD, and allergic rhinitis.  
XX  
XX Example 13; SEQ ID NO 1762; 266pp; English.  
XX  
XX The invention comprises short interfering nucleic acid (siNA) molecules  
XX which modulate vascular endothelial growth factor (VEGF) or VEGF receptor  
XX (VEGFR) gene expression. The siNA molecules of the invention are useful  
XX for treating respiratory diseases (e.g. asthma, COPD, and allergic  
XX rhinitis). The present nucleic acid represents a VEGF/VEGFR-specific  
XX siRNA sequence that was used in an example of the invention.  
XX  
XX Sequence 19 BP; 0 A; 8 C; 7 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred.No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 139 AGCGCCGACGACGAGA 155  
DB 18 AGCGCCGACGACGAGA 2  
RESULT 255  
ABD37714  
ID ABD37714 standard; RNA; 19 BP.  
XX  
XX ABD37714;  
AC  
XX  
XX 15-DEC-2005 (first entry)  
DT  
XX  
XX VEGF or VEGFR-specific siRNA sequence - SEQ ID 1515.  
DE  
XX  
XX vascular endothelial growth factor;  
XX vascular endothelial growth factor receptor; respiratory disease;  
XX respiratory-gen.; asthma; antiasthmatic;  
XX chronic obstructive pulmonary disease; allergic rhinitis; antiallergic;  
XX antiinflammatory; RNA interference; gene silencing; siRNA;  
XX short interfering RNA; ss.  
XX  
XX Unidentified.  
OS  
XX  
XX US2005222066-A1.  
PN  
XX  
XX 06-OCT-2005.  
PD  
XX  
XX 12-OCT-2004; 2004US-00962898.  
PF  
XX  
XX 18-MAY-2001; 2001US-0292217P.  
XX 20-JUL-2001; 2001US-0306883P.  
XX 13-AUG-2001; 2001US-0311865P.  
PR

PR 20-FEB-2002; 2002US-0358580P.  
PR 06-MAR-2002; 2002US-0362016P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 17-MAY-2002; 2002US-05015876.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 03-JUL-2002; 2002US-0393796P.  
PR 29-JUL-2002; 2002US-0399348P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 09-SEP-2002; 2002US-0408378P.  
PR 05-SEP-2002; 2002US-0409493P.  
PR 15-JAN-2003; 2003US-0440129P.  
PR 14-FEB-2003; 2003US-05004566.  
PR 20-FEB-2003; 2003US-05005028.  
PR 20-FEB-2003; 2003US-05005346.  
PR 20-FEB-2003; 2003US-05005476.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 16-SEP-2003; 2003US-00664767.  
PR 16-SEP-2003; 2003US-00665255.  
PR 23-SEP-2003; 2003US-00670011.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 26-JAN-2004; 2004US-00764957.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 23-APR-2004; 2004US-00831620.  
PR 30-APR-2004; 2004US-05013456.  
PR 11-MAY-2004; 2004US-00844076.  
PR 24-MAY-2004; 2004US-05016390.  
PR 09-JUN-2004; 2004US-00863973.  
PR 20-AUG-2004; 2004US-00922675.  
PR 16-SEP-2004; 2004US-00944611.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Richards I, Mcswiggen J;  
XX WPI; 2005-664178/68.  
XX  
XX  
XX New multifunctional siNA molecule comprising a structure having Formula  
XX MF-III, useful for creating a respiratory disease selected from asthma,  
XX COPD, and allergic rhinitis.  
XX  
XX Example 13; SEQ ID NO 1515; 266pp; English.  
XX  
XX The invention comprises short interfering nucleic acid (siNA) molecules  
XX which modulate vascular endothelial growth factor (VEGF) or VEGF receptor  
XX (VEGFR) gene expression. The siNA molecules of the invention are useful  
XX for treating respiratory diseases (e.g. asthma, COPD, and allergic  
XX rhinitis). The present nucleic acid represents a VEGF/VEGFR-specific  
XX siRNA sequence that was used in an example of the invention.  
XX  
XX Sequence 19 BP; 4 A; 7 C; 8 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred.No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 139 AGCGCCGACGACGAGA 155  
DB 2 AGCGCCGACGACGAGA 18  
RESULT 256  
AEF75485  
ID AEF75485 standard; RNA; 19 BP.  
XX  
XX AEF75485;  
AC  
XX  
XX 06-APR-2006 (first entry)  
DT

XX Human NOGO-A transcript target sequence/siRNA sense strand, SEQ:35.  
DE  
XX RNA interference; gene silencing; short interfering RNA; siRNA;  
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;  
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;  
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;  
KM CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;  
KM Huntingtons chorea; anticonvulsant; noctropic; dementia;  
KM Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0866;  
KM reticulon 4; RTN4; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2005261212-A1.  
PN  
XX  
XX 24-NOV-2005.  
PD  
XX  
XX 26-JUL-2002; 2002US-00206693.  
PF  
XX 11-FEB-2000; 2000US-0181797P.  
PR 09-FEB-2001; 2001US-00780533.  
PR 05-APR-2001; 2001US-00827395.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 03-APR-2002; 2002WO-US010512.  
PR 06-JUN-2002; 2002US-0386782P.  
XX  
XX (MCSW/) MCSWIGEN J A.  
PA  
XX  
XX Mcswigen JA;  
PI  
XX WPI; 2006-190836/20.  
DR  
XX  
XX New chemically modified double stranded short interfering nucleic acid  
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via  
PT RNA interference (RNAi), useful for modulating gene expression.  
XX  
XX Disclosure; SEQ ID NO 35; 171pp; English.  
PS  
XX  
XX The invention relates to chemically synthesized short interfering nucleic  
CC acids (siNAs) which downregulate expression of a NOGO receptor gene by  
CC RNA interference. The siNAs may or may not comprise ribonucleotides, can  
CC contain deoxyribonucleotides, can be chemically modified and may be  
CC double or single stranded. They further comprise sense and antisense  
CC regions, or alternatively are assembled from a sense oligonucleotide and  
CC an antisense oligonucleotide. Specifically, the siNAs include short  
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short  
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical  
CC compositions comprising an siNA targeted to a NOGO receptor mRNA. It  
CC further discloses siNAs targeted to a NOGO receptor gene, siNAs targeted  
CC to a NOGO gene itself, and expression vectors and host cells comprising  
CC an siNA of the invention. In particular, the invention discloses siRNAs  
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO  
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-  
CC AEF75902) targeted to the human NOGO-A (KIAA0866) gene of DBJ accession  
CC number AB020693. The siNAs are used to modulate expression of NOGO  
CC receptor or NOGO genes in cells, tissue explants or organisms (e.g., by  
CC ex vivo gene therapy), or in grafts and transplants for the treatment of  
CC a variety of neurodegenerative conditions such as central nervous system  
CC (CNS) injury (e.g., spinal cord injury or stroke), multiple sclerosis  
CC (MS), muscular dystrophy, chemotherapy-induced neuropathy, amyotrophic  
CC lateral sclerosis (ALS), ataxia, Parkinson's disease, Huntington's  
CC disease, dementia, Creutzfeldt-Jakob disease and especially Alzheimers  
CC disease. The siNAs may also be used in drug screening, diagnosis,  
CC therapeutic target identification and validation, genetic engineering,  
CC pharmacogenetics, studying gene function, and gene mapping (e.g., of  
CC single nucleotide polymorphisms). The present sequence represents the  
CC sense strand of a human NOGO-A-targeted double-stranded siRNA, which is  
CC identical to the NOGO-A transcript target sequence.  
XX  
XX  
XX Sequence 19 BP; 1 A; 13 C; 4 G; 0 T; 1 U; 0 Other;  
SQ

Query Match 0 9%; Score 15.4; DB 1; Length 19;  
Beat Local Similarity 88.2%; Pred. No. 2.1e+02;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 619 CCCCTCCAGCCCGGCT 635  
Db 1 CCCCGCAGCCCGGCU 17  
RESULT 257  
AEF75711/c  
ID AEF75711 standard; RNA; 19 BP.  
XX  
XX AC AEF75711;  
XX  
XX DT 06-APR-2006 (first entry)  
XX  
XX DE Human NOGO-A siRNA antisense strand, SEQ:261.  
XX  
XX RNA interference; gene silencing; short interfering RNA; siRNA;  
KM nervous system injury; spinal cord injury; neuroprotective; vulnery;  
KM cerebrovascular ischemia; cerebroprotective; multiple sclerosis;  
KM muscular dystrophy; muscular-gen.; neuropathy; motor neurone disease;  
KM CNS-gen.; ataxia; Parkinsons disease; antiparkinsonian;  
KM Huntingtons chorea; anticonvulsant; noctropic; dementia;  
KM Creutzfeldt Jakob disease; Alzheimers disease; NOGO-A; KIAA0866;  
KM reticulon 4; RTN4; ss.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2005261212-A1.  
PN  
XX  
XX 24-NOV-2005.  
PD  
XX  
XX 26-JUL-2002; 2002US-00206693.  
PF  
XX 11-FEB-2000; 2000US-0181797P.  
PR 09-FEB-2001; 2001US-00780533.  
PR 05-APR-2001; 2001US-00827395.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 03-APR-2002; 2002WO-US010512.  
PR 06-JUN-2002; 2002US-0386782P.  
XX  
XX (MCSW/) MCSWIGEN J A.  
PA  
XX  
XX Mcswigen JA;  
PI  
XX WPI; 2006-190836/20.  
DR  
XX  
XX New chemically modified double stranded short interfering nucleic acid  
PT (siRNA) molecule that directs cleavage of a NOGO receptor (NOGOR) RNA via  
PT RNA interference (RNAi), useful for modulating gene expression.  
XX  
XX Disclosure; SEQ ID NO 261; 171pp; English.  
PS  
XX  
XX The invention relates to chemically synthesized short interfering nucleic  
CC acids (siNAs) which downregulate expression of a NOGO receptor gene by  
CC RNA interference. The siNAs may or may not comprise ribonucleotides, can  
CC contain deoxyribonucleotides, can be chemically modified and may be  
CC double or single stranded. They further comprise sense and antisense  
CC regions, or alternatively are assembled from a sense oligonucleotide and  
CC an antisense oligonucleotide. Specifically, the siNAs include short  
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short  
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical  
CC compositions comprising an siNA targeted to a NOGO receptor mRNA. It  
CC further discloses siNAs targeted to a NOGO receptor gene, siNAs targeted  
CC to a NOGO gene itself, and expression vectors and host cells comprising  
CC an siNA of the invention. In particular, the invention discloses siRNAs  
CC (AEF75903-AEF76100 and AEF76101-AEF76112) targeted to the human NOGO  
CC receptor gene of GenBank accession number BC011787, and siRNAs (AEF75451-  
CC AEF75902) targeted to the human NOGO-A (KIAA0866) gene of DBJ accession  
CC number AB020693. The siNAs are used to modulate expression of NOGO



DT 05-JUN-1999 (first entry)  
XX  
XX Substance P receptor antisense oligonucleotide fragment.  
XX  
XX Antisense oligonucleotide; multiple target; antisense treatment;  
XX impaired respiration; inflammation; lung disease;  
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
XX acute asthma; allergy; asthma; impeded respiration;  
XX respiratory distress syndrome; pain; cystic fibrosis;  
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
XX prostate cancer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Myce JW;  
XX  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX Disclosure; Page 59; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AAK52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
XX -end and the juxta-section between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AAK55272-74. These multiple target oligonucleotides  
XX (specifically AAK55180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 0.8%; Score 15; DB 1; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAK54241;  
XX  
XX 05-JUN-1999 (first entry)  
DT  
XX Substance P receptor antisense oligonucleotide fragment.  
DE  
XX Antisense oligonucleotide; multiple target; antisense treatment;  
XX impaired respiration; inflammation; lung disease;  
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
XX acute asthma; allergy; asthma; impeded respiration;  
XX respiratory distress syndrome; pain; cystic fibrosis;  
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
XX prostate cancer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Myce JW;  
XX  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX Disclosure; Page 59; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AAK52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
XX -end and the juxta-section between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AAK55272-74. These multiple target oligonucleotides  
XX (specifically AAK55180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 0.8%; Score 15; DB 1; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAA33685 standard; DNA; 15 BP.  
XX AAA33685;  
AC 28-JUL-2000 (first entry)  
XX  
XX  
XX Low adenosine antisense oligonucleotide SEQ ID NO:1374.  
DB  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYCE JW;  
PI  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Claim 18; Page 436; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytosolic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinoma, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to  
CC AAA3392) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
XX Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1236 CCAGACCCAGGCGAG 1250

DB 15 CCAGACCCAGGCGAG 1  
|||||||  
RESULT 263  
AAA33684/C  
ID AAA33684 standard; DNA; 15 BP.  
XX  
XX AAA33684;  
AC 28-JUL-2000 (first entry)  
XX  
XX  
XX Low adenosine antisense oligonucleotide SEQ ID NO:1373.  
DB  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYCE JW;  
PI  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Claim 18; Page 436; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytosolic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinoma, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to  
CC AAA3392) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;  
SQ



Query Match 0.84; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 716 CAACCAAGAGACCA 730  
15 CAACCAAGAGACCA 1  
Db 15 CAACCAAGAGACCA 1  
RESULT 264  
AAFI9807/C  
ID AAFI9807 standard; DNA; 15 BP.  
XX AAFI9807;  
XX 14-MAR-2001 (first entry)  
XX Human substance P receptor polynucleotide fragment #1374.  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antiaesthetic; analgesic; hypotensive; cyostatic;  
XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.  
XX Homo sapiens.  
XX WO200062736-A2.  
XX 26-OCT-2000.  
XX 24-MAR-2000; 2000WO-US008020.  
XX 06-APR-1999; 99US-0127958P.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX (NYCE/) NYCE J W.  
XX NYCE JW;  
XX WPI; 2000-679539/66.  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.  
XX Claim 14; Page 245; 1592pp; English.  
XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (I) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiaesthetic, hypotensive and cyostatic activities.  
XX The antisense oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasoactive peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisense oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAFI8434 to AAFI21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention  
XX  
XX Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.84; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1236 CCAGACCCAGGCGAG 1250  
15 CCAGACCCAGGCGAG 1  
Db 15 CCAGACCCAGGCGAG 1  
RESULT 265  
AAFI9806/C  
ID AAFI9806 standard; DNA; 15 BP.  
XX AAFI9806;  
XX 14-MAR-2001 (first entry)  
XX Human substance P receptor polynucleotide fragment #1373.  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antiaesthetic; analgesic; hypotensive; cyostatic;  
XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.  
XX Homo sapiens.  
XX WO200062736-A2.  
XX 26-OCT-2000.  
XX 24-MAR-2000; 2000WO-US008020.  
XX 06-APR-1999; 99US-0127958P.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX (NYCE/) NYCE J W.  
XX NYCE JW;  
XX WPI; 2000-679539/66.  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.  
XX Claim 14; Page 245; 1592pp; English.  
XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (I) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiaesthetic, hypotensive and cyostatic activities.  
XX The antisense oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with

lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral factors, vasoactive peptides and transmitters, defensins, growth factors and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 15 BP: 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CAACCAAGAGACCA 730  
DB 15 CAACCAAGAGACCA 1

RESULT 266  
ABZ95501/c  
ID ABZ95501 standard; DNA; 15 BP.

AC ABZ95501;  
DT 17-OCT-2003 (first entry)

DE Human substance P receptor antisense fragment no.1365.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.

PS Disclosure; SEQ ID NO 10743; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an  
XX antiinflammatory steroid in a subject, for reducing or depleting levels  
XX of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
XX receptor, producing bronchodilation, increasing levels of adenosine or  
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 15 BP: 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 CCAGCCCGAGGCGG 1250  
DB 15 CCAGCCCGAGGCGG 1

RESULT 267  
ABZ95500/c  
ID ABZ95500 standard; DNA; 15 BP.

AC ABZ95500;  
DT 17-OCT-2003 (first entry)

DE Human substance P receptor antisense fragment no.1364.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.

PS Disclosure; SEQ ID NO 10742; 872pp; English.

XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cycostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 716 CAACCAAGAGACCA 730  
Db 15 CAACCAAGAGACCA 1

RESULT 268  
ABD19639/c  
ID ABD19639 standard; DNA; 15 BP.

XX  
XX ABD19639;

XX  
XX 29-JUL-2004 (first entry)

XX  
XX Human substance P receptor DNA fragment 1364.

XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ds.

XX  
XX Homo sapiens.

XX  
XX WO200285309-A2.

XX  
XX 31-OCT-2002.

XX  
XX 23-APR-2002; 2002WO-US013143.

XX  
XX 24-APR-2001; 2001US-0286036P.

XX  
XX (EBIG-) EPIGENESIS PHARM INC.

XX  
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S,  
XX WPI; 2003-093058/08.

XX  
XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nuclear acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX  
XX Claim 15; SEQ ID NO 10742; 763pp; English.

XX  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX  
XX Sequence 15 BP; 0 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 716 CAACCAAGAGACCA 730  
Db 15 CAACCAAGAGACCA 1

RESULT 269  
ABD19640/c  
ID ABD19640 standard; DNA; 15 BP.

XX  
XX ABD19640;

XX  
XX 29-JUL-2004 (first entry)

XX  
XX Human substance P receptor DNA fragment 1365.

XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ds.

XX  
XX Homo sapiens.

XX  
XX WO200285309-A2.

XX  
XX 31-OCT-2002.

XX  
XX 23-APR-2002; 2002WO-US013143.

PR 24-APR-2001; 2001US-0286036P.  
 XX (EPiG-) EPIGENESIS PHARM INC.  
 PA NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 PS  
 PS Claim 15; SEQ ID NO 10743; 763bp; English.  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or surfactant hypoproduction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 CC  
 XX  
 XX Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;  
 Oy 1236 CCAGACCCAGGGCAG 1250  
 DB 15 CCAGACCCAGGGCAG 1  
 RESULT 270  
 ABR03403  
 ID ABR03403 standard; RNA; 17 BP.  
 AC ABR03403;  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 XX  
 XX Human CD20 G-cleaver #18.  
 DE  
 XX  
 XX Human; ss; antisense therapy; cytostatic; anti-inflammatory; haemostatic;  
 KM cerebroprotective; neuroprotective; antiparkinsonian;  
 KM muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;  
 KM DNazyme; G-cleaver; amberyzyme; zinyzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury; multiple sclerosis;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 OS  
 PN WO200159103-A2.  
 XX  
 XX 16-AUG-2001.  
 PD  
 PD  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 XX 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWITGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 DR  
 XX  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 PT  
 XX  
 XX Claim 30; Page 152; 200pp; English.  
 PS  
 PS The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NCOG). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an NCH motif, an endolytic nucleic acid cleaving a NCH motif or  
 CC an amberyzyme (cleaving RNA with an NGN triple), a zinyzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NCOG-  
 CC targeting nucleic acid is used to cleave RNA of the NCOG gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NCOG activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NCOG. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NCOG-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NCOG expression. The present  
 CC sequence is a G-cleaver molecule of the invention  
 CC  
 XX  
 XX Sequence 17 BP; 2 A; 2 C; 6 G; 0 T; 7 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 15; DB 1; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;

```
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 802 ATCTGTGACTGTG 816
   |||:|||||:|
Db 1 AUCUGUGACUGUG 15

RESULT 271
AAA54501/c
ID AAA54501 standard; DNA; 17 BP.
XX
AC AAA54501;
XX
DT 11-APR-2001 (first entry)
XX
DE Degenerate primer for amplifying fructan exohydrolase.
XX
KM Fructan exohydrolase; FEH; transgenic plant; recombination; transgene;
KM gene expression; detergent; detergent additive; oral care composition;
KM primer; ss.
XX
OS Synthetic.
XX
PN WO20068402-A1.
XX
PD 16-NOV-2000.
XX
PF 08-MAY-2000; 2000WO-EP004226.
XX
PR 06-MAY-1999; 99BE-00000329.
XX
PA (LEUV-) LEUVEN RES & DEV.
XX
PI Van Den Ende W, Van Laere A, De Roover J, Michiels A;
XX
DR WPI; 2001-007401/01.
XX
PT Novel DNA molecules encoding enzymes having fructan exohydrolase activity
PT for use in transgenic plant production, dental care compositions, and in
PT detergents.
XX
XX Example 1; Page 15; 45pp; English.
XX
PS Transgenic plants such as Cichorium intybus, Cynara scolymus, Helianthus
CC tuberosus, Scorzonera hispanica, Oryza sativa, Zea mays, Triticum
CC aestivum, Triticum durum, Hordeum vulgare, Secale cereale, Avena sativa,
CC Sorghum vulgare, Phleum pratense, Lolium temulentum, Dactylis glomerata,
CC Pennisetum americanum, Allium cepa, Agave americanum, Agave azul
CC tegulana, Sorghum bicolor and Panicum mllaceum, transformed with a vector
CC encoding a fructan exohydrolase (FEH) enzyme are useful for the
CC recombinant production of FEH or other polypeptides having FEH activity.
CC The FEH polypeptides produced are useful in detergents or as a detergent
CC additive and in oral care compositions. This degenerate primer was
CC constructed based on peptide fragments of FEH and was then used to
CC amplify the FEH coding sequence
XX
SQ Sequence 17 BP; 2 A; 4 C; 2 G; 4 T; 0 U; 5 Other;
XX
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.8e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1208 GGCTGAAATGAATCC 1224
   |||:|||||:|
Db 17 GGYTGAAATGTAAMCC 1

RESULT 272
ABN06976
ID ABN06976 standard; DNA; 17 BP.
XX
AC ABN06976;
XX
```

```
DT 25-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6968.
XX
KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 6968; 214pp; English.
XX
PS The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.8%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 28 CAGTGCATCCAGAG 42  
 |||||  
 DB 1 CAGTGCATCCAGAG 15

RESULT 273

ABN06974  
 ID ABN06974 standard; DNA; 17 BP.

AC ABN06974;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6966.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

OS WO200192524-A2.

PN 06-DEC-2001.

PD 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) ABOMICA INC.

PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

PI WPI; 2002-179446/23.

DR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 XX or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

PS Disclosure; SEQ ID NO 6966; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and vaccine production. The hGDMLP-1  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WMO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence

SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAG 42  
 |||||  
 DB 3 CAGTGCATCCAGAG 17

RESULT 274

ABN06975  
 ID ABN06975 standard; DNA; 17 BP.

AC ABN06975;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6967.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

OS WO200192524-A2.

PN 06-DEC-2001.

PD 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) ABOMICA INC.

PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

PI WPI; 2002-179446/23.

DR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 XX or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

PS Disclosure; SEQ ID NO 6967; 214pp; English.

CC expressing the protein. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequence](http://wipo.int/pub/published_pct_sequence)  
XX  
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 0; Gaps 0;  
QY 28 CAGTGCATCCAGAG 42  
DB 2 CAGTGCATCCAGAG 16  
ACNT70065 standard; DNA; 17 BP.  
XX  
AC ACNT70065;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMLP-1 probe SEQ ID NO:6967.  
XX  
DE Human; ss; probe: myosin-like protein-1; hGDMLP-1;  
KM hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KM skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (JYX/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.

XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
DR  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
XX Disclosure; SEQ ID NO 6967; 0pp; English.  
XX  
PS The invention relates to a novel polypeptide (I) comprising a sequence  
CC (SI) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (SI), 95% deviation from (SI) which are conservative substitutions, and  
CC 65% identity to (SI). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 0; Gaps 0;  
QY 28 CAGTGCATCCAGAG 42  
DB 2 CAGTGCATCCAGAG 16  
ACNT70066 standard; DNA; 17 BP.  
XX  
AC ACNT70066;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMLP-1 probe SEQ ID NO:6968.  
XX  
DE Human; ss; probe: myosin-like protein-1; hGDMLP-1;  
KM hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KM skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.

XX (GUYY/) GU Y.  
PA (JITY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
XX  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 6966; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;  
QY 28 CAGTGCATCCAGAG 42  
Db 1 CAGTGCATCCAGAG 15  
RESULT 277  
ACN70064  
ID ACN70064 standard; DNA; 17 BP.  
XX  
AC ACN70064;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMPL-1 probe SEQ ID NO:6966.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
XX skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUYY/) GU Y.  
PA (JITY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
XX  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 6966; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;  
QY 28 CAGTGCATCCAGAG 42  
Db 3 CAGTGCATCCAGAG 17  
RESULT 278  
AAA99603  
ID AAA99603 standard; DNA; 18 BP.  
XX  
AC AAA99603;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Rat D4 receptor oligonucleotide primer ORD-403.  
XX  
KW Rat; D4 dopamine receptor; cardiovascular system; retinal tissue;  
KW vasoregulator; PCR primer; ss.  
XX  
OS Rattus sp.  
XX  
PN US6121015-A.  
PD 19-SEP-2000.  
XX  
PF 07-JUN-1995; 95US-00475742.  
XX  
PR 28-JAN-1993; 93US-00014013.



```
PR 16-JUN-1994; 94US-00261293.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Todd RD, O'malley KL;
XX
XX WPI; 2000-655527/63.
XX
XX Screening for compounds that selectively bind to a rat D4 dopamine
XX receptor (DDR), useful for identifying dopamine (ant)agonists, comprises
XX exposing cells transfected with a nucleic acid encoding the DDR to
XX candidate compounds.
XX
XX Disclosure; Col 6; 29pp; English.
XX
XX The present sequence is an oligonucleotide which was used to screen a
XX lambda Dash rat spleen genomic library for D2-like receptor sequences.
XX The primer is derived from consensus sequences in rat D2 and D3 genes.
XX This method was used to isolate the rat D4 dopamine receptor gene. A cDNA
XX encoding the rat D4 dopamine receptor was expressed in transfected
XX mammalian cells and shown to preferentially bind dopamine antagonists
XX such as clozapine. The cDNA is useful for screening drugs which
XX specifically bind to the receptor and have selective effects on the
XX cardiovascular and retinal tissues through interactions with the
XX receptor. Such compounds may act as vasoregulators or may have ionotropic
XX effects. The D4 receptor protein may be used for the production of
XX polyclonal or monoclonal antibodies which recognise the D4 receptor
XX sequence but do not recognise other dopaminergic receptors. The
XX antibodies may be used in immunocytochemical studies and for
XX identification and isolation via flow sorting of D4 expressing cell types
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 988 TGCTGGCTGCCCTTC 1002
XX 1 TGCTGGCTGCCCTTC 15
XX
XX RESULT 279
XX ABX12223
XX ID ABX12223 standard; DNA; 18 BP.
XX
XX AC ABX12223;
XX
XX DT 16-MAY-2003 (first entry)
XX
XX DE Rat dopamine D2 and D3 receptors transmembrane domain VI primer. ORD-403.
XX
XX KM Rat; ss; primer; dopamine; D4; D4 receptor; D4 dopamine receptor probe;
XX clozapine; PCR; transmembrane domain VI.
XX
XX OS Rattus norvegicus.
XX
XX US6486310-B1.
XX
XX PD 26-NOV-2002.
XX
XX PF 16-JUN-1994; 94US-00261293.
XX
XX PR 28-JAN-1993; 93US-00014013.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI O'malley KL, Todd RD;
XX
XX WPI; 2003-310438/30.
XX
XX Novel nucleic acid molecule encoding rat D4 dopamine receptor, useful as
XX a probe for related D4 dopamine receptors.
```

```
XX
XX Example 1; Col 6; 33pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding rat
XX D4 dopamine receptor. The rat D4 dopamine receptor binds dopamine
XX antagonists such as clozapine. The nucleic acid is useful as a probe for
XX related D4 dopamine receptors. The nucleic acid when expressed in cell
XX lines, is useful as an in vitro screen for drugs which specifically bind
XX to the receptor. Antibodies to the protein are useful in
XX immunocytochemical studies, identification and isolation via flow sorting
XX of D4 expressing cell types and in blocking or modifying the effects of
XX D4 agonists and/or antagonists. The present sequence represents the rat
XX dopamine D2 and D3 receptors transmembrane domain VI primer. ORD-403,
XX used to isolate the dopamine D4 receptor from a lambda Dash rat spleen
XX genomic library
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 988 TGCTGGCTGCCCTTC 1002
XX 1 TGCTGGCTGCCCTTC 15
XX
XX RESULT 280
XX ADF29051
XX ID ADF29051 standard; DNA; 18 BP.
XX
XX AC ADF29051;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Rat dopamine D4 receptor related primer seq id 5.
XX
XX KM cardiovascular; ophthalmological; rat; D4 dopamine receptor;
XX cardiovascular tissue; retinal tissue; neuronal morphology disorder;
XX neuronal connection disorder; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX US2003118506-A1.
XX
XX PD 26-JUN-2003.
XX
XX PF 11-SEP-2002; 2002US-00241313.
XX
XX PR 28-JAN-1993; 93US-00014013.
XX
XX PR 16-JUN-1994; 94US-00261293.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI O'malley KL, Todd RD;
XX
XX WPI; 2004-009074/01.
XX
XX A new nucleic acid encoding a rat D4 dopamine receptor is useful to treat
XX disorders of the cardiovascular or retinal tissue or prevent or treat
XX disorders of neuronal morphology or connections.
XX
XX Example 1; SEQ ID NO 5; 30pp; English.
XX
XX The invention describes an isolated nucleic acid encoding a rat D4
XX dopamine receptor. The invention is useful to treat disorders of the
XX cardiovascular or retinal tissue or prevent or treat disorders of
XX neuronal morphology or connections. This sequence represents a primer
XX used to isolate DNA encoding the rat dopamine D4 receptor.
XX
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 15; DB 1; Length 18;
```

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TGCTGGCTGCGCTTC 1002  
|||||  
Db 1 TGCTGGCTGCGCTTC 15

## RESULT 281

ADS41404/C  
ID ADS41404 standard; DNA; 18 BP.

AC ADS41404;

DT 16-DEC-2004 (first entry)

DE Human autoimmune disease-related PCR primer - SEQ ID 6618.

XX single nucleotide polymorphism detection; SNP detection;

XX rheumatoid arthritis; type 1 diabetes; multiple sclerosis;

KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;

KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;

KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;

KW primary systemic vasculitis; PCR; primer; ss.

XX Homo sapiens.

OS WO2004083403-A2.

XX 30-SEP-2004.

XX 18-MAR-2004; 2004WO-US008461.

XX 18-MAR-2003; 2003US-0455444P.

XX 25-APR-2003; 2003US-0465241P.

XX (APPL-) APPLERA CORP.

XX Cargill M, Begovich AB, Alexander HC;

XX WPI; 2004-728480/71.

XX Claim 21; SEQ ID NO 6618; 123pp; English.

XX The invention comprises amino acid and coding sequences containing

XX genetic polymorphisms associated with an altered risk of developing an

XX autoimmune disease (e.g. rheumatoid arthritis). The invention further

XX comprises a method of identifying an individual that has an altered risk

XX of developing an autoimmune disease, comprising detecting a single

XX nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA

XX and protein sequences of the invention are useful for diagnosing and

XX creating autoimmune diseases, such as: rheumatoid arthritis, type 1

XX diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory

XX bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious

XX anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, The

XX present DNA sequence represents a human autoimmune disease-related PCR

XX primer of the invention. NOTE: The present sequence is not shown in the

XX specification, but has been retrieved from the WIPO website.

XX Sequence 18 BP; 5 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Db 15 TTCTGGCTTCCTGC 1

## RESULT 282

ADW71322

ID ADW71322 standard; DNA; 18 BP.

AC ADW71322;

DT 07-APR-2005 (first entry)

DE Human p53 target DNA 3 fragment.

XX High throughput screening; analyte detection; p53; ds.

XX Homo sapiens.

OS US2005014246-A1.

XX 20-JAN-2005.

XX 26-MAY-2004; 2004US-00854018.

XX 14-JUL-2003; 2003JP-00196178.

XX (HITA ) HITACHI LTD.

XX Kohara Y, Okano K, Noda H;

XX WPI; 2005-111253/12.

XX High sample throughput device for chemical reaction and analysis

XX comprises a channel for receiving solution, a structure in channel having

XX a molecule immobilized on interior surface of channel.

XX Disclosure; SEQ ID NO 13; 20pp; English.

XX The present invention relates to a method of increasing the reaction

XX efficiency and to reduce the reaction time in the chemical reaction where

XX molecules immobilized on the solid phase are reacted with the molecules

XX in the solution or in the chemical analysis where molecules immobilized

XX on the solid phase capture the molecules in the solution by chemically

XX reacting with such molecules and the captured molecules are measured. The

XX invention is also helpful to improve the throughput to increase thereby

XX increase the reaction efficiency when the sample is the one at a low

XX concentration. The present sequence is human p53 target DNA fragment.

XX This sequence is used in DNA analysis using the DNA measurement device

XX 321.

XX Sequence 18 BP; 0 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 15; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 TTCTGGCTGCGCTTC 1158  
|||||

Db 2 TTCTGGCTGCGCTTC 16

RESULT 283

ADW71312/C

ID ADW71312 standard; DNA; 18 BP.

AC ADW71312;

DT 07-APR-2005 (first entry)

DE Human p53 exon specific DNA probe 3.

XX High throughput screening; analyte detection; p53; probe; ss.

XX Homo sapiens.

XX US2005014246-A1.  
 PN  
 XX  
 PD 20-JAN-2005.  
 XX  
 PF 26-MAY-2004; 2004US-00854018.  
 XX  
 PR 14-JUL-2003; 2003JP-00196178.  
 XX  
 PA (HITA ) HITACHI LTD.  
 PI Kohara Y, Okano K, Noda H;  
 XX  
 DR WPI; 2005-111253/12.  
 XX  
 PT High sample throughput device for chemical reaction and analysis  
 PT comprises a channel for receiving solution, a structure in channel having  
 PT a molecule immobilized on interior surface of channel.  
 PS  
 XX Disclosure; SEQ ID NO 3; 20pp; English.  
 CC  
 CC The present invention relates to a method of increasing the reaction  
 CC efficiency and to reduce the reaction time in the chemical reaction where  
 CC molecules immobilized on the solid phase are reacted with the molecules  
 CC in the solution or in the chemical analysis where molecules immobilized  
 CC on the solid phase capture the molecules in the solution by chemically  
 CC reacting with such molecules and the captured molecules are measured. The  
 CC invention is also helpful to improve the throughput to increase thereby  
 CC increase the reaction efficiency when the sample is the one at a low  
 CC concentration. The present sequence is human p53 exon specific DNA probe.  
 CC This sequence is used in DNA analysis using the DNA measurement device  
 CC 321.  
 XX  
 SQ Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2,1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1144 TTCGCTCTGGGCTTC 1158  
 Db 17 TTCGCTCTGGGCTTC 3  
 RESULT 284  
 AAQ36431/c  
 ID AAQ36431 standard; DNA; 18 BP.  
 XX  
 AC AAQ36431;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-MAR-1993 (first entry)  
 XX  
 DE GRP-R primer (EXT 3).  
 XX  
 KW Gastrin releasing peptide; GRP; bombesin; neuromedin B; NMB; ranatensin;  
 KW RBP; bombesin-like peptide; RBP; R2BP; R2BP; receptor; agonist;  
 KW antagonist; ligand; antibody; cancer; se.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9216623-A2.  
 XX  
 PD 01-OCT-1992.  
 XX  
 PF 13-MAR-1992; 92WO-US002091.  
 XX  
 PR 15-MAR-1991; 91US-00670603.  
 PR 03-OCT-1991; 91US-00771332.  
 XX  
 PA (BERL-) BERLEX LAB INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX

PI Batley JF, Corjay MH, Fathi Z, Feldman RI, Harkin RV;  
 PI Slatery TK, Wada B, Wu JM;  
 XX  
 DR WPI; 1992-349208/42.  
 XX  
 PT Receptors for bombesin-like peptide(s) and their DNA - useful for  
 PT screening for agonists and antagonists of the receptor ligands, also for  
 PT treating or diagnosing cancer.  
 XX  
 PS Example 12; Page 85-91; 173pp; English.  
 XX  
 CC The primers of AAQ36431-32 were used in the identification of cDNA clone  
 CC encoding the Swiss 3T3 GRP Receptor. EXT 3 (AAQ36431) was used as a gene-  
 CC specific primer for reverse transcription of Swiss 3T3 mRNA, and EXT 2  
 CC (AAQ36432) was used as a gene specific primer for Taq DNA polymerase  
 CC catalysed PCR. The DNA sequences encoding mouse R1BP; human R1BP; rat  
 CC R2BP; human R2BP and human R3BP are given in AAQ29158-62 respectively.  
 CC The receptor gene and encoded polypeptide are used for screening for  
 CC agonists and antagonists of the receptor ligands, for producing  
 CC diagnostic or therapeutic reagents, and for producing antibodies. Hosts  
 CC suffering from abnormal receptor function, e.g. proliferative cell  
 CC conditions such as cancers, may be treated. The mouse GRP receptor was  
 CC isolated from Swiss 3T3 fibroblasts and sequenced. The sequence was used  
 CC to design oligonucleotide probes to isolate DNA encoding mouse GRP  
 CC receptor from a Swiss 3T3 cDNA library. This DNA was then used as a probe  
 CC to isolate rat NMB receptor, human GRP receptor, human NMB receptor and  
 CC human R3BP (incompletely characterised homologous putative receptor) from  
 CC DNA libraries. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 5 A; 4 C; 9 G; 0 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2,3e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 982 GCCATCTGCTGGTGGCC 999  
 Db 18 GCCCTCTCTGGTGGCC 1  
 RESULT 285  
 AAV34526/c  
 ID AAV34526 standard; DNA; 18 BP.  
 XX  
 AC AAV34526;  
 XX  
 DT 20-AUG-1998 (first entry)  
 XX  
 DE Chemokine receptor CXCR4 amplifying RT-PCR primer 2.  
 XX  
 KW Chemokine receptor; gp120; fusion protein; HIV; screening; AIDS;  
 KW CD4 binding site; RT-PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9815569-A1.  
 XX  
 PD 16-APR-1998.  
 XX  
 PF 08-OCT-1997; 97WO-US018397.  
 XX  
 PR 09-OCT-1996; 96US-0027931P.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (LEUK-) LEUKOSITE INC.  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX  
 PI Sodroski J, Newman W, Wu L, Gerard N, Gerard C;  
 XX  
 DR WPI; 1998-240778/21.  
 XX  
 PT Derivatives of gp120 containing modified chemokine receptor binding site

PT - and complexes with soluble CD40, for inhibiting infectivity of human  
PT immune deficiency virus and to screen for inhibitors.  
XX  
PS Example; Page 53; 92pp; English.  
XX  
CC This primer is used for the RT-PCR amplification of a chemokine receptor  
CC CXCR4. The invention provides gp120 derivative having a conformational,  
CC discontinuous chemokine receptor binding site defined by amino acids  
CC residues present in the gp120 constant regions C2, C3 and C4, and the  
CC variable region V3, and its conformation is similar to that of the  
CC receptor binding site of wild-type gp120 complexed by CD4. Exposure of  
CC the chemokine receptor binding site is increased by having at least part  
CC of a variable or constant region of wild-type gp120 removed. A stabilised  
CC complex of gp120 CD4 binding site with a soluble CD4 molecule is used to  
CC inhibit infectivity of human immune deficiency virus (HIV). Labelled  
CC gp120 derivatives are also used to screen for inhibitors of HIV  
CC infectivity. The gp120 derivatives are used for diagnosing susceptibility  
CC to HIV infection from increased levels of the chemokine receptors (at the  
CC protein or nucleic acid levels). Transgenic animals expressing CD4 and  
CC chemokine receptor are used as models for studying development of AIDS or  
CC effect/safety of therapeutic agents  
XX  
SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 988 TGCTGCTGCTGCTTCCAC 1005  
DB 18 TGCTGCTGCTGCTTCCAC 1  
RESULT 286  
AAV49658/C  
ID AAV49658 standard; DNA; 18 BP.  
XX  
AC AAV49658;  
XX  
DT 23-OCT-1998 (first entry)  
XX  
DE Human SRCR protein PCR primer 41nrl.  
XX  
XX Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;  
KM nervous system; medullo-blastoma; glioma; breast; detection;  
KW autoantibody; PCR primer; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO9830687-A2.  
XX  
XX 16-JUL-1998.  
XX  
XX PD 09-JAN-1998; 98WO-DE000096.  
XX  
XX PR 09-JAN-1997; 97DE-01000519.  
XX  
XX PR 18-JUL-1997; 97DE-01030997.  
XX  
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
XX PI Mollenhauer J, Pousetka A;  
XX  
XX WPI; 1998-399136/34.  
XX  
XX proteins containing scavenger receptor, cysteine rich domain - useful for  
XX diagnosis and treatment of tumours.  
XX  
XX Example 1; Page 8; 54pp; German.  
XX  
XX AAV49657-V49660 are PCR primers used in the amplification of a gene which  
XX encodes a human protein which contains a SRCR (scavenger receptor,  
XX cysteine-rich) domain. The gene and encoded protein can be used to

CC diagnose or treat tumours, particularly of the nervous system (medullo-  
CC blastoma or glioma) or breast. The DNA sequence and probes derived from  
CC it, are used to identify genes that express SRCR-domain containing  
CC proteins, to determine the form in which these proteins exist and to  
CC assess the significance of individual forms on cellular properties. The  
CC protein can be used to detect the presence of autoantibodies and  
CC antibodies which regulate its expression  
XX  
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1263 CAGCGCTGAGACCCAC 1280  
DB 18 CAGCTGCTGAGACCCAC 1  
RESULT 287  
AAZ4901/C  
ID AAZ4901 standard; DNA; 18 BP.  
XX  
AC AAZ4901;  
XX  
DT 26-JAN-2000 (first entry)  
XX  
DE Human CD40 phosphorocholate antisense oligonucleotide SEQ ID NO:50.  
XX  
XX Identification; genetic target; gene modulation; human; probe;  
KM antisense oligonucleotide; phosphorocholate; PCR primer;  
KW nucleotide sequence-based technology; antisense drug discovery;  
XX target validation; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO9953101-A1.  
XX  
XX PD 21-OCT-1999.  
XX  
XX PF 13-APR-1999; 99WO-US008268.  
XX  
XX PR 13-APR-1998; 98US-0081483P.  
XX  
XX PR 28-APR-1998; 98US-00067638.  
XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX  
XX XX Cowser LM, Baker BF, Mcneil J, Freiler SM, Sasamor HM, Brooks DG;  
PI Ohsai C, Wyatt JR, Borchers AH, Vickers TA;  
XX  
XX WPI; 1999-620446/53.  
XX  
XX PT Identifying compounds which modulate expression of nucleic acids, used to  
XX provide compounds having defined physical, chemical or bioactive  
XX properties, e.g. antisense activity.  
XX  
XX Example 8; Page 77; 264pp; English.  
XX  
XX A method has been developed of defining a set of compounds that modulate  
XX the expression of a target nucleic acid (tNA) sequence via binding of the  
XX compounds with the tNA sequence. The method comprises generating a  
XX library of virtual compounds in silico according to defined criteria, and  
XX evaluating in silico the binding of the virtual compounds with the tNA  
XX according to defined criteria. Also described are: (1) a method of  
XX defining a set of oligonucleotides (ONs) that modulate the expression of  
XX a tNA sequence via binding of the ONs with the tNA sequence comprising  
XX generating a library of virtual compounds in silico according to defined  
XX criteria, and evaluating in silico the binding of the virtual ONs with  
XX the tNA according to defined criteria; and (2) a method of defining a set  
XX of compounds that modulate the expression of a tNA sequence via binding  
XX of the compounds with the tNA. The methods can be used for the generation  
XX and identification of synthetic compounds having defined physical,

CC chemical or bioactive properties. Information gathered from assays of  
CC such compounds is used to identify nucleic acid sequences that are  
CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
CC antisense drug discovery and target validation. AA240852 to AA41220, and  
CC AA52701 to AA52706, represent sequences used in the exemplification of  
CC the present invention

XX  
SQ Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 TCAGCTTCTCTCCATG 1423  
Db 18 TCGGCTTCTTCTCCATG 1

RESULT 288  
AA247734/C  
ID AA247734 standard; DNA; 18 BP.  
XX  
XX AA247734;  
XX  
XX 02-MAR-2000 (first entry)  
XX  
DE Human CD40 antisense oligonucleotide SEQ ID NO:50.  
XX  
XX Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;  
XX expression; immune disease; inflammatory disease; immunomodulatory;  
XX anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;  
XX anticancer; immuno-suppressive; anti-psoriasis; allograft rejection;  
XX hyperproliferative disease; autoimmune disease; rheumatoid arthritis;  
XX inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX WO9957320-A1.  
XX PD 11-NOV-1999.  
XX  
XX 22-APR-1999; 99WO-US008765.  
XX PF  
XX 01-MAY-1998; 98US-00071433.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Bennett CF, Cowsett LM;  
XX WPI; 2000-062158/05.  
XX DR  
XX Antisense molecules directed against nucleic acid encoding human CD40,  
XX PT for treating e.g. immune, inflammatory or hyperproliferative diseases.  
XX PS  
XX Example 9; Page 44; 102pp; English.

XX  
XX AA247685 to AA247768 represent phosphorothioate antisense  
XX oligonucleotides targeted to human CD40, which can be used to inhibit the  
XX expression of human CD40. CD40 is involved in lymphocyte activation,  
XX tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or  
XX prevent immune-associated diseases (specifically guest vs. host disease,  
XX allograft rejection or autoimmune diseases); inflammation (specifically  
XX asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel  
XX disease or psoriasis) or hyperproliferation (specifically cancer and  
XX tumours). The antisense oligonucleotides are also useful as diagnostic  
XX and research reagents. AA247769 represents the human CD40 nucleotide  
XX sequence. AA247770 to AA247773 represent human CD40 forward and reverse  
XX PCR primers, and a human CD40 PCR probe, respectively. AA247773 to  
XX AA247775 represent other PCR primers and a probe used in the  
XX exemplification of the present invention

XX  
SQ Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 TCAGCTTCTCTCCATG 1423  
Db 18 TCGGCTTCTTCTCCATG 1

RESULT 289  
AA506638  
ID AA506638 standard; DNA; 18 BP.  
XX  
XX AA506638;  
XX  
XX 12-SEP-2001 (first entry)  
XX  
XX Human alpha1-antichymotrypsin PCR primer.  
XX  
XX Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;  
XX differential display of reverse transcribed mRNAs by PCR;  
XX testicular cancer; breast cancer; prostate cancer; endometrial cancer;  
XX asthma; hypopspadia; cryptorchism; allergy; hormone replacement therapy;  
XX HRT; endocrine system; alpha1-antichymotrypsin.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200134834-A2.  
XX FN  
XX 17-MAY-2001.  
XX PD  
XX 10-NOV-2000; 2000WO-DK00628.  
XX PF  
XX 11-NOV-1999; 99DK-00001626.  
XX PR  
XX (RIGS-) RIGSHOSPITALLET.  
XX PA  
XX Leffers H, Jorgensen M, Skakkebaek NE;  
XX WPI; 2001-335941/35.  
XX DR  
XX Evaluating a cellular response to an environmental compound, for use in  
XX PT toxicological analysis, involves determining or comparing the expression  
XX PT levels of at least one endogenous gene.  
XX PF  
XX Example 2; Page 25; 77pp; English.

XX  
XX The sequence represents a PCR primer from alpha1-antichymotrypsin used in  
XX CC a DDRT-PCR experiment, demonstrating the method of the invention. The  
XX CC method relates to evaluating a cellular response to an environmental  
XX CC compound, comprising determining or comparing the expression levels of at  
XX CC least one endogenous gene e.g by differential display of reverse  
XX CC transcribed mRNAs by PCR (DDRT-PCR). The method can be adapted to  
XX CC identify compounds that act on the level of endogenous gene expression  
XX CC through activating nuclear receptors. The method is useful in  
XX CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.  
XX CC testicular, breast, prostate and endometrium), asthma, hypopspadia,  
XX CC cryptorchism and/or allergy, and for evaluating the efficiency of a  
XX CC treatment for hormonal deficiency or hormonal replacement therapy, in a  
XX CC human such as a post-menopausal female. The method is also useful for  
XX CC identifying environmental chemicals or pharmaceutical compositions that  
XX CC interact with endocrine systems, and for detecting chemicals that pose a  
XX CC health threat. Expression levels of endogenous genes are determined  
XX CC rapidly using a sensitive technique, and the expression of any gene can  
XX CC be monitored. The assays are far more informative than the currently used  
XX CC assays, and significantly reduces the number of animals required for the  
XX CC testing, as it is expected that essentially all the animals in a test  
XX CC group will respond to the compound

XX  
SQ Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 105 CCCCTGTCGCTTTAG 122  
|||  
1 CCCCTTTCTGCTTAG 18

Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1335 CACACCTGTCCTTGA 1352  
|||  
18 CACGCTCTGTCCTGA 1

RESULT 290  
AAF6209/c  
ID AAF6209 standard; DNA; 18 BP.

AC AAF6209;

DT 05-JUN-2001 (first entry)

DE Human/mouse NTRK3 RT-PCR primer, NTRK3human/mou-R.

XX Human; mouse; NTRK3; TRKC; neurotrophin-3 receptor; NTRK3-K14;  
KW transgenic mouse; human chromosome 15q24-25; anxiety disorder;  
KW panic disorder; noradrenergic neuron proliferation; agoraphobia;  
KW social phobia; depression; bipolar disorder; eating disorder; anorexia;  
KW bulimia; obesity; substance abuse; drug abuse; expression analysis;  
KW reverse transcription-PCR; RT-PCR primer; ss.

OS Homo sapiens.

OS Mus sp.

XX WO200106848-A1.

PD 01-FEB-2001.

XX 21-JUL-2000; 2000WO-ES000267.

XX 23-JUL-1999; 99ES-00001674.

XX (PALI/) ESTIVILL PALLIJA X.

PI Estiwill PalliJa X, Gratacos Mayora M, Pujana Genestar MA;

PI Fillat Fons C, Dierssen Sotos M;

DR WPI; 2001-182688/18.

PT Transgenic mice overexpressing the neurotrophin-3 receptor, useful e.g.  
PT for studying and monitoring anxiety, depression and related disorders.

XX Example; Page 15; 38pp; Spanish.

XX The invention relates to transgenic mice which express the human  
CC neurotrophin-3 receptor (NTRK3). The transgenic mice designated TgNTRK3  
CC overexpress the wild-type NTRK3 (TRKC) gene, while those designated  
CC TgNTRK3-K14 overexpress a form of NTRK3 which has a 14 amino acid  
CC residue insert in the kinase domain. Both forms of the NTRK3 gene are  
CC under the control of the PDGF (platelet-derived growth factor) promoter.  
CC The NTRK3 gene is located in the region of human chromosome 15q24-25  
CC which is duplicated in patients with anxiety disorders, and is the most  
CC likely candidate for association with these disorders. Overexpression of  
CC NTRK3 has a trophic and proliferative effect on noradrenergic neurons,  
CC increasing the response of the noradrenergic system. The transgenic mice  
CC are used as models for studying the physiopathology of anxiety disorders,  
CC panic disorder, agoraphobia, social or simple phobias, major depression,  
CC bipolar disorder, eating disorders (e.g., drug addiction). They may also be  
CC of obesity), and substance abuse (e.g., drug addiction). They may also be  
CC used for identifying, monitoring and studying phenotypes of these  
CC disorders, particularly during treatment; and for monitoring behavioural,  
CC pharmaceutical or gene therapy-based treatments for these conditions.  
CC Sequences AAF6208-AAF6209 represent NTRK3 reverse transcription-PCR  
CC primers used in the exemplifications of the invention to study NTRK3  
CC expression in transgenic mice of the invention and in control mice

XX Sequence 18 BP; 3 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 14.8; DB 1; Length 18;

RESULT 291

ABQ73036

ID ABQ73036 standard; DNA; 18 BP.

AC ABQ73036;

DT 24-SEP-2002 (first entry)

DE Human chloride channel related PCR primer SEQ ID NO:6.

XX Human; chloride channel; ClC-N3A; ClC-N3B; CFTR; cystic fibrosis;  
KW cystic fibrosis transmembrane conductance regulator; ClC-3B; respiration;  
KW PCR primer; ss.

OS Homo sapiens.

PN WO200244369-A1.

PD 06-JUN-2002.

XX 30-NOV-2001; 2001WO-UP010499.

XX 30-NOV-2000; 2000JP-00365103.

XX (BANY ) BANYU PHARM CO LTD.

PA (FURUKAWA T. FURUKAWA T.

PA (OGURA T. OGURA T.

PI Furukawa T, Ogura T;

DR WPI; 2002-557541/59.

PT Human chloride channel ClC-3B as outward rectifying chloride channel with  
PT chloride selectivity and activated by forskolin in presence of cystic  
PT fibrosis transmembrane conductance regulator, useful in diagnosis of  
PT cystic fibrosis.

XX Disclosure; Page 12; 41pp; Japanese.

XX The present invention describes a human chloride channel protein (A). (A)  
CC has respiratory activity. (A) can be used in the diagnosis of and  
CC development of drugs for cystic fibrosis. (A) is a ClC-3-selective  
CC splicing subtype, which is an outward rectifying chloride channel with  
CC chloride selectivity and is activated by forskolin in the presence of  
CC cystic fibrosis transmembrane conductance regulator (CFTR). The present  
CC sequence represents a PCR primer which is used in the exemplification of  
CC the present invention

XX Sequence 18 BP; 5 A; 10 C; 0 G; 3 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAACAATCTCCAC 260  
|||  
1 CTCGCCAACAATCTCTC 18

DB 1 CTCGCCAACAATCTCTC 18

RESULT 292

ABS64461

ID ABS64461 standard; DNA; 18 BP.

XX ABS64461;

XX ABS64461;

DT 15-NOV-2002 (first entry)  
XX  
XX Human TGF-beta binding PCR primer SFI #2.  
KW Human; NOX; neurodegenerative disease; Alzheimer's disease; anxiety;  
KW Parkinson's disease; Huntington's disease; neurological disorder;  
KW schizophrenia; manic depression; mental retardation; angina pectoris;  
KW cardiovascular disease; acute heart failure; myocardial infarction;  
KW muscular disease; muscular disorder; retinal disease; photoreception;  
KW deafness; keratinisation disorder; cancer; ovarian cancer; melanoma;  
KW immunological disorder; inflammatory disease; immune disease; diabetes;  
KW bacterial infection; fungal infection; protozoal infection; obesity;  
KW viral infection; reproductive system disorder; metabolic disturbance;  
KW anorexia; wasting disorder; chronic disease; infectious disease;  
KW dyslipidaemia; TGF-beta binding; cloning; PCR; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200264791-A2.  
XX  
XX 22-AUG-2002.  
XX  
XX 10-DEC-2001; 2001WO-US048369.  
XX  
XX 08-DEC-2000; 2000US-0254329P.  
XX 14-DEC-2000; 2000US-0255648P.  
XX 15-MAY-2001; 2001US-0281037P.  
XX 08-JUN-2001; 2001US-0297173P.  
XX 08-JUN-2001; 2001US-0309258P.  
XX 29-AUG-2001; 2001US-0315639P.  
XX 01-OCT-2001; 2001US-0326393P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Alsobrook JP, Anderson DW, Burgess CE, Boldog FL, Casman SJ;  
XX Colman SD, Edinger SR, Elleman K, Gerlach V, Gorman L, Grose WM;  
XX Guo X, Hermann JL, Kikuda R, Lepley DM, Li L, Macdougall JR;  
XX Miller I, Pena CE, Peyman JA, Rastelli L, Rieger DK, Shinkes RA;  
XX Smithson G, Sptek KA, Stone DJ, Tchernav VT, Vernet CAM, Voss EZ;  
XX Zernhsen BD, Zhong H, Zhong M;  
XX WPI; 2002-643486/69.  
XX  
XX New NOX polypeptides and polynucleotides useful for treating or  
XX preventing e.g. neurodegenerative diseases, neurological disorders,  
XX cardiovascular diseases, muscular diseases and disorders, or  
XX immunological diseases.  
XX  
XX Example 3; Page 288; 299pp; English.  
XX  
XX The present invention relates to new NOX polypeptides. The polypeptides,  
XX polynucleotides and antibodies are useful in the manufacture of a  
XX medicament for treating or preventing neurodegenerative diseases (e.g.  
XX Alzheimer's disease, Parkinson's disease, or Huntington's disease),  
XX neurological disorders (e.g. anxiety, schizophrenia, manic depression or  
XX mental retardation), cardiovascular disease (e.g. acute heart failure,  
XX angina pectoris or myocardial infarction), muscular diseases and  
XX disorders, retinal diseases (including those involving photoreception,  
XX deafness and keratinisation disorders), cancer (e.g. ovarian cancer or  
XX melanoma), immunological disorders, inflammatory and immune diseases,  
XX bacterial, fungal, protozoal and viral infections, and reproductive  
XX system disorders. The proteins of the invention may be used to screen  
XX drugs or compounds that modulate the NOX protein activity or expression,  
XX as well as to treat disorders characterised by insufficient or excessive  
XX production of NOX protein or protein forms that have decreased or  
XX aberrant activity compared to NOX wild type protein, such as diabetes,  
XX obesity, metabolic disturbances associated with obesity, anorexia and  
XX wasting disorders associated with chronic disease and various cancers,  
XX infectious diseases and various dyslipidaemias. The nucleic acid  
XX sequences of the invention may be used in chromosome mapping, identifying  
XX an individual from minute biological samples (tissue typing), and in  
XX forensic identification of a biological sample. The present nucleic acid  
XX sequence represents a cloning PCR primer that was used in the methods of

CC the invention for amplification of the NOX TGF-beta binding gene  
XX  
XX Sequence 18 BP; 3 A; 7 C; 6 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 315 GGCGCTGCTACACGCT 332  
Db 1 GGCGCGCTGCTACACGCT 18  
RESULT 293  
ADY75584/c  
ID ADY75584 standard; DNA; 18 BP.  
XX  
XX ADY75584;  
XX  
XX 02-JUN-2005 (first entry)  
XX  
XX Antisense oligonucleotide targeting human CD40, SEQ ID 89.  
XX  
XX 2'-O-methoxyethyl; 2'-MOE; ss; diagnosis; drug discovery;  
XX mass spectroscopy; phosphorochioate; antisense oligonucleotide; CD40.  
XX  
XX Homo sapiens.  
XX  
XX WO2005023986-A2.  
XX  
XX 17-MAR-2005.  
XX  
XX 07-SEP-2004; 2004WO-US028679.  
XX  
XX 04-SEP-2003; 2003US-0500723P.  
XX 04-SEP-2003; 2003US-0500724P.  
XX 04-SEP-2003; 2003US-0500730P.  
XX 04-SEP-2003; 2003US-0500732P.  
XX 04-SEP-2003; 2003US-0500824P.  
XX 11-SEP-2003; 2003US-0502007P.  
XX 17-SEP-2003; 2003US-050495P.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;  
XX WPI; 2005-233282/24.  
XX  
XX Selecting a target molecule having affinity for a ligand that is equal  
XX to/greater than a baseline affinity by introducing a target molecule into  
XX a ligand and standard target test mixture and identifying complex by mass  
XX spectrometer.  
XX  
XX Example 63; SEQ ID NO 89; 314pp; English.  
XX  
XX The invention relates to selecting a target molecule that has an affinity  
XX for a ligand that is equal to or greater than a baseline affinity,  
XX comprises introducing a target molecule into a test mixture of the ligand  
XX and a standard target, introducing the test mixture into a mass  
XX spectrometer and identifying any complexes of the target molecule and the  
XX ligand. Also included are a method of detecting a ligand-target complex  
XX having an affinity as expressed as a dissociation constant of nanomolar-  
XX 100 millimolar, a method for determining the relative interaction between  
XX at least two molecules determining target a ligand, a method of  
XX determining binding interaction (between a first target molecule and a  
XX second target molecule with respect to a ligand), a method of determining  
XX the relative proximity of binding sites for a first target molecule and a  
XX second target molecule on a ligand, a method of determining the relative  
XX orientation of a first target molecule to a second target molecule when  
XX bound to a ligand, a method for screening target molecules having binding  
XX affinity to a ligand, a method for modulating the binding affinity of a  
XX target molecule for a ligand, a method for refining the binding of a





RESULT 295  
ID AEC52834 standard; DNA; 18 BP.  
AC AEC52834;  
XX  
DT 17-NOV-2005 (first entry)  
DE Antisense oligonucleotide targeting human TGF-beta-3 #1232.  
XX  
KM Transforming growth factor beta; TGF-beta-3; antisense therapy;  
KM antisense oligonucleotide; ss; cancer; cytostatic.  
XX  
OS Homo sapiens.  
PN WO2005084712-A2.  
PD 15-SEP-2005.  
PF 28-FEB-2005; 2005WO-EP002101.  
XX  
PR 27-FEB-2004; 2004EP-00004478.  
PR 01-APR-2004; 2004US-0558135P.  
XX  
PA (ANTI-) ANTISENSE PHARMA GMBH.  
PI Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;  
PI Bischof A, Halner M, Egger T;  
DR WPI; 2005-630685/64.  
XX  
PT New antisense oligonucleotides inhibiting the synthesis of proteins  
PT involved in the formation of metastases such as transforming growth  
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for  
PT treating cancer.  
XX  
XX Claim 4; Page 72; 106pp; English.  
XX  
XX The invention relates to an antisense oligonucleotide or its active  
XX derivative selected from AEC46374-AEC46395, targeting human interleukin-  
XX 10 (IL-10). Also included are a process of manufacturing the antisense  
XX oligonucleotide (or its active derivative, by adding consecutive  
XX nucleosides and linker stepwise or by cutting the oligonucleotide out of  
XX longer oligonucleotide chain), a pharmaceutical composition comprising a  
XX composition for treating cancer. The oligonucleotide is an antisense  
XX oligonucleotide inhibiting the synthesis of proteins involved in the  
XX formation of metastases. The oligonucleotide is an antisense  
XX oligonucleotide inhibiting the production of transforming growth factor  
XX (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules  
XX (CAMs), integrins, selectins, metalloproteases (MMPs), their tissue  
XX inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are  
XX useful for the preparation of a pharmaceutical composition for inhibiting  
XX the formation of metastases in cancer treatment. The oligonucleotides are  
XX useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,  
XX brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the  
XX kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical  
XX carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,  
XX endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder  
XX cancer, gastric cancer, head and neck cancer, hepatocellular cancer,  
XX liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell  
XX bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma, papillary  
XX carcinoma, papillary adenocarcinoma, prostate cancer, small  
XX intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland  
XX carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,  
XX testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,  
XX trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,  
XX Ewing's tumor, craniopharyngioma, ependyoma, medulloblastoma,  
XX hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,  
XX neuroblastoma, pinealoma, retinoblastoma, sarcoma, seminoma, teratoma,  
XX Wilms tumor and/or myeloma, multiple. The present sequence is an  
XX antisense oligonucleotide targeting human TGF-beta-3.

SO Sequence 18 BP; 2 A; 10 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 240 CCTCTCCCAAAATCTC 257  
DB 1 CCTCTCCCAATGATCTC 18  
RESULT 296  
ID AEC51657 standard; DNA; 18 BP.  
AC AEC51657;  
XX  
DT 17-NOV-2005 (first entry)  
DE Antisense oligonucleotide targeting human TGF-beta-3 #55.  
XX  
KM Transforming growth factor beta; TGF-beta-3; antisense therapy;  
KM antisense oligonucleotide; ss; cancer; cytostatic.  
XX  
OS Homo sapiens.  
PN WO2005084712-A2.  
PD 15-SEP-2005.  
PF 28-FEB-2005; 2005WO-EP002101.  
XX  
PR 27-FEB-2004; 2004EP-00004478.  
PR 01-APR-2004; 2004US-0558135P.  
XX  
PA (ANTI-) ANTISENSE PHARMA GMBH.  
PI Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;  
PI Bischof A, Halner M, Egger T;  
DR WPI; 2005-630685/64.  
XX  
PT New antisense oligonucleotides inhibiting the synthesis of proteins  
PT involved in the formation of metastases such as transforming growth  
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for  
PT treating cancer.  
XX  
XX Claim 4; Page 70; 106pp; English.  
XX  
XX The invention relates to an antisense oligonucleotide or its active  
XX derivative selected from AEC46374-AEC46395, targeting human interleukin-  
XX 10 (IL-10). Also included are a process of manufacturing the antisense  
XX oligonucleotide (or its active derivative, by adding consecutive  
XX nucleosides and linker stepwise or by cutting the oligonucleotide out of  
XX longer oligonucleotide chain), a pharmaceutical composition comprising a  
XX composition for treating cancer. The oligonucleotide is an antisense  
XX oligonucleotide inhibiting the synthesis of proteins involved in the  
XX formation of metastases. The oligonucleotide is an antisense  
XX oligonucleotide inhibiting the production of transforming growth factor  
XX (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules  
XX (CAMs), integrins, selectins, metalloproteases (MMPs), their tissue  
XX inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are  
XX useful for the preparation of a pharmaceutical composition for inhibiting  
XX the formation of metastases in cancer treatment. The oligonucleotides are  
XX useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,  
XX brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the  
XX kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical  
XX carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,  
XX endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder  
XX cancer, gastric cancer, head and neck cancer, hepatocellular cancer,  
XX liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell  
XX bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma,

CC papillary carcinoma, papillary adenocarcinoma, prostate cancer, small  
 CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland  
 CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,  
 CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,  
 CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,  
 CC Ewing's tumor, craniopharyngioma, ependyoma, medulloblastoma,  
 CC hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,  
 CC neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,  
 CC Wilms tumor and/or myeloma, multiple. The present sequence is an  
 CC antisense oligonucleotide targeting human TGF-beta-3.  
 XX  
 SQ Sequence 18 BP; 3 A; 4 C; 9 G; 2 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 15 GCGGCGACGCGCGCAGTG 32  
 1 GCGGCGACTGACGCGCAGTG 18  
 Db

RESULT 297  
 AEC52974  
 ID AEC52974 standard; DNA; 18 BP.  
 XX  
 AC AEC52974;  
 XX  
 DT 17-NOV-2005 (first entry)  
 XX  
 DE Antisense oligonucleotide targeting human TGF-beta-3 #1372.  
 XX  
 KW Transforming growth factor beta; TGF-beta-3; antisense therapy;  
 KW antisense oligonucleotide; ss; cancer; cytostatic.  
 OS  
 XX Homo sapiens.  
 OS  
 PN WO2005084712-A2.  
 XX  
 PD 15-SEP-2005.  
 XX  
 PF 28-FEB-2005; 2005WO-BP002101.  
 XX  
 PR 27-FEB-2004; 2004EP-00004478.  
 PR 01-APR-2004; 2004US-0558135P.  
 XX  
 PA (ANTI-) ANTISENSE PHARMA GMBH.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;  
 PI Bischof A, Halner M, Egger T;  
 XX  
 DR WPI; 2005-630685/64.  
 XX  
 XX New antisense oligonucleotides inhibiting the synthesis of proteins  
 PT involved in the formation of metastases such as transforming growth  
 PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for  
 PT treating cancer.  
 XX  
 PS Claim 4; Page 73; 106pp; English.  
 XX  
 XX The invention relates to an antisense oligonucleotide or its active  
 CC derivative selected from AEC46374-AEC46395, targeting human interleukin-  
 CC 10 (IL-10). Also included are a process of manufacturing the antisense  
 CC oligonucleotide (or its active derivative, by adding consecutive  
 CC nucleosides and linker stepwise or by cutting the oligonucleotide out of  
 CC longer oligonucleotide chain), a pharmaceutical composition comprising a  
 CC the antisense oligonucleotide and a TGF-beta 2 antagonist for preparing a  
 CC composition for treating cancer. The oligonucleotide is an antisense  
 CC oligonucleotide inhibiting the synthesis of proteins involved in the  
 CC formation of metastases. The oligonucleotide is an antisense  
 CC oligonucleotide inhibiting the production of transforming growth factor  
 CC (TGF)-beta 1, TGF-beta 2, TGF-beta 3 cell-cell adhesion molecules  
 CC (CAMs), integrins, selectins, metalloproteinases (MMPs), their tissue

CC inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are  
 CC useful for the preparation of a pharmaceutical composition for inhibiting  
 CC the formation of metastases in cancer treatment. The oligonucleotides are  
 CC useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,  
 CC brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the  
 CC kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical  
 CC carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,  
 CC endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder  
 CC cancer, gastric cancer, head and neck cancer, hepatocellular cancer,  
 CC liver carcinoma, lung carcinoma, ovarian cancer, pancreas carcinoma,  
 CC bronchogenic/lung carcinoma, papillary adenocarcinoma, prostate cancer, small  
 CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland  
 CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,  
 CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,  
 CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,  
 CC Ewing's tumor, craniopharyngioma, ependyoma, medulloblastoma,  
 CC hemangioblastoma, medulloblastoma, melanoma, mesothelioma, neuroblastoma,  
 CC neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,  
 CC Wilms tumor and/or myeloma, multiple. The present sequence is an  
 CC antisense oligonucleotide targeting human TGF-beta-3.  
 CC  
 XX  
 SQ Sequence 18 BP; 2 A; 10 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 241 CTCTCCCAACATCTCC 258  
 1 CTCTCCCAATGCAATCTCC 18  
 Db

RESULT 298  
 AEC27781/C  
 ID AEC27781 standard; DNA; 18 BP.  
 XX  
 AC AEC27781;  
 XX  
 DT 17-NOV-2005 (first entry)  
 XX  
 DE Human allele-specific oligonucleotide #3801.  
 XX  
 KW Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;  
 KW major histocompatibility complex; MHC; HLA; human leukocyte antigen;  
 KW immune disorder; inflammation; inflammatory bowel disease;  
 KW ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes;  
 KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;  
 KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;  
 KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;  
 KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;  
 KW idiopathic thrombocytopenia purpura; Sjogrens syndrome;  
 KW multiple sclerosis; Reiter's syndrome; psoriasis; anti-inflammatory;  
 KW gastrointestinal-gen.; antitumor; immunomodulator; immunosuppressive;  
 KW antiarthritic; antirheumatic; antidiabetic; muscular-gen.;  
 KW neuroprotective; dermatological; antihypertensive; hepatotropic; antianemic;  
 KW hemostatic; ophthalmological; uropathic; antiporiatic; ss;  
 KW SNP detection.  
 XX  
 OS  
 XX Homo sapiens.  
 OS  
 PN WO2005082110-A2.  
 XX  
 PD 09-SEP-2005.  
 XX  
 PF 28-FEB-2005; 2005WO-US006628.  
 XX  
 PR 26-FEB-2004; 2004US-0547823P.  
 XX  
 PA (ILDU-) ILLUMINA INC.  
 XX  
 PI Oliphant A, Murray S;  
 XX

DR WPI; 2005-638856/65.

PT Identifying single nucleotide polymorphism (SNP) haplotype that  
PT correlates with the HLA type, useful for diagnosing an immunological or  
PT inflammatory condition, comprises providing SNPs in the major  
PT histocompatibility complex region.

XX  
PS Example 1; SEQ ID NO 3801, 175bp; English.

XX  
CC The invention relates to a method of identifying the nucleotide for each  
CC of a set of single nucleotide polymorphisms (SNPs) in the major  
CC histocompatibility complex (MHC) region in a population of individuals,  
CC comprising providing the HLA type for the individuals and identifying an  
CC SNP haplotype in the population that correlates with the HLA type, where  
CC the SNP haplotype comprises the SNPs in the MHC region. The invention  
CC also relates to a method of predicting the HLA type of an individual, a  
CC method of determining the presence or absence of an allelic variant of an  
CC MHC gene in an individual, a method of identifying an SNP haplotype that  
CC correlates with susceptibility to a disease or condition, and a method of  
CC determining the susceptibility of an individual to a disease or  
CC condition. The disease or condition is an immune disorder or inflammatory  
CC condition selected from inflammatory bowel disease, ulcerative colitis,  
CC Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,  
CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease, systemic  
CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic  
CC lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,  
CC pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia  
CC purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and  
CC psoriasis. This sequence represents a human allele-specific  
CC oligonucleotide used in the scope of the invention.

XX  
SQ Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1292 TGGTGGGGGCCCCAGAGG 1309  
DB 18 TGGTGGAGGCCCTCGAGG 1  
|||||  
|||||

RESULT 299  
ABK12174  
ID ABK12174 standard; DNA; 15 BP.  
XX  
AC ABK12174;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #4.  
XX  
KW Human; 88; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;  
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
KW opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN W0200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001MO-USO26663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anaestasio AE, Kazemi A;  
XX  
DR WPI; 2002-280907/32.

PT Novel isolated polynucleotide which is a polymorphic variant of  
PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
PT isoform used in screening drug candidates to treat pain, depression,  
PT vomiting.

XX  
PS Claim 17; Page 14; 89pp; English.

XX  
CC The invention relates to an isolated polynucleotide sequence which  
CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
CC 16 SG as given in specification, where each SG comprises specific regions  
CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,  
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
CC of an individual by determining either the haplotype of one or both  
CC copies of the TACR1 gene, predicting the haplotype pair for the TACR1  
CC gene of an individual, identifying an association between a trait and a  
CC haplotype pair, an isolated oligonucleotide for detecting the  
CC polymorphisms, a computer system for storing and analysing polymorphism  
CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
CC for studying expression and function of TACR1 and expressing TACR1  
CC protein for use in screening for candidate drugs to treat diseases  
CC related to TACR1 activity. The polymorphism and haplotype data is useful  
CC for validating whether TACR1 is a suitable target for drugs to treat  
CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
CC addiction. Screening for such drugs and reducing bias in clinical trials  
CC of such drugs. The genotyping method is useful for determining whether an  
CC individual has one of the haplotype pairs. The haplotyping method is  
CC useful for improving efficiency and outcome of several steps in discovery  
CC and development of drugs for treating the diseases. The haplotyping  
CC method is also useful for validating TACR1 as a candidate target for  
CC treating a specific condition or disease predicted to be associated with  
CC TACR1 activity. The method is also useful for screening compounds to  
CC treat a specific condition or disease predicted to be associated with  
CC TACR1 activity. The methods are useful for identifying an association  
CC between susceptibility to a disease, straging of a disease, or response to  
CC a drug. The gene for TACR1 is located on human chromosome 2. The present  
CC sequence is an allele specific oligonucleotide (ASO) probe used to detect  
CC polymorphisms in the TACR1 gene

XX  
SQ Sequence 15 BP; 2 A; 6 C; 1 G; 5 T; 0 U; 1 Other;

Query Match 0.8%; Score 14.6; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 536 ACTCTTCCCATCG 550  
DB 1 ACTCTTCCCATCG 15  
|||||  
|||||

RESULT 300  
ABK12178  
ID ABK12178 standard; DNA; 15 BP.  
XX  
AC ABK12178;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #8.  
XX  
KW Human; 88; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;  
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
KW opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN W0200216399-A2.  
XX  
PD 28-FEB-2002.

27-AUG-2001; 2001WO-US026663.  
 25-AUG-2000; 2000US-0227815P.  
 (GENA-) GENNAISSANCE PHARM INC.  
 Anastasio AE, Kazemi A;  
 WPI; 2002-280907/32.  
 Novel isolated polynucleotide which is a polymorphic variant of  
 tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 isoform used in screening drug candidates to treat pain, depression,  
 vomiting.  
 Claim 17; Page 14; 89pp; English.  
 The invention relates to an isolated polynucleotide sequence which  
 comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 16 SG as given in specification, where each SG comprises specific regions  
 of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
 94501, 94821, 94892, 94960. Also included are fragments of the TACR1  
 isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
 the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
 of an individual by determining either the haplotype of one or both  
 copies of the TACR1 gene, predicting an association between a trait and a  
 gene of an individual, identifying an association between a trait and a  
 haplotype pair, an isolated oligonucleotide for detecting the  
 polymorphisms, a computer system for storing and analysing polymorphism  
 data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
 for studying expression and function of TACR1 and expressing TACR1  
 protein for use in screening for candidate drugs to treat diseases  
 related to TACR1 activity. The polymorphism and haplotype data is useful  
 for validating whether TACR1 is a suitable target for drugs to treat  
 pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
 addiction, screening for such drugs and reducing bias in clinical trials  
 of such drugs. The genotyping method is useful for determining whether an  
 individual has one of the haplotype pairs. The haplotyping method is  
 useful for improving efficiency and outcome of several steps in discovery  
 and development of drugs for treating the diseases. The haplotyping  
 method is also useful for validating TACR1 as a candidate target for  
 treating a specific condition or disease predicted to be associated with  
 TACR1 activity. The method is also useful for screening compounds to  
 treat a specific condition or disease predicted to be associated with  
 TACR1 activity. The methods are useful for identifying an association  
 between susceptibility to a disease, staging of a disease, or response to  
 a drug. The gene for TACR1 is located on human chromosome 2. The present  
 sequence is an allele specific oligonucleotide (ASO) probe used to detect  
 polymorphisms in the TACR1 gene  
 Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1628 ATGCTGTGACTCA 1642  
 |||||:|||||  
 1 ATGCTGTGACTCA 15  
 Db  
 RESULT 301  
 ABK12184  
 ID ABK12184 standard; DNA; 15 BP.  
 XX  
 XX  
 AC ABK12184;  
 XX  
 AC  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human Tachykinin Receptor 1 allele specific oligonucleotide primer #5.  
 XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;

single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
 depression; vomiting; acute inflammatory diarrhoea; ASO;  
 opiate addiction; drug screening; allele specific oligonucleotide.  
 Homo sapiens.  
 WO200216399-A2.  
 28-FEB-2002.  
 27-AUG-2001; 2001WO-US026663.  
 25-AUG-2000; 2000US-0227815P.  
 (GENA-) GENNAISSANCE PHARM INC.  
 Anastasio AE, Kazemi A;  
 WPI; 2002-280907/32.  
 Novel isolated polynucleotide which is a polymorphic variant of  
 tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 isoform used in screening drug candidates to treat pain, depression,  
 vomiting.  
 Claim 17; Page 14; 89pp; English.  
 The invention relates to an isolated polynucleotide sequence which  
 comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 16 SG as given in specification, where each SG comprises specific regions  
 of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
 94501, 94821, 94892, 94960. Also included are fragments of the TACR1  
 isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
 the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
 of an individual by determining either the haplotype of one or both  
 copies of the TACR1 gene, predicting an association between a trait and a  
 gene of an individual, identifying an association between a trait and a  
 haplotype pair, an isolated oligonucleotide for detecting the  
 polymorphisms, a computer system for storing and analysing polymorphism  
 data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
 for studying expression and function of TACR1 and expressing TACR1  
 protein for use in screening for candidate drugs to treat diseases  
 related to TACR1 activity. The polymorphism and haplotype data is useful  
 for validating whether TACR1 is a suitable target for drugs to treat  
 pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
 addiction, screening for such drugs and reducing bias in clinical trials  
 of such drugs. The genotyping method is useful for determining whether an  
 individual has one of the haplotype pairs. The haplotyping method is  
 useful for improving efficiency and outcome of several steps in discovery  
 and development of drugs for treating the diseases. The haplotyping  
 method is also useful for validating TACR1 as a candidate target for  
 treating a specific condition or disease predicted to be associated with  
 TACR1 activity. The method is also useful for screening compounds to  
 treat a specific condition or disease predicted to be associated with  
 TACR1 activity. The methods are useful for identifying an association  
 between susceptibility to a disease, staging of a disease, or response to  
 a drug. The gene for TACR1 is located on human chromosome 2. The present  
 sequence is an allele specific oligonucleotide (ASO) PCR primer used to  
 detect polymorphisms in the TACR1 gene  
 Sequence 15 BP; 1 A; 8 C; 1 G; 4 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 100 TTCCACCCCTCTGTC 114  
 |||||:|||||  
 1 TTCCACCCCTCTGTC 15  
 Db  
 RESULT 302

ABK12192  
ID ABK12192 standard; DNA; 15 BP.  
XX  
AC ABK12192;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 ASO primer #13.  
XX  
KW Human; 89; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
XX opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anastasio AE, Kazemi A;  
XX  
XX WPI; 2002-280907/32.  
XX  
DR Novel isolated polynucleotide which is a polymorphic variant of  
XX tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
PT isoform used in screening drug candidates to treat pain, depression,  
PT vomiting.  
XX  
XX Claim 17; Page 14; 89pp; English.  
XX  
XX The invention relates to an isolated polynucleotide sequence which  
XX comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
XX 16 SG as given in specification, where each SG comprises specific regions  
XX of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
XX polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
XX 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
XX isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
XX the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
XX of an individual by determining either the haplotype of one or both  
XX copies of the TACR1 gene, predicting an association between a trait and a  
XX haplotype pair, an isolated oligonucleotide for detecting the  
XX polymorphisms, a computer system for storing and analysing polymorphism  
XX data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
XX for studying expression and function of TACR1 and expressing TACR1  
XX protein for use in screening for candidate drugs to treat diseases  
XX related to TACR1 activity. The polymorphism and haplotype data is useful  
XX for validating whether TACR1 is a suitable target for drugs to treat  
XX pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
XX addiction, screening for such drugs and reducing bias in clinical trials  
XX of such drugs. The genotyping method is useful for determining whether an  
XX individual has one of the haplotype pairs. The haplotyping method is  
XX useful for improving efficiency and outcome of several steps in discovery  
XX and development of drugs for treating the diseases. The haplotyping  
XX method is also useful for validating TACR1 as a candidate target for  
XX treating a specific condition or disease predicted to be associated with  
XX TACR1 activity. The method is also useful for screening compounds to  
XX treat a specific condition or disease predicted to be associated with  
XX TACR1 activity. The methods are useful for identifying an association  
XX between susceptibility to a disease, staging of a disease, or response to  
XX a drug. The gene for TACR1 is located on human chromosome 2. The present  
XX sequence is an allele specific oligonucleotide (ASO) PCR primer used to  
XX detect polymorphisms in the TACR1 gene  
XX  
XX Sequence 15 BP; 3 A; 7 C; 2 G; 2 T; 0 U; 1 Other; '

Query Match 0.8%; Score 14.6; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1331 AGGCCACACCTCGT 1345  
DB 1 AGGCCACACCTCGT 15  
RESULT 303  
ABK12193/c  
ID ABK12193 standard; DNA; 15 BP.  
XX  
AC ABK12193;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 ASO primer #14.  
XX  
KW Human; 89; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
KM single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
XX opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anastasio AE, Kazemi A;  
XX  
XX WPI; 2002-280907/32.  
XX  
DR Novel isolated polynucleotide which is a polymorphic variant of  
XX tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
PT isoform used in screening drug candidates to treat pain, depression,  
PT vomiting.  
XX  
XX Claim 17; Page 14; 89pp; English.  
XX  
XX The invention relates to an isolated polynucleotide sequence which  
XX comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
XX 16 SG as given in specification, where each SG comprises specific regions  
XX of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
XX polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
XX 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
XX isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
XX the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
XX of an individual by determining either the haplotype of one or both  
XX copies of the TACR1 gene, predicting an association between a trait and a  
XX haplotype pair, an isolated oligonucleotide for detecting the  
XX polymorphisms, a computer system for storing and analysing polymorphism  
XX data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
XX for studying expression and function of TACR1 and expressing TACR1  
XX protein for use in screening for candidate drugs to treat diseases  
XX related to TACR1 activity. The polymorphism and haplotype data is useful  
XX for validating whether TACR1 is a suitable target for drugs to treat  
XX pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
XX addiction, screening for such drugs and reducing bias in clinical trials  
XX of such drugs. The genotyping method is useful for determining whether an  
XX individual has one of the haplotype pairs. The haplotyping method is  
XX useful for improving efficiency and outcome of several steps in discovery  
XX and development of drugs for treating the diseases. The haplotyping  
XX method is also useful for validating TACR1 as a candidate target for  
XX treating a specific condition or disease predicted to be associated with

CC TACR1 activity. The method is also useful for screening compounds to  
 CC treat a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The methods are useful for identifying an association  
 CC between susceptibility to a disease, staging of a disease, or response to  
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present  
 CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to  
 CC detect polymorphisms in the TACR1 gene  
 CC  
 XX Sequence 15 BP; 3 A; 3 C; 6 G; 2 T; 0 U; 1 Other;  
 SQ  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1343 CGTCCCTGACCTGA 1357  
 Db 15 CRTCCCTGACCTGA 1  
 RESULT 304  
 ABK12194  
 ID ABK12194 standard; DNA; 15 BP.  
 XX  
 AC ABK12194;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Human Tachykinin Receptor 1 ASO primer #15.  
 DE  
 XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
 XX single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
 KM opiate addiction; drug screening; allele specific oligonucleotide.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200216399-A2.  
 PN  
 XX 28-FEB-2002.  
 PD  
 XX 27-AUG-2001; 2001WO-US026663.  
 PF  
 XX 25-AUG-2000; 2000US-0227815P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Anastasio AE, Kazemi A;  
 PI  
 XX WPI; 2002-280907/32.  
 DR  
 XX Novel isolated polynucleotide which is a polymorphic variant of  
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 PT isoform used in screening drug candidates to treat pain, depression,  
 PT vomiting.  
 PT  
 XX Claim 17; Page 14; 89pp; English.  
 PS  
 XX The invention relates to an isolated polynucleotide sequence which  
 CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 CC 16 SG as given in specification, where each SG comprises specific regions  
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,  
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
 CC of an individual by determining either the haplotype of one or both  
 CC copies of the TACR1 gene, predicting an association between a trait and a  
 CC haplotype pair, identifying an association for detecting the  
 CC polymorphisms, a computer system for storing and analysing polymorphism  
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
 CC for studying expression and function of TACR1 and expressing TACR1  
 CC protein for use in screening for candidate drugs to treat diseases

CC related to TACR1 activity. The polymorphism and haplotype data is useful  
 CC for validating whether TACR1 is a suitable target for drugs to treat  
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
 CC addiction, screening for such drugs and reducing bias in clinical trials  
 CC of such drugs. The genotyping method is useful for determining whether an  
 CC individual has one of the haplotype pairs. The haplotyping method is  
 CC useful for improving efficiency and outcome of several steps in discovery  
 CC and development of drugs for treating the diseases. The haplotyping  
 CC method is also useful for validating TACR1 as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The method is also useful for screening compounds to  
 CC treat a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The methods are useful for identifying an association  
 CC between susceptibility to a disease, staging of a disease, or response to  
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present  
 CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to  
 CC detect polymorphisms in the TACR1 gene  
 CC  
 XX Sequence 15 BP; 2 A; 5 C; 2 G; 5 T; 0 U; 1 Other;  
 SQ  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1622 ACCCTCATGCTGTGT 1636  
 Db 1 ACCCTCATGCTGTGT 15  
 RESULT 305  
 ABK12195/c  
 ID ABK12195 standard; DNA; 15 BP.  
 XX  
 AC ABK12195;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Human Tachykinin Receptor 1 ASO primer #15.  
 DE  
 XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
 XX single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
 KM opiate addiction; drug screening; allele specific oligonucleotide.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200216399-A2.  
 PN  
 XX 28-FEB-2002.  
 PD  
 XX 27-AUG-2001; 2001WO-US026663.  
 PF  
 XX 25-AUG-2000; 2000US-0227815P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Anastasio AE, Kazemi A;  
 PI  
 XX WPI; 2002-280907/32.  
 DR  
 XX Novel isolated polynucleotide which is a polymorphic variant of  
 PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 PT isoform used in screening drug candidates to treat pain, depression,  
 PT vomiting.  
 PT  
 XX Claim 17; Page 14; 89pp; English.  
 PS  
 XX The invention relates to an isolated polynucleotide sequence which  
 CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 CC 16 SG as given in specification, where each SG comprises specific regions  
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,  
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1

isogenes and TACR1 cDNA, a transgenic non-human animal transformed with the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1 of an individual by determining either the haplotype of one or both copies of the TACR1 gene, predicting the haplotype pair for the TACR1 gene of an individual, identifying an association between a trait and a haplotype pair, an isolated oligonucleotide for detecting the polymorphisms, a computer system for storing and analysing polymorphism data and a genome anthology for TACR1 gene. The TACR1 isogene is useful for studying expression and function of TACR1 and expressing TACR1 protein for use in screening for candidate drugs to treat diseases related to TACR1 activity. The polymorphism and haplotype data is useful for validating whether TACR1 is a suitable target for drugs to treat pain, depression, vomiting, acute inflammatory diarrhoea and opiate addiction, screening for such drugs and reducing bias in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one of the haplotype pairs. The haplotyping method is useful for improving efficiency and outcome of several steps in discovery and development of drugs for treating the diseases. The haplotyping method is also useful for validating TACR1 as a candidate target for treating a specific condition or disease predicted to be associated with TACR1 activity. The method is also useful for screening compounds to treat a specific condition or disease predicted to be associated with TACR1 activity. The methods are useful for identifying an association between susceptibility to a disease, staging of a disease, or response to a drug. The gene for TACR1 is located on human chromosome 2. The present sequence is an allele specific oligonucleotide (ASO) PCR primer used to detect polymorphisms in the TACR1 gene

Sequence 15 BP; 3 A; 1 C; 4 G; 6 T; 0 U; 1 Other;

Query Match  
Best Local Similarity 93.3%; Score 14.6; DB 1; Length 15;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1634 TGTGACTCAACCA 1648  
15 TKTGACTCAACCAA 1

RESULT 306  
ABK12187/c  
ID ABK12187 standard; DNA; 15 BP.  
XX  
AC ABK12187;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 allele specific oligonucleotide primer #8.  
XX  
KW Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
KW opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Anaestasio AB, Kazemi A;  
XX  
XX WPI; 2002-280907/32.  
XX  
XX  
XX Novel isolated polynucleotide which is a polymorphic variant of  
PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
PT isoform used in screening drug candidates to treat pain, depression,

vomiting.

Claim 17; Page 14; 89pp; English.

The invention relates to an isolated polynucleotide sequence which comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of 16 SG as given in specification, where each SG comprises specific regions of the TACR1 genomic DNA appearing as ABK12189, and is defined by polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915, 94601, 94821, 94892, 94960. Also included are fragments of the TACR1 isogenes and TACR1 cDNA, a transgenic non-human animal transformed with the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1 of an individual by determining either the haplotype of one or both copies of the TACR1 gene, predicting the haplotype pair for the TACR1 gene of an individual, identifying an association between a trait and a haplotype pair, an isolated oligonucleotide for detecting the polymorphisms, a computer system for storing and analysing polymorphism data and a genome anthology for TACR1 gene. The TACR1 isogene is useful for studying expression and function of TACR1 and expressing TACR1 protein for use in screening for candidate drugs to treat diseases related to TACR1 activity. The polymorphism and haplotype data is useful for validating whether TACR1 is a suitable target for drugs to treat pain, depression, vomiting, acute inflammatory diarrhoea and opiate addiction, screening for such drugs and reducing bias in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one of the haplotype pairs. The haplotyping method is useful for improving efficiency and outcome of several steps in discovery and development of drugs for treating the diseases. The haplotyping method is also useful for validating TACR1 as a candidate target for treating a specific condition or disease predicted to be associated with TACR1 activity. The method is also useful for screening compounds to treat a specific condition or disease predicted to be associated with TACR1 activity. The methods are useful for identifying an association between susceptibility to a disease, staging of a disease, or response to a drug. The gene for TACR1 is located on human chromosome 2. The present sequence is an allele specific oligonucleotide (ASO) PCR primer used to detect polymorphisms in the TACR1 gene

Sequence 15 BP; 3 A; 3 C; 7 G; 1 T; 0 U; 1 Other;

Query Match  
Best Local Similarity 93.3%; Score 14.6; DB 1; Length 15;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

542 TTCCCATGCCGCTG 556  
15 TYCCCATGCCGCTG 1

RESULT 307  
ABK12177  
ID ABK12177 standard; DNA; 15 BP.  
XX  
AC ABK12177;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #7.  
XX  
KW Human; ss; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;  
KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
KW opiate addiction; drug screening; allele specific oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200216399-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026663.  
XX  
PR 25-AUG-2000; 2000US-0227815P.  
XX  
XX



XX (GENA-) GENAISSANCE PHARM INC.  
 PA Anastasio AE, Kazemi A;  
 XX WPI; 2002-280907/32.  
 DR Novel isolated polynucleotide which is a polymorphic variant of  
 XX tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 PT isoform used in screening drug candidates to treat pain, depression,  
 PT vomiting.  
 XX Claim 17, Page 14; 89pp; English.  
 PS The invention relates to an isolated polynucleotide sequence which  
 XX comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 CC 16 SG as given in specification, where each SG comprises specific regions  
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
 CC of an individual by determining either the haplotype of one or both  
 CC copies of the TACR1 gene, predicting an association between a trait and a  
 CC haplotype pair, an isolated oligonucleotide for detecting the  
 CC polymorphisms, a computer system for storing and analysing polymorphism  
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
 CC for studying expression and function of TACR1 and expressing TACR1  
 CC protein for use in screening for candidate drugs to treat diseases  
 CC related to TACR1 activity. The polymorphism and haplotype data is useful  
 CC for validating whether TACR1 is a suitable target for drugs to treat  
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
 CC addiction, screening for such drugs and reducing bias in clinical trials  
 CC of such drugs. The genotyping method is useful for determining whether an  
 CC individual has one of the haplotype pairs. The haplotyping method is  
 CC useful for improving efficiency and outcome of several steps in discovery  
 CC and development of drugs for treating the diseases. The haplotyping  
 CC method is also useful for validating TACR1 as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The method is also useful for screening compounds to  
 CC treat a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The methods are useful for identifying an association  
 CC between susceptibility to a disease, staging of a disease, or response to  
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present  
 CC sequence is an allele specific oligonucleotide (ASO) probe used to detect  
 CC polymorphisms in the TACR1 gene  
 XX  
 XX Sequence 15 BP; 1 A; 8 C; 2 G; 3 T; 0 U; 1 Other;  
 SO  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1337 CACCCTGCTCCCTGG 1351  
 Db 1 CACCCTGCTCCCTGG 15  
 RESULT 308  
 ABK12186  
 ID ABK12186 standard; DNA; 15 BP.  
 XX  
 XX ABK12186;  
 AC  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Human Tachykinin Receptor 1 allele specific oligonucleotide primer #7.  
 DB  
 XX Human; ss; primer; TACR1; Tachykinin receptor 1; chromosome 2; PCR; SNP;  
 KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;  
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;  
 KW opiate addiction; drug screening; allele specific oligonucleotide.

XX Homo sapiens.  
 OS  
 XX WO200216399-A2.  
 XX  
 XX 28-FEB-2002.  
 PD  
 XX 27-AUG-2001; 2001WO-US026663.  
 PF  
 XX 25-AUG-2000; 2000US-0227815P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA Anastasio AE, Kazemi A;  
 XX WPI; 2002-280907/32.  
 DR Novel isolated polynucleotide which is a polymorphic variant of  
 XX tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein  
 PT isoform used in screening drug candidates to treat pain, depression,  
 PT vomiting.  
 XX Claim 17, Page 14; 89pp; English.  
 PS The invention relates to an isolated polynucleotide sequence which  
 XX comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of  
 CC 16 SG as given in specification, where each SG comprises specific regions  
 CC of the TACR1 genomic DNA appearing as ABK12169, and is defined by  
 CC polymorphisms at positions (p) 3164, 3319, 3906, 4339, 4444, 92915,  
 CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1  
 CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with  
 CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1  
 CC of an individual by determining either the haplotype of one or both  
 CC copies of the TACR1 gene, predicting an association between a trait and a  
 CC gene of an individual, identifying an association for detecting the  
 CC polymorphisms, a computer system for storing and analysing polymorphism  
 CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful  
 CC for studying expression and function of TACR1 and expressing TACR1  
 CC protein for use in screening for candidate drugs to treat diseases  
 CC related to TACR1 activity. The polymorphism and haplotype data is useful  
 CC for validating whether TACR1 is a suitable target for drugs to treat  
 CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate  
 CC addiction, screening for such drugs and reducing bias in clinical trials  
 CC of such drugs. The genotyping method is useful for determining whether an  
 CC individual has one of the haplotype pairs. The haplotyping method is  
 CC useful for improving efficiency and outcome of several steps in discovery  
 CC and development of drugs for treating the diseases. The haplotyping  
 CC method is also useful for validating TACR1 as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The method is also useful for screening compounds to  
 CC treat a specific condition or disease predicted to be associated with  
 CC TACR1 activity. The methods are useful for identifying an association  
 CC between susceptibility to a disease, staging of a disease, or response to  
 CC a drug. The gene for TACR1 is located on human chromosome 2. The present  
 CC sequence is an allele specific oligonucleotide (ASO) PCR primer used to  
 CC detect polymorphisms in the TACR1 gene  
 XX  
 XX Sequence 15 BP; 3 A; 6 C; 0 G; 5 T; 0 U; 1 Other;  
 SO  
 Query Match 0.8%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 530 TCCACACTTCTTC 544  
 Db 1 TCCACACTTCTTC 15  
 RESULT 309  
 ADU94981  
 ID ADU94981 standard; RNA; 16 BP.  
 XX





CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammation  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addition disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, edema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected,  
CC reducing side effects of treatment. ABK3834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
SQ Sequence 16 BP; 3 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 207 CGAATGATACGTC 222  
Db 16 CAAATGATACGTC 1

RESULT 311  
AAV93332  
ID AAV93332 standard; RNA; 17 BP.  
XX  
XX AAV93332;  
AC  
XX  
XX 18-FEB-1999 (first entry)  
DT  
XX  
XX Human B-raf substrate nucleotide position 426.  
DE  
XX  
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW stenosis; rheumatoid arthritis; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9850530-A2.  
PN  
XX  
XX 12-NOV-1998.  
PD  
XX  
XX 05-MAY-1998; 98WO-US009249.  
PF  
XX  
XX 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
FA  
XX  
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisch K, Bellon L,  
PI Parry T, Beigelman L, Mcswigen JA, Karpelsky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;

XX  
XX WPI; 1999-009494/01.  
DR  
XX  
XX Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT resensitis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synons.  
PS  
XX  
XX Claim 177; Page 166; 259pp; English.

A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Oy 1004 ACACTCTTCTCCCTCT 1019  
Db 2 ACACUCUCUCUCUCUCU 17

RESULT 312  
ABK03470  
ID ABK03470 standard; RNA; 17 BP.  
XX  
XX ABK03470;  
AC  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX  
XX Human CD20 Zinzyne #21.  
DE  
XX  
XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Synthetic.  
OS  
XX  
XX WO200159103-A2.  
PN  
XX  
XX 16-AUG-2001.  
PD  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
PF  
XX  
XX

PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J.  
 PA (CHOW/) CHOWIRRA B M.  
 XX  
 PI Blatt L, Mcswigen J, Chowirra BM;  
 XX  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX  
 XX Claim 30; Page 154; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a  
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapiers. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOCO. The treatment may further comprise the use of one or more  
 CC therapiers. In particular, the NOCO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOCO expression. The present  
 CC sequence is a zinzyme molecule of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;  
 XX  
 Query Match 0.84; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Qy 799 CACATCTGTGTACTG 814  
 Db 2 CCACUCCUGUGAGUCG 17  
 |||:|:|:|:|:|:|:|:|  
 RESULT 313  
 ABRK00920  
 ID ABRK00920 standard; RNA; 17 BP.  
 AC ABRK00920;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Inozyme #190.

KW Human; ss; antisense therapy; cyrostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian; ribozyme;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; Inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 KW  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PD 09-FEB-2001; 2001WO-US004273.  
 PF  
 XX  
 XX 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J.  
 PA (CHOW/) CHOWIRRA B M.  
 XX  
 PI Blatt L, Mcswigen J, Chowirra BM;  
 XX  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX  
 XX Claim 88; Page 81; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a  
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapiers. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOCO. The treatment may further comprise the use of one or more  
 CC therapiers. In particular, the NOCO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOCO expression. The present  
 CC sequence is an Inozyme of the invention

```
XX SQ Sequence 17 BP; 2 A; 11 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCCAGCCCGGC 634
    |||||
Db 2 CCCCGCAGCCCGGC 17

RESULT 314
ADV06518/c
ID ADV06518 standard; RNA; 17 BP.
XX AC
XX AC ADV06518;
XX DT 10-FEB-2005 (first entry)
XX DE Human BACE DNAzyme substrate sequence #478.
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200116312-A2.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000WO-US023998.
XX PR 31-AUG-1999; 99US-0151713P.
XX PR 27-SEP-1999; 99US-00406643.
XX PR 27-SEP-1999; 99US-0156236P.
XX PR 08-NOV-1999; 99US-00436430.
XX PR 06-DEC-1999; 99US-0169100P.
XX PR 29-DEC-1999; 99US-00474432.
XX PR 29-DEC-1999; 99US-0173612P.
XX PR 30-DEC-1999; 99US-00476387.
XX PR 04-FEB-2000; 2000US-00498824.
XX PR 20-MAR-2000; 2000US-00531025.
XX PR 14-APR-2000; 2000US-0197769P.
XX PR 23-MAY-2000; 2000US-00578223.
XX PR 09-AUG-2000; 2000US-00636385.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A,
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B,
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX DR WPI; 2001-244406/25.
XX PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX PT obesity and heart disease.
XX PS Example 4; Page 386; 717pp; English.
XX CC The present invention relates to the use of enzymatic nucleic acid
XX CC molecules (e.g. ribozymes) to modulate gene expression. The invention
XX CC also methods for their use to down regulate or inhibit the expression of
```

```
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a DNAzyme used in the
CC examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX SQ Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1275 GACCACATCTCCACA 1290
    |||||
Db 17 GTCCACATCTCCACA 2

RESULT 315
ADU86311
ID ADU86311 standard; DNA; 17 BP.
XX AC
XX AC ADU86311;
XX DT 10-FEB-2005 (first entry)
XX DE Human TERT hammerhead ribozyme substrate sequence #342.
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ds.
XX OS Homo sapiens.
XX PN WO200116312-A2.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000WO-US023998.
XX PR 31-AUG-1999; 99US-0151713P.
XX PR 27-SEP-1999; 99US-00406643.
XX PR 27-SEP-1999; 99US-0156236P.
XX PR 08-NOV-1999; 99US-00436430.
XX PR 06-DEC-1999; 99US-0169100P.
XX PR 29-DEC-1999; 99US-00474432.
XX PR 29-DEC-1999; 99US-0173612P.
XX PR 30-DEC-1999; 99US-00476387.
XX PR 04-FEB-2000; 2000US-00498824.
XX PR 20-MAR-2000; 2000US-00531025.
XX PR 14-APR-2000; 2000US-0197769P.
XX PR 23-MAY-2000; 2000US-00578223.
XX PR 09-AUG-2000; 2000US-00636385.
```

XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J, Usman N, Blact L, Beigelman L, Burgin A;  
PI Karpelesky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sprout BS;  
XX WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
XX Example 1; Page 274; 717pp; English.  
XX  
XX The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/C-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
CC zinczyme, and/or DNAzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.  
XX  
XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1687 GACCAGCTTTTCTCA 1702  
DB 1 GGCACGCTTTCCTCA 16  
RESULT 316  
ABK63841/C  
ID ABK63841 standard; DNA; 17 BP.  
XX  
XX ABK63841;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #5.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KM immune disorder; autoimmune disorder; cardiovascular disorder;  
KM vascular disorder; airway disorder; neuropathic disorder; pain;  
KM psychiatric disorder; central nervous system disorder; inflammation;  
KM respiratory condition; opthalmic condition; intestinal condition;  
KM demyelinating disease; small cell lung cancer; depression;  
KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KM neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-IB001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNIV MCGILL.  
XX  
XX Henry JL, Cahill CM, Yaehpal K;  
PI WPI; 2002-241835/29.  
DR  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Claim 24; Page 65; 100pp; English.  
PS  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), opthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastrointestinal tract inflammation, and inflammatory diseases such as  
CC inflammatory bowel diseases. Other disorders and diseases include  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected.  
CC reducing side effects of treatment. ABK63841-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
XX Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 207 CGAATGATAGTACGTC 222  
DB 16 CAAATGATACGTC 1  
RESULT 317  
ACA07747  
ID ACA07747 standard; RNA; 17 BP.  
XX

AC ACA07747;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE NFKB sub-unit modulating zinzyme substrate #146.  
 XX  
 KM Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KM G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;  
 KM lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KM oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KM cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KM lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KM chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KM cyclophosphamide; doxorubicin; fluorouracil cardioplatin; edatrexate;  
 KM gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KM rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KM gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KM transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KM allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002177568-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PP 23-MAY-2001; 2001US-00864785.  
 XX  
 PR 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 XX  
 PA (STIN/) STINGCOMB D T.  
 PA (MCSW/) MCSWIGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 PI Stinchcomb DT, Mcswigen J, Draper KG;  
 XX  
 DR WPI; 2003-340953/32.  
 XX  
 PT Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX  
 PS Claim 3; Page 39; 72pp; English.  
 XX  
 CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil cardioplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury,  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 134 GCCCCAGCGCCAGCC 149  
 DB 2 GCCCCAGCGCCAGCC 17  
 ID ABZ61190 standard; RNA; 17 BP.  
 XX ABZ61190/c  
 AC ABZ61190;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human K-Ras DNAzyme substrate #1302.  
 XX  
 KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KM anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PP 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswigen J;  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 PS Claim 58; Page 110; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ6531, ABZ6520 - ABZ6524,  
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
 QY Query Match 0.8%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 DB 834 CCTGCTGGTGTGTTGGC 849  
 17 CCTGCTGGTGTGTTGGC 2  
 RESULT 319

ADK13263/c  
ID ADK13263 standard; DNA; 17 BP.  
XX  
AC ADK13263;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human glioma endothelial marker (GEM) long tag SEQ ID NO:441.  
XX  
KW glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;  
KM anticancer; anti-glioma; immune response; cytoskeletal;  
KM multi-drug sensitive glioma; human; long tag; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN MO2004016758-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 15-AUG-2003; 2003WO-US025614.  
XX  
PR 15-AUG-2002; 2002US-0403390P.  
PR 01-APR-2003; 2003US-0458978P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Madden SJ, Wang CJ, Cook BP, Lattera J, Walter K;  
XX  
DR WPI; 2004-247973/23.  
XX  
PT Diagnosing glioma by detecting expression product of any one of 255  
PT genes; glioma endothelial markers, in brain tissue sample suspected of  
PT being neoplastic, and comparing the expression with expression in normal  
PT brain tissue sample.  
XX  
XX  
PS Example 2; SEQ ID NO 441; 114pp; English.  
XX  
CC The present invention describes a method (M1) for aiding in the diagnosis  
CC of glioma. (M1) involves detecting an expression product of at least one  
CC gene (I) in a first brain tissue sample (T) suspected of being  
CC neoplastic, where (I) is chosen from any one of 255 genes (glioma  
CC endothelial markers (GEMs)) as given in specification, and comparing the  
CC expression of (I) in (T) with expression of (I) in a second normal brain  
CC tissue sample (R), where increased expression of (I) in (T) relative to  
CC (R), identifies (T) as likely to be neoplastic. Also described: (1)  
CC treating (M2) glioma involves contacting cells of the glioma with an  
CC antibody that specifically binds to a extracellular epitope; (2)  
CC identifying (M3) a test compound as potential anticancer or anti-glioma  
CC drug involves contacting a test compound with the cell which expresses  
CC (I), monitoring an expression product of the at least one gene and  
CC identifying test compound as a potential anticancer drug if it decreases  
CC the expression of at least one gene; (3) identifying (M4) a test compound  
CC as potential anticancer or anti-glioma drug involves contacting a test  
CC compound with the cell which expresses mRNA of at least one gene  
CC identified by a tag as described above, monitoring mRNA of the gene, and  
CC identifying the test compound as a potential anticancer drug if it  
CC decreases the expression of at least one gene; and (4) inducing (M5) an  
CC immune response to glioma involves administering to a mammal, a protein  
CC or (I). (I) have cytostatic activities, and can be used to trigger immune  
CC destruction of glioma cells, and as immune response inducers. (M1) is  
CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi-  
CC drug sensitive glioma in a human. (M5) is useful for inducing an immune  
CC response to a glioma in a mammal having glioma or in a mammal who has had  
CC a glioma surgically removed. The present sequence represents a human GEM  
CC long tag oligonucleotide, which is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 17 BP; 5 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1415 CCTCCAAATGCTCTC 1430  
|||  
Db 16 CCTCCAAATGCTCTC 1  
|||  
RESULT 320  
ADN00720  
ID ADN00720 standard; DNA; 17 BP.  
XX  
AC ADN00720;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human SLT related PCR primer, SEQ ID 19.  
XX  
KW Anorectic; nootropic; neuroprotective; antidiabetic; transgenic animal;  
KM SLT; obesity; eating disorder; insulin resistance; puberty disturbance;  
KM memory damage; sexual function disorder; anorexia; anaemia; human; PCR;  
KM primer; ss.  
XX  
OS Synthetic.  
XX  
PN MO2004023870-A1.  
XX  
PD 25-MAR-2004.  
XX  
PF 09-SEP-2003; 2003WO-JP011501.  
XX  
PR 10-SEP-2002; 2002JP-00264054.  
XX  
PA (TAKEDA ) TAKEDA CHEM IND LTD.  
XX  
PI Mori M, Sugo T, Nishida M, Kaeuga H, Takeomi S;  
XX  
DR WPI; 2004-269810/25.  
XX  
PT Human SLT transgenic animals for evaluating SLT inhibitors and screening  
PT drugs for obesity, eating hyperactivity, insulin resistance, disturbances  
PT during puberty, memory damage or disorder of sexual function.  
XX  
XX  
PS Example 2; SEQ ID NO 19; 79pp; Japanese.  
XX  
CC The present invention relates to a transgenic SLT animal. The transgenic  
CC animal is useful for evaluating SLT inhibitors and screening drugs for  
CC obesity, eating hyperactivity, insulin resistance, disturbances during  
CC puberty, memory damage or disorder of sexual function, or preventives or  
CC remedies for anorexia, anaemia accompanying anorexia or hypoproteinemia,  
CC including clarification of pathological mechanism of these diseases. The  
CC present sequence is a PCR primer, used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 309 CCTTTGGGAGCTGCC 324  
|||  
Db 2 CCTTTGGGAGCTTCC 17  
|||  
RESULT 321  
AD230264/c  
ID AD230264 standard; RNA; 17 BP.  
XX  
AC AD230264;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Human K-Ras substrate RNA sequence SEQ ID NO:1302.  
XX



KW short interfering RNA; siRNA; RNA interference; gene silencing;  
KM cytosolic; cancer; Ras gene; substrate; ss.  
OS Homo sapiens.  
PN US2005080031-A1.  
XX  
XX 14-APR-2005.  
PD  
XX 26-NOV-2003; 2003US-00724270.  
PF  
XX 18-MAY-2001; 2001US-0292217P.  
PR 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 20-JUL-2001; 2001US-0306883P.  
PR 13-AUG-2001; 2001US-0311865P.  
PR 10-SEP-2001; 2001US-0318471P.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 06-MAR-2002; 2002US-0362016P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 20-MAY-2002; 2002WO-US015876.  
PR 29-MAY-2002; 2002US-00157580.  
PR 06-JUN-2002; 2002WO-US016840.  
PR 06-JUN-2002; 2002US-00163552.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 10-SEP-2002; 2002US-00283700.  
PR 15-JAN-2003; 2003US-0440129P.  
PR 20-FEB-2003; 2003WO-US005028.  
PR 20-FEB-2003; 2003WO-US005346.  
PR 16-APR-2003; 2003US-00417012.  
PR 24-APR-2003; 2003US-00422704.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 29-AUG-2003; 2003US-00652791.  
PR 23-OCT-2003; 2003US-00693059.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PI Mcswiggen J;  
XX  
XX WPI; 2005-331166/34.  
DR  
XX  
XX Novel double-stranded short interfering RNA molecule having first  
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,  
PT and second nucleotide sequence having complementarity to first sequence,  
PT useful for treating cancer.  
XX  
XX Example 1; SEQ ID NO 1302; 143pp; English.  
PS  
XX The invention relates to a double-stranded short interfering RNA (siRNA)  
XX molecule (I) comprising a first nucleotide sequence having 19-23  
CC nucleotides complementary to an RNA sequence encoding HER2 or its  
CC portion, and a second nucleotide sequence having 19-23 nucleotides  
CC exhibiting complementarity to the first sequence, and including at least  
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also  
CC described is a method of producing a class of nucleic acid-based gene  
CC modulating agents that exhibit a high degree of specificity for RNA of a  
CC desired target. (I) is useful for modulating HER2 activity in a cell, and  
CC for treating diseases or conditions related to levels of HER2 gene  
CC expression. (I) is useful for treating cancer, such as pancreatic cancer,  
CC bladder cancer, lung cancer, breast cancer or prostate cancer. The  
CC present sequence represents a human K-Ras substrate RNA sequence for a  
CC DNAzyme (ribozyme), which is used in an example from the present  
CC invention for the identification of potential target sites in human Ras  
CC RNA.  
XX  
XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 834 CCTGCTGGTGAATTGC 849  
|||  
Db 17 CCTGCTGGTGAATTGC 2  
RESULT 322  
AED88220/c  
ID AED88220 standard; DNA; 17 BP.  
XX  
XX AED88220;  
AC  
XX 26-JAN-2006 (first entry)  
DT  
XX Human Leukocyte Antigen B allele identification probe, SEQ ID 103.  
XX  
XX HLA; Leukocyte; Antigen; transplant rejection; histocompatibility;  
KM preclinical testing; cancer; cytostatic; diabetes mellitus; antidiabetic;  
KW probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX JP2005185172-A.  
PN  
XX 14-JUL-2005.  
PD  
XX 25-DEC-2003; 2003JP-00430554.  
PF  
XX 25-DEC-2003; 2003JP-00430554.  
PR  
XX 25-DEC-2003; 2003JP-00430554.  
PR  
XX (CANO) CANON KK.  
PA  
XX Tsukada M;  
PI  
XX WPI; 2006-013379/02.  
DR  
XX  
XX Probe set for specific identification of an HLA-B allele in a sample,  
PT useful e.g. in matching transplant donors and recipients, and in  
PT determining suitable treatment for patients with conditions such as  
PT cancer and diabetes mellitus.  
XX  
XX Claim 2; SEQ ID NO 103; 152pp; Japanese.  
PS  
XX The invention relates to a novel probe set for the identification of a  
XX Human Leukocyte Antigen (HLA)-B allele in a sample. The invention further  
CC includes a method for identifying an HLA-B allele using the probe set.  
CC The probe set and method are useful for identifying an HLA-B allele in a  
CC sample. The information gained is useful, for example, in matching organ  
CC donors and recipients, and in guiding clinical decisions in the treatment  
CC of diseases such as cancer and diabetes mellitus. This oligo sequence  
CC represents a probe used in the identification of a Human Leukocyte  
CC Antigen B allele of the invention.  
XX  
XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 438 CGCGAGGCGCTTCATG 453  
|||  
Db 17 CGCGAGGCGCTTCATG 2  
RESULT 323  
AAQ85449/c  
ID AAQ85449 standard; DNA; 18 BP.  
XX  
XX AAQ85449;  
AC  
XX 25-MAR-2003 (revised)  
DT 05-OCT-1995 (first entry)



```
XX PCR primer for HARDS clone p3H226.
DE
XX
XX Hantavirus-Associated Respiratory Distress Syndrome; epitope;
KM immunodiagnostic; vaccine; antigenic; amplification; ss.
XX
XX Synthetic.
OS
XX
XX W09506250-A1.
PN
XX
XX 02-MAR-1995.
PD
XX
XX 25-AUG-1994; 94WO-US009416.
PF
XX
XX 25-AUG-1993; 93US-00111519.
PR 13-SEP-1993; 93US-00120096.
PR 26-OCT-1993; 93US-00141035.
PR 22-MAR-1994; 94US-00210762.
XX
XX (UYNE-) UNIV NEW MEXICO STATE.
PA
XX
XX Hjelle B, Jenison S;
PI
XX
XX WPI; 1995-106942/14.
DR
XX
XX Recombinant antigens of HARDS virus - useful in immuno-diagnostic(s),
PT prophylactics and therapeutics for HARDS virus.
XX
XX
XX Example; Page 14; 78pp; English.
PS
XX
XX The sequence is that of a PCR primer used to amplify clone p3H226 from
CC Hantavirus-Associated Respiratory Distress Syndrome virus. See also
CC AA085436-50, AA086100-10. (Updated on 25-MAR-2003 to correct PW field.)
CC
XX
XX Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 0 U; 2 Other;
SQ
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX 129 CCTGAGCCCGCAGCGCCA 146
Qy |||||:|||||
Db 18 CCTGARCCTCGATGCMCCA 1
XX
XX
XX RESULT 324
XX AAT41606
XX ID AAT41606 standard; DNA; 18 BP.
XX
XX
XX AAT41606;
AC
XX
XX 04-JUN-1997 (first entry)
DT
XX
XX Oligonucleotide containing core DNA regulatory element.
DE
XX
XX Regulatory element; STAT; protein; cytokine; responsive; host cell;
KM transfection; agonist; antagonist; mediated; STAT5; transcription;
KM modulation; signalling pathway; STAT6; Oligonucleotide;
KM electrophoretic mobility shift assay; EMSA; ds.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 5..18
FT /*tag= a
FT /note= "core DNA regulatory element"
XX
XX W09630515-A1.
PN
XX
XX 03-OCT-1996.
PD
XX
XX 25-MAR-1996; 96WO-US004012.
PF
XX
```

```
PR 27-MAR-1995; 95US-00411020.
XX
XX (LIGA-) LIGAND PHARM INC.
XX
XX Seidel HM, Lamb IP, Tian Chan S;
PI
XX
XX WPI; 1996-455362/45.
DR
XX
XX DNA construct for screening modulators of cytokine-mediated transcription
PT - contg. regulatory element and a cytokine-sensitive promoter operably
PT linked to a heterologous gene.
XX
XX
XX Example 1; Page 26; 72pp; English.
PS
XX
XX A novel DNA construct comprises the present oligonucleotide (ON), which
CC contains a core a regulatory element, operably linked to a promoter,
CC which is operably linked to a heterologous gene (preferably a marker
CC gene). The gene is under the transcriptional control of the promoter and
CC the ON sequence when the ON is bound by a STAT protein activated in
CC response to IL-2, IL-3, G-CSF, GM-CSF, erythropoietin, thrombopoietin, or
CC preferably IL-4, IL-7, IL-9, IL-13 or IL-15. Cytokine responsive host
CC cells transfected with the DNA construct can be used to measure the
CC ability of a compound to act as an agonist or antagonist of cytokine
CC mediated gene transcription. In particular, they can be used to screen
CC for cytokine modulators involved in the STAT5 and/or STAT6 protein
CC signalling pathway. Following an electrophoretic mobility shift assay the
CC DNA construct was found to bind IL-4 moderately and IL-13 not determined
CC
XX
XX Sequence 18 BP; 5 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1717 TCCATTTCGGAAGTG 1732
Qy |||||:|||||
Db 3 TCCATTTCGGAATG 18
XX
XX
XX RESULT 325
XX AAX73505/C
XX ID AAX73505 standard; RNA; 18 BP.
XX
XX
XX AAX73505;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flk-1 VEGF receptor hairpin ribozyme substrate #52.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;
KM KDR; hammethead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fme-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX
XX Mus sp.
OS
XX
XX W09715662-A2.
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
PF
XX
XX 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI
XX
XX WPI; 1997-259017/23.
DR
XX
```

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 152; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (Flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 CC  
 SQ Sequence 18 BP; 7 A; 5 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 662 TCTGTGTCATCTGGGT 677  
 Db 18 TCTGTGTCATCTGAGT 3  
 RESULT 326  
 AAX84480  
 ID AAX84480 standard; DNA; 18 BP.  
 AC AAX84480;  
 XX  
 DT 10-SEP-1999 (first entry)  
 XX  
 DE PCR primer for Human EDIRF II coding sequence.  
 XX  
 KW Embryo derived interleukin related factor; diagnosis; detection; therapy;  
 KW EDIRF-related disease; immune disorder; haematopoietic disorder;  
 KW developmental disorder; inflammatory disease; arthritis; psoriasis;  
 KW EDIRF II; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN MO9932632-A1.  
 PD 01-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98MO-US027068.  
 XX  
 PR 19-DEC-1997; 97US-0094890.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX  
 PI Holtzman DA;  
 XX  
 DR WPI; 1999-418929/35.  
 XX  
 PT Nucleic acid encoding embryo-derived interleukin-related factors.  
 XX  
 XX Example 2; Page 75; 116pp; English.  
 XX  
 CC This sequence is a PCR primer for DNA encoding the embryo-derived  
 CC interleukin-related factor (EDIRF) of the invention, designated human  
 CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),  
 CC antibodies (Ab) specific for EDIRF, and other modulators are used; (i) in  
 CC screening and detection assays, e.g. for chromosome mapping, tissue  
 CC typing or forensic studies; (ii) in diagnosis, prognosis or monitoring  
 CC clinical trials; and (iii) for treating or preventing EDIRF-related  
 CC diseases (especially immune, haematopoietic, differentiative,  
 CC developmental or inflammatory disease, including arthritis and psoriasis.

CC The EDIRF coding sequence, or its fragments, are also useful as probes  
 CC and primers (for detecting related sequences and disease-associated  
 CC mutations, also for mutagenesis), for expressing recombinant EDIRF and as  
 CC source of antisense, ribozyme and peptide nucleic acids for inhibiting  
 CC translation of EDIRF-derived mRNA. EDIRF is used to raise Ab (useful for  
 CC detecting EDIRF, including forms with aberrant post-translational  
 CC modification, for affinity purification and therapeutically) and to  
 CC screen for specific modulators (e.g. peptides or peptidomimetics)  
 CC  
 SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1450 GCAGGTGACGCCCA 1465  
 Db 2 GCAGGTGACGCCCA 17  
 RESULT 327  
 AAA07036/c  
 ID AAA07036 standard; DNA; 18 BP.  
 AC AAA07036;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:9.  
 XX  
 XX Integrin beta 3; human endothelial glycoprotein; GP3A, GPIIb; ITGB3;  
 KW C6b1; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor;  
 KW fibronectin receptor; expression inhibition; antisense; tumour formation;  
 KW cancer invasion; bleeding disorder; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US6037176-A.  
 PD 14-MAR-2000.  
 XX  
 PF 25-JUN-1999; 99US-00344520.  
 XX  
 PR 25-JUN-1999; 99US-00344520.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowsett LM, Monia BP;  
 XX  
 DR WPI; 2000-246189/21.  
 XX  
 PT New antisense compound that inhibits human integrin beta3, useful e.g.  
 PT for treating or preventing infection, inflammation and tumors.  
 XX  
 PS Claim 1; Col 39; 33pp; English.  
 XX  
 CC Sequences AAA07035-A07074 represent antisense oligonucleotides targeted  
 CC to the human integrin beta 3 gene, which inhibit its expression. The  
 CC antisense oligonucleotides were designed to target different regions of  
 CC the human integrin beta 3 RNA, and were analysed for their effect on  
 CC integrin beta 3 mRNA levels by quantitative real-time PCR. GAPDH  
 CC (glyceraldehyde-3-phosphate) mRNA levels were measured as a control.  
 CC Integrins constitute one of four classes of cellular adhesion molecules,  
 CC and play an important role in cell migration, cell anchorage to  
 CC substrates and cytoadhesion signalling pathways. They are heterodimeric  
 CC cation-dependent membrane glycoproteins composed of an alpha and beta  
 CC subunit. Integrin beta 3 (also known as human endothelial glycoprotein,  
 CC GP3A, GPIIb, ITGB3, C6b1 and platelet glycoprotein 3a) is the common  
 CC beta subunit partner of the members of the beta-3 subfamily of integrins.  
 CC This family consists of the vitronectin receptor (alpha-V-beta-3) and the  
 CC fibronectin receptor (alpha-III-beta-3). Cells expressing this class of  
 CC integrin can adhere to various matrix proteins and participate in various  
 CC cytoadhesion-driven cellular responses. Integrin beta 3 is implicated in

CC conditions such as vascular stenosis, excessive bone resorption,  
CC angiogenesis (in melanoma), tumour invasion, platelet aggregation and  
CC Glanzmann's thrombasthenia. The oligonucleotides of the invention are  
CC useful for diagnosis, prevention and treatment of conditions associated  
CC with integrin beta 3 expression, such as tumour formation, inflammation,  
CC infections and the diseases mentioned above  
XX  
SQ Sequence 18 BP; 5 A; 8 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 804 CTGTGTACTGTGCTG 819  
DB 18 CTGGGTGACTGTGCTG 3  
RESULT 328  
AAZ48483  
ID AAZ48483 standard; DNA; 18 BP.  
XX  
AC AAZ48483;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18876.  
XX  
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;  
KW inflammation; tumour formation; TNFR1; anticancer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US6007995-A.  
XX  
PD 28-DEC-1999.  
XX  
PF 26-JUN-1998; 98US-00106038.  
XX  
PR 26-JUN-1998; 98US-00106038.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Baker BF, Cowbert LM;  
XX  
DR WPI; 2000-105333/09.  
XX  
PT Antisense inhibition of tumor necrosis factor type 1 expression for  
PT diagnosis, treatment and prevention of disease, particularly tumors.  
PS Example 10; Col 24; 34pp; English.  
XX  
XX The invention provides antisense compounds targeted to human tumour  
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds  
CC can be used in a method of inhibiting the expression of TNFR1 human cells  
CC or tissues. The antisense compounds specifically hybridize with one or  
CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid  
CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1  
CC produced. The antisense compounds and method are useful as research  
CC reagents and diagnostics, and in the treatment and prophylaxis of  
CC infection, inflammation or tumour formation. Sequences AAZ48482-565  
CC represent antisense oligos used for inhibition of the human TNFR1 mRNA  
XX  
SQ Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 105 CCTCTCTGTCTGCTTT 120  
DB 3 CCTCTCTCTGCTTT 18

RESULT 329  
AAZ59805/C  
ID AAZ59805 standard; DNA; 18 BP.  
XX  
AC AAZ59805;  
XX  
DT 19-APR-2000 (first entry)  
XX  
DE Human Smad3 phosphorothioate antisense oligonucleotide, SEQ ID NO:17.  
XX  
KW Smad3; MADH3; hMAD3; JVI5-2; TGF-beta signalling pathway;  
KW transcription factor; expression inhibition; antisense therapy;  
KW tumour formation; inflammation; antisense; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6013788-A.  
XX  
PD 11-JAN-2000.  
XX  
PF 09-APR-1999; 99US-00289376.  
XX  
PR 09-APR-1999; 99US-00289376.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Cowbert LM;  
XX  
DR WPI; 2000-126072/11.  
XX  
PT Antisense inhibition of the human Smad3 gene, useful for diagnosing,  
PT preventing and treating conditions associated with Smad3 expression e.g.  
PT inflammation.  
XX  
PS Claim 11; Col 38; 31pp; English.  
XX  
XX Sequences AAZ49796-259835 represent antisense oligonucleotides targeted  
CC to the human Smad3 gene, which inhibit its expression. The antisense  
CC oligonucleotides were designed to target different regions of the human  
CC Smad3 RNA, and were analysed for their effect on Smad3 mRNA levels by  
CC quantitative real-time PCR. The Smad proteins are a family of cytosolic  
CC proteins which are involved in TGF-beta superfamily signal transduction.  
CC On ligand binding, TGF-beta superfamily proteins (such as bone  
CC morphogenetic protein (BMP), activin and TGF-betas themselves)  
CC phosphorylate Smad proteins, which then homo- or heterodimerise and  
CC translocate to the nucleus to activate target gene transcription. Smad3  
CC (also known as MADH3, hMAD3 and JVI5-2) is a member of a subgroup of Smad  
CC family transcription factors, the pathway-restricted Smads, which are  
CC regulated by TGF-beta and activins. It can heterodimerise with Smad4  
CC (US6013787-A, AAY69622), the complex being able to activate TGF-beta  
CC inducible transcription. The oligonucleotides of the invention are useful  
CC for diagnosis, prevention and treatment of conditions associated with  
CC Smad3 expression, such as tumour formation, inflammation and certain  
CC infections  
XX  
SQ Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1118 TCATCTACTGCTGCTT 1133  
DB 18 TCATCTACTGCCGCTT 3  
RESULT 330  
AAZ76614  
ID AAZ76614 standard; DNA; 18 BP.  
XX  
AC AAZ76614;

XX 10-SEP-2001 (first entry)  
 XX Human biallelic marker downstream amplification primer SEQ ID NO:10970.  
 DE  
 XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO9954500-A2.  
 PN  
 XX 28-OCT-1999.  
 PD  
 XX 21-APR-1999; 99WO-IB000822.  
 PP  
 XX 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 PR  
 XX (GBST ) GENSET.  
 PA  
 XX Cohen D, Blumenfeld M, Chumakov I,  
 PI  
 XX WPI, 2000-013267/01.  
 DR  
 XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX  
 PS Claim 9, Page 2569; 2745BP; English.  
 XX  
 CC AAZ6564 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence listing from the  
 CC present invention  
 CC  
 SQ Sequence 18 BP; 1 A; 9 C; 0 G; 8 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1404 CTTGACCTTCTCTCC 1419  
 |||||  
 DB 2 CTTGATCTTCTCTCC 17  
 |||||  
 RESULT 331  
 AAH37701/C  
 ID AAH37701 standard; DNA; 18 BP.  
 XX  
 XX AAH37701;  
 AC  
 XX 14-AUG-2001 (first entry)  
 DT  
 XX SNP specific upper PCR primer SEQ ID 497.  
 DE  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 PN MO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 PD  
 PF 13-OCT-2000; 2000WO-US028436.  
 PF  
 XX 15-OCT-1999; 99US-0160096P.  
 PR  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 PA  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 XX WPI, 2001-290930/30.  
 DR  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PS  
 XX Claim 1; Page 52; 83bp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC diseases of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 CC  
 SQ Sequence 18 BP; 4 A; 4 C; 8 G; 2 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1223 CCACCCGGGTATCTCA 1238  
 |||||  
 DB 18 CCACCCGGGTCTCCA 3  
 |||||  
 RESULT 332  
 ABT04979  
 ID ABT04979 standard; DNA; 18 BP.  
 XX  
 XX ABT04979;  
 AC  
 XX 11-OCT-2002 (first entry)  
 DT  
 XX TNFR1 expression modulation related antisense oligo SEQ ID No 9.  
 DE  
 XX Antisense compound; tumour necrosis factor receptor 1; liver disease;  
 KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;

KM human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200248168-A1.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 22-OCT-2001; 2001WO-US051224.  
 XX  
 PR 24-OCT-2000; 2000US-00695451.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Baker BF, Cowsett LM, Zhang H, Dean NM;  
 XX  
 DR WPI; 2002-583481/62.  
 XX  
 PT Novel antisense compound targeted to nucleic acid molecule encoding tumor  
 PT necrosis factor receptor 1 (TNFR1), useful for treating humans having  
 PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.  
 XX  
 PS Example 10; Page 44; 121pp; English.  
 XX  
 CC The invention relates to an antisense compound 8 to 30 nucleotides in  
 CC length targeted to nucleic acid molecule encoding tumour necrosis factor  
 CC receptor 1 (TNFR1), where the antisense compound inhibits expression of  
 CC TNFR1. The antisense compound is useful for inhibiting the expression of  
 CC TNFR1 in cells or tissues. The antisense compound is also useful for  
 CC treating an animal (preferably human) having a disease or condition  
 CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver  
 CC injury) or a hyperproliferative disorder such as cancer, by inhibiting  
 CC the expression of TNFR1. The antisense compound is useful for  
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
 CC This polynucleotide sequence represents a human oligonucleotide relating  
 CC to the TNFR1 of the invention  
 XX  
 SO Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 105 CCCCTCGTCTGCTT 120  
 Db 3 CCCCTCTCTGCTT 18  
 XX  
 RESULT 333  
 ABK63840/c  
 ID ABK63840 standard; DNA; 18 BP.  
 XX  
 AC ABK63840;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #4.  
 XX  
 KM Human; neurokinin receptor-1; NK-1; dermatological disorder;  
 KM immune disorder; autoimmune disorder; cardiovascular disorder;  
 KM vascular disorder; airway disorder; neuropathic disorder; pain;  
 KM psychiatric disorder; central nervous system disorder; inflammation;  
 KM respiratory condition; ophthalmic condition; intestinal condition;  
 KM demyelinating disease; small cell lung cancer; depression;  
 KM hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
 KM neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
 KM neuro-pathological disorder; stress; antisense; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200213799-A2.  
 XX  
 PD 21-FEB-2002.

XX  
 PF 17-AUG-2001; 2001WO-IB001510.  
 XX  
 PR 18-AUG-2000; 2000US-0226086P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Henry JL, Cahill CM, Yashpal K;  
 XX  
 DR WPI; 2002-241835/29.  
 XX  
 PT Treating pathological condition involving neurokinin receptor-1, e.g.  
 PT pain or inflammation, by administering oligonucleotide or a non-  
 PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
 PT pathway.  
 XX  
 PS Claim 24; Page 65; 100pp; English.  
 XX  
 CC The invention relates to a method of treating a pathological condition  
 CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
 CC receptor, especially treating, attenuating or preventing pain or  
 CC inflammatory condition. The method comprises administering to a mammal, a  
 CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
 CC which interferes with function or production of NK-1 receptors. The  
 CC method is useful for treating a pathological condition characterised by  
 CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
 CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
 CC psychosia, schizophrenia), gut inflammation, arthritis, and central or  
 CC peripheral aspects of chronic or acute pain, and for treating,  
 CC attenuating or preventing pain or inflammation such as peripheral,  
 CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
 CC pain relating to psychiatric disorders and central nervous system  
 CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
 CC in a mammal, in particular human. NK-1 receptor related disorders,  
 CC diseases, or pathological conditions treatable by this method include  
 CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
 CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
 CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
 CC Crohn's disease), cardiovascular conditions (stroke), chronic  
 CC gastrointestinal tract inflammation, and inflammatory diseases such as  
 CC inflammatory bowel diseases. Other disorders and diseases include  
 CC cardiovascular pathologies including stroke, chronic inflammatory  
 CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
 CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
 CC disorders such as allergies and poison ivy, vasospastic diseases such as  
 CC angina, addiction disorders such as alcoholism, neurodegenerative  
 CC disorders such as acquired immune deficiency syndrome (AIDS) related  
 CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
 CC disorders such as peripheral neuropathy, edema, stress related and  
 CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
 CC effectively treat chronic conditions and other pathological states  
 CC without the co-administration of substance P, and reduce the number of  
 CC activated receptors while not reducing the number of quiescent NK-1  
 CC receptors. Receptors not chronically stimulated are less affected.  
 CC reducing side effects of treatment. ABK63834-ABK6396 represent NK-1  
 CC receptor coding sequences and oligonucleotides of the invention  
 XX  
 SO Sequence 18 BP; 3 A; 3 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 207 CGAATGATGATACGTC 222  
 Db 16 CAAATGATGATACGTC 1  
 XX  
 RESULT 334  
 ADD40778/c  
 ID ADD40778 standard; DNA; 18 BP.  
 XX

```

AC ADD40778;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human tenascin-W PCR primer #6.
XX
XX Tenascin-W; stem cell marker; cancer; thrombosis; wound healing;
XX atherosclerosis; osteogenesis; bone healing; osteoporosis;
XX excessive bone growth; cytosatic; osteopathic; anticoagulant;
XX thrombolytic; vulnerary; antiarteriosclerotic;
XX extracellular matrix molecule; metastatic tumour; peritoneum; human; PCR;
XX primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003080663-A2.
XX
XX 02-OCT-2003.
XX
XX 26-MAR-2003; 2003WO-EP003150.
XX
XX 27-MAR-2002; 2002GB-00007224.
XX
XX (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
XX
XX Chiquet-Ehrismann R, Scherberich A;
XX
XX WPI; 2003-876907/81.
XX
XX New tenascin-W polypeptide and nucleic acid molecule, useful for
XX manufacturing a medicament for the prophylaxis or treatment of cancer, or
XX a condition requiring increased tenascin-W levels, e.g. wound healing or
XX atherosclerosis.
XX
XX Example 3; SEQ ID NO 22; 84bp; English.
XX
XX The present invention relates to tenascin-W proteins (ADD40758 and
XX ADD40760) and their coding sequences (ADD40757 and ADD40759). Tenascin-W
XX is an extracellular matrix molecule that is specifically expressed in
XX metastatic tumour cells and in the peritoneum, the stem cell compartment
XX for osteogenesis. Tenascin-W is useful as a stem cell marker and are
XX useful for the treatment of cancer, including metastatic cancer (e.g. a
XX solid tumour, glioblastoma, prostate, lung, colorectal, osteo- or breast
XX carcinoma), any disease or condition requiring increased tenascin-W
XX levels (e.g. thrombosis, wound healing or atherosclerosis), a condition
XX ameliorated by the promotion of osteogenesis (e.g. bone healing or
XX osteoporosis) or a bone disease resulting from excessive bone growth. The
XX present sequence is a PCR primer, which was used to isolate the coding
XX sequence for human tenascin-W.
XX
XX Sequence 18 BP; 2 A; 1 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1276 ACCACCATCTCCACAG 1291
XX |||||
XX Db 16 ACCACCTCTCCACAG 1
XX
XX RESULT 335
XX ADE13426/c
XX ID ADE13426 standard; DNA; 18 BP.
XX
XX ADE13426;
XX
XX 29-JAN-2004 (first entry)
XX
XX HLA class I allele specific primer #42.
XX
XX ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.
XX

```

```

OS Homo sapiens.
XX
XX US2003165884-A1.
XX
XX 04-SEP-2003.
XX
XX 25-APR-2002; 2002US-00133779.
XX
XX 20-DEC-1999; 99US-0172768P.
XX 20-DEC-2000; 2000US-00747391.
XX
XX (STEM-) STEMCTYE INC.
XX
XX Chow R, Tonaï R;
XX
XX WPI; 2003-874916/81.
XX
XX Identifying class I or II Human Leukocyte Antigen genotypes using
XX hybridization and amplification assays.
XX
XX Claim 7; SEQ ID NO 42; 66bp; English.
XX
XX The invention relates to a method of identifying a class I or II Human
XX Leukocyte Antigen (HLA) genotype of a subject using hybridisation and
XX amplification assay. The method is used for determining the HLA genotype
XX of a subject. The present sequence represents a HLA class I allele
XX specific primer.
XX
XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.8%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 2.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 438 CGCGAGGCGCTTCATG 453
XX |||||
XX Db 18 CGCGAGGCGCTTCATG 3
XX
XX RESULT 336
XX ADL09276/c
XX ID ADL09276 standard; DNA; 18 BP.
XX
XX ADL09276;
XX
XX 06-MAY-2004 (first entry)
XX
XX HLA locus-specific capture oligonucleotide #42.
XX
XX ss; primer; human leukocyte antigen; HLA; HLA genotyping; human; PCR.
XX
XX Homo sapiens.
XX
XX US6670124-B1.
XX
XX 30-DEC-2003.
XX
XX 20-DEC-2000; 2000US-00747391.
XX
XX 20-DEC-1999; 99US-0172768P.
XX
XX (STEM-) STEMCTYE INC.
XX
XX Chow R, Tonaï R;
XX
XX WPI; 2004-068584/07.
XX
XX Identifying an HLA genotype of a subject by hybridizing the amplification
XX products with an HLA locus-specific capture oligonucleotide and detecting
XX the detectable complexes to identify the HLA genotype of the subject.
XX
XX Example 1; SEQ ID NO 42; 66bp; English.
XX

```

CC The invention describes a method of identifying a human leukocyte antigen  
CC (HLA) genotype of a subject comprising: obtaining a sample comprising a  
CC template nucleic acid from the subject; amplifying the template nucleic  
CC acid with HLA allele-specific forward primers and HLA allele-specific  
CC reverse primers to form amplification products; hybridizing the  
CC amplification products with an HLA locus-specific capture oligonucleotide  
CC ; and detecting the detectable complexes to identify the HLA genotype of  
CC the subject. The present sequence represents one of 276 HLA locus-  
CC specific capture oligonucleotides of the invention.

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGAGGCGCTTCATG 453  
|||  
18 CGCGAGGCGCTTCATG 3

RESULT 337

ADN35828  
ID ADN35828 standard; DNA; 18 BP.

XX  
AC ADN35828;

XX 01-JUL-2004 (first entry)

XX Human NSCLC gene antisense-S oligonucleotide #44.

XX ss; cytosratic; gene therapy; vaccine; non-small cell lung cancer; NSCLC;

KW diagnosis; cancer; URLC1; antisense.

XX Homo sapiens.

PN W0204031413-A2.

XX 15-APR-2004.

XX 22-SEP-2003; 2003WO-JP012072.

XX 30-SEP-2002; 2002US-0414673P.

PR 28-FEB-2003; 2003US-0451374P.

PR 28-APR-2003; 2003US-0466100P.

PA (ONCO-) ONCOTHERAPY SCI INC.

PA (UITY) UNIV TOKYO.

PI Nakamura Y, Daigo Y, Nakatsuru S;

DR WPI; 2004-330206/30.

XX Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)  
PT comprises determining an expression level of an NSCLC-associated gene in  
PT a sample.

XX Disclosure; SEQ ID NO 509; 394bp; English.

XX The invention relates to a method of diagnosing non-small cell lung  
CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by  
CC determining the expression level of a NSCLC-associated gene in a  
CC biological sample derived from the subject, where an increase or decrease

CC of the level compared to a normal control level of the gene indicates  
CC that the subject suffers from or is at risk of developing NSCLC. The  
CC method is useful in diagnosing NSCLC or a predisposition to developing  
CC NSCLC in a subject. The compound, polynucleotide and the encoded  
CC polypeptide and composition are useful in treating or preventing NSCLC.

CC This sequence corresponds to an antisense oligonucleotide of genes that  
CC are differentially expressed in NSCLC cells.

XX Sequence 18 BP; 4 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1277 CCACCATCTCCACAGT 1292  
|||  
3 CGGCATCTCCACAGT 18

RESULT 338

ADRO6011  
ID ADRO6011 standard; DNA; 18 BP.

XX  
AC ADRO6011;

XX 21-OCT-2004 (first entry)

XX Human TNFR1 antisense oligonucleotide seqid 9.

XX cytosratic; gene therapy; apoptosis inhibitor;

KW radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;

XX human; antisense oligonucleotide; antisense technology; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..18

FT /\*cag= b

FT /mod\_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone"

FT modified\_base 1..4

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)

FT nucleotides"

FT /\*cag= c

FT /mod\_base= OTHER

FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)

FT nucleotides"

FT US2004147471-A1.

XX 29-JUL-2004.

XX 06-NOV-2003; 2003US-00702817.

XX 26-JUN-1998; 98US-00106038.

PR 17-JUN-1999; 99WO-US013763.

PR 24-OCT-2000; 2000US-00695451.

XX (ZHAN/) ZHANG H.

PA Zhang H;

PI WPI; 2004-561407/54.

XX Inhibiting radiation-induced apoptosis in a cell or tissue comprises  
PT administering to the cell or tissue an antisense oligonucleotide targeted  
PT to a nucleic acid molecule encoding tumor necrosis factor receptor 1.  
XX Example 10; SEQ ID NO 9; 24bp; English.

SQ Sequence 18 BP; 0 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 105 CCCCTCTGCTGCTTT 120  
 |||||  
 DB 3 CCTCTCTCTGCTTT 18

RESULT 339  
 ADX58092/c  
 ID ADX58092 standard; DNA; 17 BP.  
 XX  
 AC ADX58092;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Primer Gamma 15 for single chain antibody heavy chain variable fragment.  
 XX  
 XX virucide; vaccine; single chain antibody; HSV; glycoprotein;  
 KM glycoprotein D; herpes simplex virus; HSV infection; RT-PCR; primer; ss;  
 KM heavy chain.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005011580-A2.  
 XX  
 PD 10-FEB-2005.  
 XX  
 PP 26-JUL-2004; 2004WO-US024013.  
 XX  
 PR 25-JUL-2003; 2003US-0489984P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Simmons A, Chen J;  
 XX  
 DR WPI; 2005-142827/15.  
 XX  
 PT New single chain antibody that specifically binds to a Herpes Simplex  
 PT Virus (HSV) glycoprotein, useful in preparing a composition for  
 PT preventing or treating a HSV infection.  
 XX  
 PS Example 1; SEQ ID NO 30; 99bp; English.

CC The specification describes a single chain antibody that specifically  
 CC binds to a herpes simplex virus (HSV) glycoprotein, e.g. glycoprotein D.  
 CC The single chain antibody of the invention is useful for preparing a  
 CC composition for preventing or treating a HSV infection. C region RT-PCR  
 CC primer ADX58077 with gamma degenerate signal sequence RT-PCR primers  
 CC ADX58078-ADX58094 were used to amplify cDNA encoding single chain  
 CC antibody heavy chain variable fragments. The amplicons were used to  
 CC generate single chain antibodies of the invention.  
 CC  
 CC Sequence 17 BP; 5 A; 4 C; 5 G; 1 T; 0 U; 2 Other;

Query Match 0.8%; Score 14.2; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 310 CTTTGGGAGCTGCC 324  
 |||||  
 DB 17 CTTTGGGAGCTGCC 3

RESULT 340  
 AAT76447/c  
 ID AAT76447 standard; DNA; 14 BP.  
 XX  
 AC AAT76447;  
 XX

DT 16-SEP-1997 (first entry)

DE Substance P receptor antisense oligonucleotide.  
 XX  
 XX Asclma; airway epithelium; adenosine free; cystic fibrosis;  
 KM chronic obstructive pulmonary disease; bronchitis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640162-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PP 06-JUN-1996; 96WO-US009306.  
 XX  
 PR 07-JUN-1995; 95US-00474497.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW, Metzger WJ;  
 XX  
 DR WPI; 1997-051871/05.  
 XX  
 PT Treatment of airway diseases such as asthma - by topically applying  
 PT adenosine-free antisense oligonucleotide to airway epithelium of  
 PT subject.  
 XX  
 PS Example 5; Page 40; 71pp; English.

CC A method for treating airway disease in a subject has been produced,  
 CC which involves the topical administration of an essentially adenosine  
 CC free antisense oligonucleotide (ON) to the airway epithelium of the  
 CC subject. The present sequence is an antisense oligonucleotide specific  
 CC for the substance P receptor. The method can be used to treat airway  
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary  
 CC disease, bronchitis and other airway diseases characterised by an  
 CC inflammatory response. By eliminating adenosine from the antisense ON,  
 CC its liberation upon antisense degradation is prevented, thereby  
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-  
 CC reactive airways

SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 AGCCGACAAAGAA 397  
 |||||  
 DB 14 AGCCGACAAAGAA 1

RESULT 341  
 AAX54238/c  
 ID AAX54238 standard; DNA; 14 BP.  
 XX  
 AC AAX54238;  
 XX  
 DT 05-JUL-1999 (first entry)

DE Substance P receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;  
 XX impaired respiration; inflammation; lung disease;  
 XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KM acute asthma; allergy; asthma; impeded respiration;  
 KM respiratory distress syndrome; pain; cystic fibrosis;  
 KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KM prostate cancer; ss.  
 XX



OS Synthetic.  
XX  
XX W09913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nycce JW;  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX Disclosure; Page 59; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AA52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
XX end and the junction between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AA55272-74. These multiple target oligonucleotides  
XX (specifically AA55180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impaired respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 384 AGCCCAAAAAGAA 397  
DB 14 AGCCCAAAAAGAA 1  
RESULT 342  
AA333682/C  
ID AA333682 standard; DNA; 14 BP.  
XX  
XX AAA33682;  
AC  
XX  
XX 28-JUL-2000 (first entry)  
XX  
XX Low adenosine antisense oligonucleotide SEQ ID NO:1371.  
XX  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
XX phosphorocholate; impaired respiration; inflammation; allergy;  
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
XX antiallergic; antiaesthetic; cyostatic; analgesic; impaired airway;  
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
XX cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX

OS Homo sapiens.  
XX  
XX W0200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nycce JW;  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers.  
XX  
XX Claim 18; Page 436; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets  
XX nucleic acids involved in bronchoconstriction, allergies, and/or  
XX inflammation. The ON can have antiinflammatory, antiallergic,  
XX antiaesthetic, cyostatic and analgesic activities. The compositions are  
XX useful for the treatment of diseases associated with inflammation,  
XX impaired airways, including lung disease and diseases whose secondary  
XX effects afflict the lungs of a subject. They can be used for treating  
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
XX impaired respiration, respiratory distress syndrome, pain, cystic  
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
XX pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
XX carcinomas, and cancers which may metastasize to the lungs, including  
XX breast and prostate cancer. The reduction of the adenosine content of the  
XX ONs reduces side effects. The A-containing ONs break down with the  
XX release of deoxyadenosine which activates adenosine receptors causing  
XX bronchoconstriction and inflammation. AA32313 to AA35312 represent the  
XX nucleotide sequences given in the sequence listing from the present  
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AA32313 to  
XX AA3392) are specifically claimed ONs from the present invention. N.B.  
XX Sequences given in the disclosure of the present invention do not match  
XX up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing  
SQ  
Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
QY 384 AGCCCAAAAAGAA 397  
DB 14 AGCCCAAAAAGAA 1  
RESULT 343  
AA289118  
ID AA289118 standard; DNA; 14 BP.  
XX  
XX AA289118;  
AC  
XX  
XX 02-JUN-2000 (first entry)  
XX  
XX Rice OPR17 PCR primer #1.  
XX  
XX Molecular marker; rice; PCR primer; PABD marker; SCAR marker; ss.  
XX  
XX Oryza sativa.  
OS

XX CN1237328-A.  
PN 08-DEC-1999.  
XX 10-APR-1999; 99CN-00103764.  
XX 10-APR-1999; 99CN-00103764.  
XX (ANHU-) ANHU ACAD AGRIC SCI.  
XX Yang J, Wang X, Li L;  
XX WPI; 2000-238142/21.  
XX Application of molecular marking technique in quick determination of true  
PT or false and purity of hybrid rice seed.  
XX Example 5; Page 10; 12pp; Chinese.  
XX This invention describes a novel molecular marking technique which allows  
CC the quick and accurate determination of authenticity and purity of rice  
CC hybridized combination and hybrid species. The method involves designing  
CC stable PCR primers from a PAPD marker and utilizing SCAR markers to make  
CC the determination of authenticity and purity of rice hybridized  
CC combination and hybrid species in 1-2 days. Accuracy is identical to that  
CC of planting determination, and is reliable. AA89110-289135 represent  
CC primers used in the method of the invention  
XX  
SQ Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 232 GACTCAGACCTCTC 245  
DB 1 GACTCAGACCTCTC 14  
RESULT 344  
AAF19804/c  
ID AAF19804 standard; DNA; 14 BP.  
XX AAF19804;  
AC  
XX 14-MAR-2001 (first entry)  
DT  
XX  
DE Human substance P receptor polynucleotide fragment #1371.  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; analgesic; hypotensive; cytostatic;  
KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200062736-A2.  
PN  
XX 26-OCT-2000.  
PD  
XX 24-MAR-2000; 2000WO-US008020.  
PF  
XX 06-APR-1999; 99US-0127958P.  
PR  
XX (UYEC-) UNITV EAST CAROLINA.  
PA (NYCE/) NYCE J W.

XX NYCE JW;  
PI WPI; 2000-679539/66.  
XX  
DR Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.  
XX  
XX  
PS Claim 14; Page 245; 1592pp; English.  
XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (i) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antisthmatic, hypotensive and cyostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive proteins. The  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 384 AGCCCAAAAAGAA 397  
DB 14 AGCCCAAAAAGAA 1  
RESULT 345  
AB272765  
ID AB272765 standard; RNA; 14 BP.  
XX AB272765;  
AC  
XX 09-APR-2003 (first entry)  
DT  
XX  
DE Rod opsin hairpin ribozyme target oligonucleotide SEQ ID NO:5.  
XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;  
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;  
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;  
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200288320-A2.  
PN  
XX 07-NOV-2002.  
PD  
XX

PF 01-MAY-2002; 2002WO-US013679.  
XX  
XX 01-MAY-2001; 2001US-00847601.  
XX  
XX (UYFL ) UNIV FLORIDA.  
XX  
XX Lewin AS, Shaw LC, Grant MB;  
XX WPI; 2003-111880/10.  
XX  
XX A recombinant adeno-associated virus-vectored ribozyme composition,  
PT useful for treating a disease or dysfunction of the mammalian eye e.g.  
PT retinal disease, e.g. diabetic retinopathy or age-related macular  
PT degeneration.  
XX  
XX Claim 1; Page 61; 115pp; English.  
XX  
XX The present invention describes a recombinant adeno-associated virus  
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a  
CC first ribozyme that specifically cleaves an mRNA encoding a protein,  
CC polypeptide, or peptide selected from the group of rod opsin, INOS,  
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin  
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a  
CC vector comprising a polynucleotide encoding the ribozyme, where the  
CC polynucleotide operably positioned downstream of at least a first  
CC promoter that directs expression of the polynucleotide in a selected  
CC mammalian cell transformed with the vector; (c) a viral particle  
CC comprising the ribozyme or the polynucleotide; or (d) an AAV vector  
CC comprising the ribozyme or the polynucleotide; or (e) a host cell  
CC comprising the ribozyme or the polynucleotide. Also described is a method  
CC for decreasing the amount of mRNA encoding a selected polypeptide in a  
CC retinal cell of a mammalian eye, comprising providing to the eye the  
CC composition described above, and for a time effective to specifically  
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can  
CC be used in gene therapy. (I) can be used for treating a disease or  
CC dysfunction of the mammalian eye, such as a retinal disease or retinal  
CC degeneration. (I) is also useful for manufacturing a medicament for  
CC treating the diseases mentioned above, including autoimmune dominant  
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
CC for treating, decreasing the severity, or ameliorating the symptoms of a  
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,  
CC blindness, a reduction in central or peripheral vision, or a reduction in  
CC total vision. AB272763 to AB272953 represent sequences used in the  
CC exemplification of the present invention  
XX  
XX Sequence 14 BP; 0 A; 7 C; 3 G; 0 T; 4 U; 0 Other;  
SQ  
XX  
XX Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 689 TGCTGCGCTTCCCC 702  
||:|||||:  
Db 1 UGUGGCGCCUCCCC 14  
||:|||||:  
RESULT 346  
AB295498/C  
ID AB295498 standard; DNA; 14 BP.  
XX  
XX  
XX AB295498;  
AC  
XX  
XX 17-OCT-2003 (first entry)  
DT  
XX  
XX Human substance P receptor antisense fragment no.1362.  
DE  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

XX  
XX Homo sapiens.  
OS  
XX  
XX WO200285308-A2.  
PN  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
DR  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 10740; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cycostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 384 AGCCCAAAAGAA 397  
|||||||:  
Db 14 AGCCCAAAAGAA 1  
|||||||:  
RESULT 347  
ABD19637/C  
ID ABD19637 standard; DNA; 14 BP.  
XX  
XX  
XX ABD19637;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Human substance P receptor DNA fragment 1362.  
DE  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;

emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
pulmonary transplantation rejection; de.  
Homo sapiens.  
WO200285309-A2.  
31-OCT-2002.  
23-APR-2002; 2002WO-US013143.  
24-APR-2001; 2001US-0286036P.  
(EPIC-) EPIGENESIS PHARM INC.  
Myce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;  
Miller S, Tang L, Shahabuddin S;  
MPI, 2003-093058/08.  
Pharmaceutical composition for treating asthma, has antisense  
oligonucleotide containing less percentage of adenosine, targeted to  
nucleic acids associated with lung airway or lung dysfunction, and  
bronchodilating agent.  
Claim 15; SEQ ID NO 10740; 763bp; English.  
This invention describes a novel composition (a) a first active agent,  
comprising oligonucleotides, effective for alleviating  
bronchoconstriction, respiratory tract inflammation, allergies and  
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
surfactant depletion or hyposecretion, when administered to a mammal. The  
oligonucleotides are derived from a gene encoding or regulating  
expression of a target polypeptide associated with lung airway or lung  
dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
The invention also describes a kit, that comprises: (a) a delivery  
device, in separate containers, (b) the oligonucleotides, (c)  
instructions for adding a carrier and for use of the kit. The composition  
of the invention has antiallergic, antiinflammatory, antiasthmatic, is a  
beta-adrenergic, hypotensive, immunosuppressive and cytostatic activity, is a  
beta-adrenergic agonist. The composition is useful for preventing or  
treating a respiratory, lung or malignant disease. The administered  
composition comprises oligo and is administered to reduce the production  
or availability, or to increase the degradation of the target mRNA or to  
reduce the amount of target polypeptide present in the lungs. The  
pulmonary obstruction, and/or bronchoconstriction and/or lung  
inflammation, allergies and/or surfactant hypoproduction are associated  
with a disease or condition such as pulmonary vasoconstriction,  
inflammation, allergies, asthma, impeded respiration, respiratory  
distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
transplantation rejection, pulmonary infections, bronchitis or cancer.  
The reduced adenosine content of the anti-sense oligos corresponding to  
c thymidines present in the target RNA serves to prevent the breakdown of  
the oligonucleotides into products that free adenosine into the system  
e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
prevent any unwanted effects due to it  
Sequence 14 BP; 0 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AA090578;  
01-FEB-1996 (first entry)  
Encodes recombinant bile salt-activated lipase N-terminal sequence.  
Bile salt activated lipase; BAL; C-terminal repeat; ss.  
Synthetic.  
JP0711891-A.  
02-MAY-1995.  
30-SEP-1993; 93JP-00245079.  
30-SEP-1993; 93JP-00245079.  
(MEIP ) MEIJI MILK PROD CO LTD.  
MPI, 1995-196318/26.  
P-PSDB; AAR75106.  
New recombinant bile salt-activating lipase(s), DNA encoding them and  
vectors - useful for high level expression of the lipase(s) by fermenter-  
culturing.  
Claim 3; Page 10; 31pp; Japanese.  
New lipases are ones in which 1-15 repeats of any of the sequences  
AAR75099-R75105 (encoded by AA090570-090576) are attached to the C-  
terminus of the bile salt-activated lipase (BAL) of sequence AAR75098  
(encoded by AA090569) and/or in which the amino acid sequence SMTGS  
(encoded by AA090578) is attached to the N-terminus of the BAL. The  
recombinant lipases can be produced by fermentation in transformed Pichia  
pastoris GS 115 host cells  
Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1133 TCAATGACAGGTTTC 1146  
1 TCAATGACAGGTTTC 14  
RESULT 349  
AAV93851  
ID AAV93851 standard; RNA; 15 BP.  
AAV93851;  
18-FEB-1999 (first entry)  
Target sequence with sequence homology to c-raf and B-raf position 426.  
Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
screening; identification; synthesis; deprotection; purification; cancer;  
inflammation; psoriasis; non-hepatic ascites; infection; genetic diffc;  
restenosis; rheumatoid arthritis; ss.  
Homo sapiens.  
WO98050530-A2.  
12-NOV-1998.  
05-MAY-1998; 98WO-US009249.  
09-MAY-1997; 97US-0046059P.

PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUN-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L,  
PI Parry T, Beigelman L, Mcswigen JA, Karpelisy A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX WPI; 1999-009494/01.  
XX  
XX Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX  
XX Claim 180; Page 177; 259pp; English.  
XX  
XX A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalyzes (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-rat. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV91877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX  
SQ Sequence 15 BP; 2 A; 6 C; 0 G; 0 T; 7 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
Qy 1004 ACATCTTCTTCCTC 1017  
Db 1 ACATCTTCTTCCTC 14  
RESULT 350  
ABK63843/C  
ID ABK63843 standard; DNA; 15 BP.  
XX  
AC ABK63843;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Neurokinin 1 receptor (NK-1) antisense oligonucleotide #7.  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
KW immune disorder; autoimmune disorder; cardiovascular disorder;  
KW vascular disorder; airway disorder; neuropathic disorder; pain;  
KW psychiatric disorder; central nervous system disorder; inflammation;  
KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.

XX  
XX Homo sapiens.  
OS  
XX WO200213799-A2.  
PN  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2001; 2001WO-IB001510.  
PE  
XX 18-AUG-2000; 2000US-0226086P.  
PR  
XX (UYMC-) UNIV MCGILL.  
PA  
XX Henry JL, Cahill CM, Yaehpal K;  
PI WPI; 2002-241835/29.  
DR  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Claim 24; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
CC receptor, especially treating, attenuating or preventing pain or  
CC inflammatory condition. The method comprises administering to a mammal, a  
CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
CC which interferes with function or production of NK-1 receptors. The  
CC method is useful for treating a pathological condition characterised by  
CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
CC psychiatric and central nervous system disorders (e.g. anxiety,  
CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
CC peripheral aspects of chronic or acute pain, and for treating,  
CC attenuating or preventing pain or inflammation such as peripheral,  
CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
CC pain relating to psychiatric disorders and central nervous system  
CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
CC in a mammal, in particular human. NK-1 receptor related disorders,  
CC diseases, or pathological conditions treatable by this method include  
CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
CC (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and  
CC Crohn's disease), cardiovascular conditions (stroke), chronic  
CC gastro-intestinal tract inflammation, and inflammatory diseases such as  
CC cardiovascular pathologies including stroke, chronic inflammatory  
CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
CC disorders such as allergies and poison ivy, vasospastic diseases such as  
CC angina, addiction disorders such as alcoholism, neurodegenerative  
CC disorders such as acquired immune deficiency syndrome (AIDS) related  
CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
CC disorders such as peripheral neuropathy, oedema, stress related and  
CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
CC effectively treat chronic conditions and other pathological states  
CC without the co-administration of substance P, and reduce the number of  
CC activated receptors while not reducing the number of quiescent NK-1  
CC receptors. Receptors not chronically stimulated are less affected.  
CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
CC receptor coding sequences and oligonucleotides of the invention  
XX  
SQ Sequence 15 BP; 3 A; 3 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 209 AATGATTAACGTC 222  
Db 14 AATGATTAACGTC 1

RESULT 351  
 AAT94355  
 ID AAT94355 standard; DNA; 16 BP.  
 XX  
 AC AAT94355;  
 XX  
 DT 04-MAR-1998 (first entry)  
 XX  
 DE Human DPC4 sequence tagged site sense primer D18s479.  
 XX  
 KW DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;  
 KW tumour suppressor gene; proliferative disease; PCR primer;  
 KW sequence tagged site; STS; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9726271-A1.  
 XX  
 PD 24-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-US000827.  
 XX  
 PR 19-JAN-1996; 96US-00588821.  
 XX  
 PA (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX  
 PI Kern SE, Hahn SA;  
 XX  
 DR WPI; 1997-385290/35.  
 XX  
 PT Deleted in Pancreatic Cancer locus 4 polypeptide - and related nucleic  
 PT acids, used in diagnosis and treatment of proliferative diseases, e.g.  
 PT cancer of pancreas or other organs.  
 XX  
 PS Example 2; Page 56; 104pp; English.  
 XX  
 CC The present sequence represents a sequence tagged site (STS) primer used  
 CC in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,  
 CC locus 4) region, and gene identification. DPC4 is a tumour suppressor  
 CC gene. Detection of truncated DPC4 protein, or of homozygous deletions or  
 CC intragenic mutations in nucleic acids encoding it, is used to diagnose (in  
 CC vivo or in vitro) proliferative diseases, especially pancreatic  
 CC carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,  
 CC colitis-associated neoplasia or chronic ulcerative colitis. These  
 CC conditions, where associated with a homozygous deletion, can be treated  
 CC by administering an agent that: (a) modulates DPC4 expression,  
 CC specifically a sense DPC4 sequence (particularly in the form of a vector,  
 CC i.e. by gene therapy), but also an antisense sequence where DPC4 protein  
 CC is over expressed or (b) mimics the activity of DPC4. DPC4 nucleic acid  
 CC is also used as hybridisation probes for detecting presence/absence of  
 CC human chromosome 18q21.1 fragments. When a homozygous deletion is  
 CC detected in this region, an agent can be administered that accumulates  
 CC within, or kills, only cells which contain such a deletion. This agent  
 CC exploits the absence of an enzyme (or other protein) encoded by a  
 CC neighbouring gene and lost by the deletion, i.e. it has a highly  
 CC selective action  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.8%; Score 14; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 730 ATGCCAGCAGAGT 743  
 2 ATGCCAGCAGAGT 15  
 RESULT 352  
 AAV11865

ID AAV11865 standard; cDNA; 17 BP.  
 XX  
 AC AAV11865;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE Mus musculus Tub Interactor gene PCR primer.  
 XX  
 KW PCR primer; tub interactor; treatment; obesity; cachexia;  
 KW anorexia nervosa; diabetes; cell cycle progression; apoptosis;  
 KW neurodegenerative disease; Alzheimer's disease; drug screening;  
 KW Parkinson's disease; Huntington's chorea; detection; diagnosis;  
 KW amyotrophic lateral sclerosis; spinocerebellar degeneration; ss.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 XX  
 PN WO9812302-A1.  
 XX  
 PD 26-MAR-1998.  
 XX  
 PF 05-SEP-1997; 97WO-US015627.  
 XX  
 PR 17-SEP-1996; 96US-00715032.  
 XX  
 PR 21-JUL-1997; 97US-00897340.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Gimeno CJ, Errada PR;  
 XX  
 DR WPI; 1998-217246/19.  
 XX  
 PT Tub interactor genes - used to develop products for the treatment of  
 PT obesity, cachexia, anorexia nervosa or related disorders e.g. diabetes.  
 XX  
 PS Disclosure; Page 81; 120pp; English.  
 XX  
 CC The sequence is that of a PCR primer used in the identification of Tub  
 CC Interactor (TI) gene mTI-3  
 CC  
 CC  
 SQ Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 571 TACTCCATGACGCG 584  
 3 TACTCCATGACGCG 16  
 RESULT 353  
 AAV93331  
 ID AAV93331 standard; RNA; 17 BP.  
 XX  
 AC AAV93331;  
 XX  
 DT 18-FEB-1999 (first entry)  
 XX  
 DE Human B-raf substrate nucleotide position 425.  
 XX  
 KW Human; c-raf; A-raf; B-raf; hamsterhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalytic; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9850530-A2.  
 XX  
 PD 12-NOV-1998.  
 XX

[illegible]

PN	WO200047618-A2.
XX	
PD	17-AUG-2000.
XX	
PF	10-FEB-2000; 2000WO-US003819.
XX	
PR	10-FEB-1999; 99US-0119571P.
XX	
PA	15-JUN-1999; 99US-0139172P.
XX	
PI	(ELAN-) ELAN PHARM INC.
PJ	Anderson JP, Baai G, Doane MT, Frigon N, John V, Power M;
XX	Sinha S, Tateumo G, Tung J, Wang S, Mcconlogue L,
XX	WPI: 2000-533011/48.
DR	
PT	Purified beta-secretase protein used in assays to discover inhibitors
XX	which can be used for the treatment of amyloidogenic diseases e.g.
PP	Alzheimer's disease.
XX	
PS	Example 3, Page 66, 121pp; English.
XX	
CC	The specification describes a beta-secretase enzyme. The enzyme cleaves
CC	beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC	enzyme is therefore implicated in the production of amyloid plaque
CC	components which accumulate in the brains of individuals afflicted with
CC	Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC	mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC	like pathology to test if they maintain or improve cognitive ability or
CC	reduce the plaque burden. The compounds are used for the treatment of
CC	amyloidogenic diseases e.g. Alzheimer's disease. PCR primers AAA59530-49
CC	were used to amplify DNA encoding beta-secretase enzyme
XX	
SQ	Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 0 U; 3 Other;
XX	
Query Match	0.8%; Score 14; DB 1; Length 17;
Best Local Similarity	82.4%; Pred. No. 2.6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
OY	1306 GAGGAGGACCGCAGAGA 1322    :  :      1 GAYGARGAGCCNGAGGA 17
DB	
RESULT 355	
ABK03568	
ID	ABK03568 standard; RNA; 17 BP.
XX	
AC	ABK03568;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human CD20 DNAzyme #22.
KM	Human; B6; antiense therapy; cyostatic; antiinflammatory; haemostatic;
KM	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KM	Muscular; CD20; neurite growth inhibitor gene; NOGO; hammethead ribozyme;
KM	DNAzyme; incyzyme; G-C-leaver; amberzyme; zinczyme; lymphoma; leukaemia;
KM	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
KM	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM	MCI; immunocytoema; IMC; immune thrombocytopaenia; stroke; dementia;
KM	Inflammation; arthropathy; central nervous system injury;
KM	chemobrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM	Parkinson's disease; ataxia; Huntington's disease;
KM	Creutzfeldt-jakob disease; muscular dystrophy; neurodegenerative disease.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200159103-A2.
XX	
PD	16-AUG-2001.
XX	



XX 09-FEB-2001; 2001MO-US004273.  
 PF 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 DR WPI; 2001-607195/69.  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 PS Claim 30; Page 159; 200pp; English.  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNAzyme) an NCH motif, a G-cleaver (cleaving RNA with an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an NCH motif) or  
 CC an amberzyme (cleaving RNA with an NCH motif), a zinczyme (cleaving RNA  
 CC with a XGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOCO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOCO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemo-therapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOCO expression. The present  
 CC sequence is a DNAzyme molecule of the invention  
 XX Sequence 17 BP; 1 A; 2 C; 7 G; 0 T; 7 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 2.6e02; Indels 0; Gaps 0;  
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 803 TCTGTGTCAGTGTG 816  
 DB 1 UCUUGUGUACUGUG 14  
 RESULT 356  
 ADV07675/c  
 ID ADV07675 standard; RNA; 17 BP.  
 XX ADV07675;  
 AC  
 XX 10-FEB-2005 (first entry)  
 DT

XX Human BACE amberzyme ribozyme substrate sequence #488.  
 DE Enzymatic nucleic acid molecule; gene expression; down regulation;  
 XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW beta-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammethead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberzyme; zinczyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX WO200116312-A2.  
 PN  
 XX 08-MAR-2001.  
 PD  
 XX 30-AUG-2000; 2000MO-US023998.  
 PF  
 XX 31-AUG-1999; 99US-0151713P.  
 PR 27-SEP-1999; 99US-00406643.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.  
 PR 29-DEC-1999; 99US-0173512P.  
 PR 30-DEC-1999; 99US-00476387.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 10-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA Mcswiggen J, Uman N, Blatt L, Beigelman L, Burgin A;  
 PI Kowalsky J, Matulis-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 DR WPI; 2001-244406/25.  
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 XX Example 4; Page 403; 717pp; English.  
 PS The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention of  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zinczyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for a ribozyme used in  
 CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
 CC more than once in the specification, but these have different sequences  
 CC associated with them.  
 CC



Sequence 17 BP; 3 A; 0 C; 8 G; 0 T; 6 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1277 CCACCATCTCCACA 1290  
DB 16 CCACCATCTCCACA 3  
RESULT 357  
ADU86313  
ID ADU86313 standard; DNA; 17 BP.  
AC ADU86313;  
XX 10-FEB-2005 (first entry)  
XX Human TERT hammerhead ribozyme substrate sequence #344.  
DE Enzymatic nucleic acid molecule; gene expression; down regulation;  
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HBR2;  
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KM amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
de.  
XX Homo sapiens.  
OS WO200116312-A2.  
XX 08-MAR-2001.  
PD 30-AUG-2000; 2000MO-US023998.  
PF 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcswiggen J, Uzman N, Blact L, Beigelman L, Burgin A;  
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sprout BS;  
XX WPI; 2001-244406/25.  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX Example 1; Page 274; 717pp; English.  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine

CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,  
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.  
XX  
XX Sequence 17 BP; 3 A; 8 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1689 CCAGCTTTCTCTCA 1702  
DB 1 CCAGCTTTCTCTCA 14  
RESULT 358  
ADU86312  
ID ADU86312 standard; DNA; 17 BP.  
AC ADU86312;  
XX 10-FEB-2005 (first entry)  
XX Human TERT hammerhead ribozyme substrate sequence #343.  
DE Enzymatic nucleic acid molecule; gene expression; down regulation;  
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HBR2;  
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KM amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
de.  
XX Homo sapiens.  
OS WO200116312-A2.  
XX 08-MAR-2001.  
PD 30-AUG-2000; 2000MO-US023998.  
PF 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.

PA (RIBO-) RIBOZYME PHARM INC.  
 XX Maswiggen J, Uman N, Blatt L, Beigelman L, Burgin A,  
 PI Karpelisky A, Matulic-Adamic J, Swedler D, Draper K, Chowrira B,  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 DR WPI; 2001-244406/25.  
 XX  
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 XX  
 XX Example 1; Page 274; 717pp; English.  
 XX  
 XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,  
 CC zincyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for a ribozyme used in  
 CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
 CC more than once in the specification, but these have different sequences  
 CC associated with them.  
 XX  
 XX Sequence 17 BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 0.8%; Score 14; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1689 CCAGCTTTCTCTCA 1702  
 Db 2 CCAGCTTTCTCTCA 15  
 XX  
 XX RESULT 359  
 XX ABN06977  
 ID ABN06977 standard; DNA; 17 BP.  
 XX  
 XX ABN06977;  
 DT 29-MAY-2002 (first entry)  
 XX  
 XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6969.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200192524-A2.  
 PN  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR  
 XX 21-SEP-2000; 2000US-0234687P.  
 PR  
 XX 27-SEP-2000; 2000US-0236359P.  
 PR  
 XX 04-OCT-2000; 2000GB-00024263.  
 OS

PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 DR  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 PT  
 XX Disclosure; SEQ ID NO 6969; 214pp; English.  
 PS  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 CC  
 XX Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 0.8%; Score 14; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 29 AGTGCATCCAGAG 42  
 Db 1 AGTGCATCCAGAG 14  
 XX  
 XX RESULT 360  
 XX ABN06973  
 ID ABN06973 standard; DNA; 17 BP.  
 XX  
 XX ABN06973;  
 DT 29-MAY-2002 (first entry)  
 XX  
 XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6965.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 XX Homo sapiens.  
 OS

XX WO200192524-A2.  
PN  
XX  
XX 06-DEC-2001.  
PD  
XX  
XX 25-MAY-2001; 2001WO-US016381.  
PF  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX 30-JAN-2001; 2001WO-US000661.  
PR  
XX 30-JAN-2001; 2001WO-US000662.  
PR  
XX 30-JAN-2001; 2001WO-US000663.  
PR  
XX 30-JAN-2001; 2001WO-US000664.  
PR  
XX 30-JAN-2001; 2001WO-US000665.  
PR  
XX 30-JAN-2001; 2001WO-US000666.  
PR  
XX 30-JAN-2001; 2001WO-US000667.  
PR  
XX 30-JAN-2001; 2001WO-US000668.  
PR  
XX 30-JAN-2001; 2001WO-US000669.  
PR  
XX 05-FEB-2001; 2001US-0266860P.  
PR  
XX  
XX (ABOM-) AEOMICA INC.  
PA  
XX  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
PI  
XX WPI; 2002-179446/23.  
DR  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
PT  
XX  
XX Disclosure; SEQ ID NO 6965; 214pp; English.  
PS  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acid can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ffp.wipo.int/pub/published\_pcc\_sequence  
CC  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ADM54123;  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX  
XX Human GRID mRNA substrate sequence #398.  
DE  
XX  
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;  
KW NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNAzyme; amberzyme; Inozyme;  
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003134806-A1.  
PN  
XX  
XX 17-JUL-2003.  
PD  
XX  
XX 23-FEB-2001; 2001US-00792818.  
PF  
XX  
XX 10-FEB-2000; 2000US-0181594P.  
PR  
XX  
XX (JARV/) JARVIS T.  
PA (CARL/) CARLOWITZ I V.  
PA (MCSW/) MCSWIGEN J.  
PA (HAMB/) HAMBILIN P A.  
PA (ELLI/) ELLIS J H.  
XX  
XX Jarvis T, Carlowitz IV, Mcswigen J, Hamblin PA, Ellis JH;  
PI  
XX WPI; 2003-829646/77.  
DR  
XX  
XX New nucleic acid molecule that down-regulates expression of Grb2-related  
PT with insert domain (GRID) gene, useful for treating a condition and  
PT associated with the level of GRID, e.g. tissue/graft rejection and  
PT leukemia.  
PT  
XX  
XX Claim 4; SEQ ID NO 398; 74pp; English.  
PS  
XX  
XX The invention relates to a nucleic acid molecule that down-regulates  
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a  
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNAzyme,  
CC amberzyme, Inozyme and hairpin ribozyme. Also include are a mammalian cell  
CC including the novel nucleic acid molecule, reducing GRID activity in a  
CC cell by contacting the cell with the novel nucleic acid molecule,  
CC treating a patient having a condition associated with the level of GRID  
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with  
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by  
CC contacting the cell with the novel nucleic acid molecule, an expression  
CC vector comprising a nucleic acid sequences (encoding at least the novel  
CC nucleic acid molecule in a manner that allows its expression), a  
CC mammalian cell including the expression vector and an enzymatic nucleic  
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid  
CC molecule is useful for treating a condition associated with the level of  
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is  
CC a target region for the enzymatic nucleic acids of the invention.  
CC  
XX  
SQ Sequence 17 BP; 5 A; 9 C; 1 G; 0 T; 2 U; 0 Other;  
XX  
XX  
XX Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 361  
ADM54123  
ID ADM54123 standard; mRNA; 17 BP.  
XX

RESULT 362  
ADL82294  
ID ADL82294 standard; DNA; 17 BP.  
XX  
XX ADL82294;  
XX  
XX 20-MAY-2004 (first entry)  
DT

XX Human ER+ breast cancer differentially expressed sequence #264.  
DE gene therapy; de; breast cancer; human; ER+ breast cancer.  
XX Homo sapiens.  
XX US2003166026-A1.  
XX 04-SEP-2003.  
XX 08-JAN-2003; 2003US-00339782.  
XX 09-JAN-2002; 2002US-0348053P.  
XX (LYNX-) LYNX THERAPEUTICS INC.  
XX Goodman LJ, Bowen BA;  
XX WPI, 2004-069003/07.  
XX Vector containing nucleic acid associated with breast cancer, useful for  
XX treating, diagnosing and characterizing breast cancer, also related  
XX polypeptides and antibodies.  
XX Claim 1, SEQ ID NO 265; 61pp; English.  
XX  
XX The invention relates to a composition which contains at least one vector  
XX (B) containing a nucleic acid (I) associated with breast cancer. The  
XX vector (B), also polypeptides (II) encoded by (I), are used for treatment  
XX of breast cancer. Arrays based on (I), (II), or their fragments, and (II)  
XX -specific antibodies (Ab) are used to predict characteristics (e.g.  
XX invasiveness or stage) of breast cancer, and (I), or its fragments, are  
XX used to modulate characteristics of such cells; to identify breast cancer  
XX genes and to detect breast cancer (by detecting polymorphic nucleic acid  
XX or its products). The present sequence represents a human ER+ breast  
XX cancer differentially expressed sequence.  
SQ Sequence 17 BP; 2 A; 10 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 617 ATCCCTCCAGCCC 630  
Db 2 ATCCCTCCAGCCC 15  
RESULT 363  
ADR31412/C  
ID ADR31412 standard; DNA; 17 BP.  
XX ADR31412;  
XX 04-NOV-2004 (first entry)  
XX Bovine RORCGH DNA specific PCR primer, RORCGH3.  
XX  
XX Marbling; RORC; retinoid related orphan receptor C (gamma);  
XX RAR-related orphan receptor gamma; nuclear receptor ROR-gamma;  
XX retinoic acid-binding receptor gamma; fat deposit; bovine; RORCGH; PCR;  
XX primer; ss.  
XX  
XX Bos sp.  
XX WO2004070055-A1.  
XX 19-AUG-2004.  
XX 04-FEB-2004; 2004WO-AU000127.  
XX 04-FEB-2003; 2003AU-00900454.  
XX

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX (OUE-) STATE QUEENSLAND DEPT PRIMARY IND.  
XX (LYNE-) UNIV NEW ENGLAND.  
XX (NEMS-) NEW SOUTH WALES DEPT AGRIC.  
XX (MEAT-) MEAT & LIVESTOCK AUSTRALIA LTD.  
XX  
XX Barendse W;  
XX WPI, 2004-604466/58.  
XX  
XX Assessing propensity for marbling in animal meat useful for selecting  
XX animal to improve marbling in herd, involves detecting alleles of  
XX retinoid related orphan receptor C gamma gene associated with increased  
XX fat deposition in muscle.  
XX  
XX Disclosure; SEQ ID NO 10; 53pp; English.  
XX  
XX The present invention relates to a method for assessing the propensity  
XX for marbling in meat derived from an animal. The method involves testing  
XX the animal for the presence or absence of one or more alleles of the gene  
XX encoding the retinoid related orphan receptor C (gamma) (RORC) also known  
XX as RAR-related orphan receptor gamma, nuclear receptor ROR-gamma and  
XX retinoic acid-binding receptor gamma associated with increased fat  
XX deposition in muscle tissue and genetic variation located external to the  
XX RORC gene which shows allelic association with it. The invention is  
XX useful for selection and breeding of animal with improved fat deposition  
XX characteristics, particularly high marbling scores. The present sequence  
XX is bovine RORC allelic variant, RORCGH DNA specific PCR primer.  
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1235 TCCGAGCCCGGGC 1248  
Db 16 TCCGAGCCCGGGC 3  
RESULT 364  
ACN70067  
ID ACN70067 standard; DNA; 17 BP.  
XX ACN70067;  
XX 02-DEC-2004 (first entry)  
XX Human GDMLP-1 probe SEQ ID NO:6969.  
XX  
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
XX hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
XX skeletal muscle function.  
XX  
XX Homo sapiens.  
XX US2004137589-A1.  
XX 15-JUL-2004.  
XX 26-NOV-2003; 2003US-00723361.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-0004263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX

PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-026860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
PI Gu Y, JI Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
DR WPI; 2004-533378/51.  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 6969; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 AGTGCATCCAGAG 42  
DB 1 AGTGCATCCAGAG 14  
RESULT 365  
ACNT0063  
ID ACN70063 standard; DNA; 17 BP.  
XX  
XX ACN70063;  
XX  
XX 02-DEC-2004 (first entry)  
DT  
XX  
DE Human GDMPL-1 probe SEQ ID NO:6965.  
XX  
KM Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KM hGDMPL-1 agonist; hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
KM skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
XX 26-NOV-2003; 2003US-00723361.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-026860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
XX (GUY/) GU Y.  
XX (JIY/) JI Y.  
XX (PENN/) PENN S G.  
XX (HANZ/) HANZEL D K.  
XX (RANK/) RANK D.  
XX (CHEN/) CHEN W.  
XX (SHAN/) SHANNON M E.  
PI Gu Y, JI Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
DR WPI; 2004-533378/51.  
XX  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 6965; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 CAGTGCATCCAGAA 41  
DB 4 CAGTGCATCCAGAA 17  
RESULT 366  
ADS41403/c  
ID ADS41403 standard; DNA; 17 BP.  
XX  
XX ADS41403;  
AC  
XX  
XX 16-DEC-2004 (first entry)  
DT  
XX  
DE Human autoimmune disease-related PCR primer - SEQ ID 6617.  
XX  
KM single nucleotide polymorphism detection; SNP detection;  
KM rheumatoid arthritis; type 1 diabetes; multiple sclerosis;  
KM systemic lupus erythematosus; inflammatory bowel disease; psoriasis;  
KM thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;  
KM glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;  
KM primary systemic vasculitis; PCR; primer; ss.

XX Homo sapiens.  
XX WO2004083403-A2.  
XX 30-SEP-2004.  
XX 18-MAR-2004; 2004WO-US008461.  
XX 18-MAR-2003; 2003US-0455444P.  
XX 25-APR-2003; 2003US-0465241P.  
XX (APPL-) APPLERA CORP.  
XX Cargill M, Begovich AB, Alexander HC;  
XX WPI, 2004-728480/71.  
XX New isolated nucleic acid molecule comprises at least 8 contiguous  
XX nucleotides where one of the nucleotides is a single nucleotide  
XX polymorphism (SNP), useful for diagnosing or treating autoimmune  
XX diseases, e.g. rheumatoid arthritis.  
XX Claim 21; SEQ ID NO 6617; 123pp; English.  
XX The invention comprises amino acid and coding sequences containing  
XX genetic polymorphisms associated with an altered risk of developing an  
XX autoimmune disease (e.g. rheumatoid arthritis). The invention further  
XX comprises a method of identifying an individual that has an altered risk  
XX of developing an autoimmune disease, comprising detecting a single  
XX nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA  
XX and protein sequences of the invention are useful for diagnosing and  
XX treating autoimmune diseases, such as: rheumatoid arthritis, type 1  
XX diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory  
XX bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious  
XX anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,  
XX myocarditis, Sjogren's disease, or primary systemic vasculitis. The  
XX present DNA sequence represents a human autoimmune disease-related PCR  
XX primer of the invention. NOTE: The present sequence is not shown in the  
XX specification, but has been retrieved from the WIPO website.  
XX Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0;  
Qy 677 TCCGCTCTCTCTG 690  
Db 14 TCTGCTCTCTCTG 1  
RESULT 367  
AAQ30775  
ID AAQ30775 standard; DNA; 17 BP.  
XX AAQ30775;  
AC  
XX 25-MAR-2003 (revised)  
DT 22-MAR-1993 (first entry)  
XX  
DE PCR primer rspr284h to amplify human NKIR sF core region.  
XX Neurokinin-1 receptor short form; arthritis; Substance P;  
XX polymerase chain reaction; rat NKIR; ss.  
XX Synthetic.  
XX EP514207-A2.  
XX 19-NOV-1992.  
XX 15-MAY-1992; 92EP-00304432.  
PF

XX 17-MAY-1991; 91US-00701930.  
XX 17-MAY-1991; 91US-00701935.  
XX 17-MAY-1991; 91US-00701937.  
XX (MERI ) MERCK & CO INC.  
XX Strader CD, Fong TM;  
XX WPI, 1992-384034/47.  
XX New human neurokinin-1 receptor short form protein - useful for  
XX identifying and determining substance P antagonists in arthritic  
XX patients.  
XX Example 1; Page 8; 36pp; English.  
XX Human mRNA was prepared from 3 glioblastoma cell lines T98G, CCF-SSTG1  
XX and U87MG. First strand cDNA was synthesised and used as template with  
XX rat primers rspr284, rspr284h and rspr7a2 (AAQ30774-6) in first round PCR  
XX amplification. Secondary PCR was performed on the amplified product using  
XX the same 3 primers prior to a third round of amplification, this time  
XX using the primers rspr284, rspr284h, rspr7a1 (AAQ30777) and rspr7a1h  
XX (AAQ30778). The tertiary PCR product was sequenced and was found to have  
XX 90% identity at the nucleotide level with the central core region of the  
XX rat NKIR from amino acid 91 to 280. Primer rspr284h is a sense primer  
XX based on the rat NKIR sequence 238-255 (numbering as in J.Biol.Chem. 264:  
XX 17649-17652, 1989), but designed to incorporate the human codon bias.  
XX (updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2;  
Qy 448 TCCATGCTGTCATTCAA 464  
Db 1 TGATGCTGCTCTTCAA 17  
RESULT 368  
AAQ47255/C  
ID AAQ47255 standard; DNA; 17 BP.  
XX AAQ47255;  
AC  
XX 25-MAR-2003 (revised)  
DT 25-JAN-1994 (first entry)  
XX  
DE PCR primer for amplifying tachykinin receptor specific mRNA from human  
XX leukocytes.  
XX Polynucleotide; synthesis; solid support; ss.  
XX Synthetic.  
XX WO9315228-A1.  
XX 05-AUG-1993.  
XX 29-JAN-1993; 93WO-US001040.  
XX 29-JAN-1992; 92US-00827975.  
XX (HITB ) HITACHI CHEM CO LTD.  
XX (HITB ) HITACHI CHEM RES CENT INC.  
XX Keller C, Misuhashi M, Akitaya T;  
XX WPI, 1993-258700/32.  
XX Predn. of double stranded cDNA immobilised support - by binding  
PT

PT polynucleotide with sequence complementary to poly-adenylic acid tail of  
PT mRNA to insol. support.  
XX  
XX Example 3; Page 26; 54pp; English.  
XX  
CC A polynucleotide is immobilised on an insoluble solid support and used to  
CC synthesize ds-cDNA, ss-cDNA and both sense and antisense mRNA. The  
CC advantage of this system is that RNA bound to the solid support need not  
CC be precipitated when changing solutions. Two primers were used to amplify  
CC tachykinin receptor specific mRNA after its synthesis using the above  
CC method (AA047254, AA047255). (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 983 CCATCTGCTGCTGCC 999  
DB 17 CCATCTGCTGCTGCC 1  
RESULT 369  
AAx71369/c  
ID AAx71369 standard; RNA; 17 BP.  
XX  
AC AAx71369;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Human KDR VEGF receptor hammerhead ribozyme substrate #381.  
XX  
KM Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;  
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KM foetal liver kinase 1; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Payco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX  
DR WPI; 1997-259017/23.  
XX  
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
XX Claim 4; Page 108; 218pp; English.  
XX  
XX The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAx67275 to AAx75752 represent specific examples

CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1505 TTCACTCGAACCATCA 1521  
DB 17 TTCACTCGAATCCATGA 1  
RESULT 370  
AAx72795/c  
ID AAx72795 standard; RNA; 17 BP.  
XX  
AC AAx72795;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #228.  
XX  
KM Vascular endothelial growth factor receptor; VEGF receptor; flk-1; flk-1;  
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KM foetal liver kinase 1; ss.  
XX  
XX Mus sp.  
XX  
XX WO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Payco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX  
DR WPI; 1997-259017/23.  
XX  
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
XX Claim 4; Page 129; 218pp; English.  
XX  
XX The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAx67275 to AAx75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 3 C; 6 G; 0 T; 8 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 714 CTCACCCAGAGACCA 730  
DB 17 CACACCCAGAGACCA 1

RESULT 371  
AAK72944/c  
ID AAK72944 standard; RNA; 17 BP.  
XX  
AC AAK72944;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #377.  
XX  
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
OS Mus sp.  
XX  
PN MO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PP 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
XX  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX (CHIR ) CHIRON CORP.  
XX  
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;  
XX  
DR WPI; 1997-259017/23.  
XX  
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability- useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 134; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAK67275 to AAK75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 0 T; 4 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1505 TTGATCTGGAAACCATCA 1521  
DB 17 TTGATCTGGATCATCA 1  
XX  
RESULT 372  
AAK71197/c  
ID AAK71197 standard; RNA; 17 BP.  
XX  
AC AAK71197;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Human KDR VEGF receptor hammerhead ribozyme substrate #209.  
XX

XX  
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PP 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
XX  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX (CHIR ) CHIRON CORP.  
XX  
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;  
XX  
DR WPI; 1997-259017/23.  
XX  
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability- useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 103; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAK67275 to AAK75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 3 C; 6 G; 0 T; 8 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 714 CTCACACACAGACCA 730  
DB 17 CACACACAGACCA 1  
XX  
RESULT 373  
AAK62890/c  
ID AAK62890 standard; RNA; 17 BP.  
XX  
AC AAK62890;  
XX  
DT 16-JUL-1999 (first entry)  
XX  
DE Delta-9 desaturase hammerhead ribozyme target SEQ ID NO:765.  
XX  
KW Maize; corn; Zea mays; delta-9 desaturase; GBSs; target; substrate;  
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;  
KW modulation; gene expression; transgenic plant; cleavage; canola plant;  
KW caffeine synthesis; coffee plant; nicotine production; tobacco;  
KW fruit ripening; flower pigmentation; lignin production; ss.  
XX  
OS Zea mays.  
XX  
PN MO9710328-A2.  
XX



PD 20-MAR-1997.  
XX  
XX 12-JUL-1996; 96WO-US011689.  
XX  
XX 13-JUL-1995; 95US-0001135P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX (DMC ) DOWELANCO.  
XX  
XX Zwick MG, Edington BE, Mcswigen JA, Merlo PAO, Guo L, Skokut TA,  
PI Young SA, Folkerts O, Merlo DJ;  
XX  
XX WPI; 1997-202224/18.  
XX  
XX Ribozyyme which modulates plant gene expression - preferably modulates  
PT expression of DELTA-9 desaturase or granule bound starch synthase in  
PT maize or canola.  
XX  
XX  
XX Claim 38; Page 86; 155pp; English.  
XX  
XX The present invention describes an enzymatic nucleic acid molecule (1)  
CC with RNA cleaving activity, which modulates the expression of a plant  
CC gene. Also described is a gene comprising a cDNA sequence encoding maize  
CC Delta-9 desaturase. (1) can be used to modulate expression of a gene,  
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)  
CC gene, in a plant (preferably a maize or canola plant). (1) can be used to  
CC modulate caffeine synthesis in a coffee plant, nicotine production in a  
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum  
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or  
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine  
CC plant  
XX  
XX  
SQ Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 636 GTCAGCCACGACCA 652  
DB 17 GTCAGCCACGACCA 1  
RESULT 374  
AAV97463/c  
ID AAV97463 standard; RNA; 17 BP.  
XX  
XX AAV97463;  
AC  
XX  
XX 17-MAR-1999 (first entry)  
DT  
XX  
XX Human EGF-R target sequence nucleotide position 2148.  
DE  
XX  
XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;  
KM hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;  
KM cancer; genetic drift; detection; mutation; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9833893-A2.  
PN  
XX  
XX 06-AUG-1998.  
PD  
XX  
XX 14-JAN-1998; 98WO-US000730.  
PF  
XX  
XX 31-JAN-1997; 97US-0036476P.  
PR  
XX 04-DEC-1997; 97US-00985162.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (UTAS-) UNITV ASTON.  
XX  
XX Akhtar S, Fell P, Mcswigen JA;  
PI

DR WPI; 1998-437449/37.  
XX  
XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
PT growth factor receptor, useful for inhibiting cell proliferation and for  
PT treating cancers.  
XX  
XX  
XX Claim 5; Page 73; 109pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules (NMs)  
CC which specifically cleave RNA derived from an epidermal growth factor  
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090  
CC represent specifically claimed target sequence from human EGF-R. AAV98044  
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and  
CC hairpin ribozymes respectively for human EGF-R. The NMs are useful for  
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR  
CC expression levels e.g. to inhibit cell proliferation in the prevention or  
CC treatment of cancers. The NMs can also be used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of EGF-R RNA in a cell  
XX  
XX  
SQ Sequence 17 BP; 0 A; 7 C; 5 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1313 AGCCAGAGAGCGCCCC 1329  
DB 17 AGCCAGAGAGCGCCCC 1  
RESULT 375  
AAA20669/c  
ID AAA20669 standard; RNA; 17 BP.  
XX  
XX AAA20669;  
AC  
XX  
XX 19-JUN-2000 (first entry)  
DT  
XX  
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3895.  
DE  
XX  
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
KM hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;  
KM opthalmitic; antiinflammatory; antiarthritic; antipodiatric; ARMD;  
KM dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
KM age related macular degeneration; inflammation; neovascular glaucoma;  
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;  
KM tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
KM Kippel-Trennauy-Weber syndrome; Osher-Weber-Rendu syndrome; ss.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9950403-A2.  
PN  
XX  
XX 07-OCT-1999.  
PD  
XX  
XX 24-MAR-1999; 99WO-US006507.  
PF  
XX  
XX 27-MAR-1998; 98US-0079678P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;  
PI WPI; 1999-591315/50.  
XX  
XX Novel ribozymes for modulating the synthesis, expression and/or stability  
PT of an mRNA encoding an angiogenic factors.  
XX  
XX Claim 55; Page 160; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with RNA  
CC

cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, CC AAA17167 and AAA17560 and AAA17623 to AAA17684 represent their CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to CC AAA19154 represent ribozyme sequences for Tie-2, and AAA19386 to AAA19086 CC and AAA19155 to AAA19222 represent their corresponding target sequences; CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and CC AAA21596 to AAA21688 represent their corresponding target sequences; CC AAA21689 to AAA22475 and AAA23263 to AAA23342 representing ribozyme sequences for integrin subunit beta 3, and AAA23246 to AAA23262, AAA23343 to CC AAA23422 represent their corresponding target sequences. The ribozymes of CC the invention are used for modulating the synthesis, expression and/or CC stability of an mRNA encoding integrin subunit alpha-6, or Tie-2. They are CC especially used to treat cancer, diabetic retinopathy, age related CC macular degeneration (ARMD), inflammation, and arthritis, as well as CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, CC angiodioma of tuberous sclerosis, pot-wine stains, Sturge Weber CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, CC and other syndromes and diseases related to the levels of ARNT, Tie-2, CC integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1720 ATTTCGAGAGTACTT 1736  
17 ACTTCTGAGAGTCAATT 1

Db

RESULT 376  
AAH94825/c  
ID AAH94825 standard; RNA; 17 BP.  
AC AAH94825;  
XX  
XX 09-OCT-2001 (first entry)  
DT  
XX  
XX Human Chk1 ribozyme substrate SEQ ID NO: 250.  
DE  
XX  
XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;  
KW RNA cleavage; cancer; ss.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157206-A2.  
FN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 02-FEB-2001; 2001WO-US003504.  
PP  
XX  
XX 03-FEB-2000; 2000US-0179983P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (PAT/) PATTALEY A R.  
PA  
XX  
XX Pattaley AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;  
PI  
XX  
XX WPI, 2001-496922/54.  
DR  
XX  
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid  
PT molecules, which downregulate expression of a checkpoint kinase-1 gene,  
PT useful for treating colorectal, lung, breast or prostate cancers.  
PT  
XX  
XX Claim 4; Page 57; 115pp; English.  
CC  
XX  
XX The present invention provides nucleic acid molecules capable of

downregulating the expression of the human checkpoint kinase-1 (Chk1) CC gene. These may be antisense or ribozyme sequences, and are useful in the CC treatment of diseases associated with conditions affected by Chk1 levels, CC including cancer. The present sequence is an oligonucleotide described in CC the exemplification of the invention

Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1369 TCTTCACGAGTCACTC 1385  
17 TCTTCACGAGTCTCTC 1

Db

RESULT 377  
ABK01580  
ID ABK01580 standard; RNA; 17 BP.  
AC ABK01580;  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX  
XX Human NOGO G-Cleaver #36.  
DE  
XX  
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNAAzyme; inozyme; G-cleaver; amberyne; zinyne; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; CVA; Huntington's disease; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX Synthetic.  
OS  
XX  
XX WO200159103-A2.  
FN  
XX  
XX 16-AUG-2001.  
PD  
XX  
XX 09-FEB-2001; 2001WO-US004273.  
PP  
XX  
XX 11-FEB-2000; 2000US-0181797P.  
PR  
XX  
XX 28-FEB-2000; 2000US-0185516P.  
PR  
XX  
XX 06-MAR-2000; 2000US-0187128P.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOM/) CHOMRIRA B M.  
PA  
XX  
XX Blatt L, Mcswiggen J, Chowrira BM;  
PI  
XX  
XX WPI, 2001-607195/69.  
DR  
XX  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
PT  
XX  
XX Claim 88; Page 92; 200pp; English.  
PS  
XX  
XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulate expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ .  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a G-cleaver molecule of the invention  
XX  
SQ Sequence 17 BP; 1 A; 9 C; 3 G; 0 T; 4 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 2.8e+02;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 545 CCAATGCCGCTGCTTC 561  
1 CCAATCCCGCGCTGCTTC 17  
Db  
RESULT 378  
ABK02357/c  
ID ABK02357 standard; RNA; 17 BP.  
XX  
XX ABK02357;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NOGO Amberzyme #29.  
XX  
KW Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammetthead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001, 2001WO-US004273.  
XX  
PR 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX  
PI Blatt L, Mcswigen J, Chowrira BM;  
XX  
XX WPI; 2001-607195/69.  
DR  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
PS Claim 88; Page 131; 200pp; English.  
XX  
CC The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ .  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is an amberzyme molecule of the invention  
XX  
SQ Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.9; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1003 CACATCTTCTTCTCCT 1019  
17 CTCCTCTTCTTCTCCT 1  
Db  
RESULT 379  
ABK02363  
ID ABK02363 standard; RNA; 17 BP.  
XX  
XX ABK02363;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NOGO Amberzyme #35.  
XX  
KW Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KW

muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
DNAzyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;  
B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
inflammatory arthropathy; central nervous system injury;  
cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
Parkinson's disease; ataxia; Huntington's disease;  
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Homo sapiens.  
Synthetic.  
WO200159103-A2.  
16-AUG-2001.  
09-FEB-2001; 2001WO-US004273.  
11-FEB-2000; 2000US-0181797P.  
28-FEB-2000; 2000US-0185516P.  
06-MAR-2000; 2000US-0187128P.  
(RIBO-) RIBOZYME PHARM INC.  
(BLATT/) BLATT L.  
(MCSW/) MCSWIGEN J.  
(CHOW/) CHOWRIRA B M.  
Blatt L, Mcswigen J, Chowrira BM;  
WPI; 2001-607195/69.  
Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
constructs, which down regulate expression of a CD20 gene or neurite  
growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
central nervous system injury.

Claim 88; Page 131; 200PP; English.

The invention relates to a nucleic acid molecule which down regulates  
expression of a CD20 gene and a nucleic acid molecule which down  
regulates expression of a neurite growth inhibitor gene (NOGO). The  
nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
DNAzyme) (an endolytic nucleic acid cleaving an RNA motif) or  
possessing an NCH motif), a G-cleaver (cleaving RNA with a NTR motif) or  
an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
Furthermore, it may be contacted with a condition associated with the level  
of CD20. The treatment may further comprise the use of one or more  
therapies. In particular, the CD20 targeting nucleic acid may be used to  
treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
nucleic acid may be contacted with a cell to reduce NOGO activity of the  
cell and treat a patient having a condition associated with the level of  
NOGO. The treatment may further comprise the use of one or more  
therapies. In particular, the NOGO-targeting nucleic acid may be used to  
treat central nervous system (CNS) injury and cerebrovascular accident  
(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
disease, muscular dystrophy, and/or other neurodegenerative disease  
states which respond to the modulation of NOGO expression. The present  
sequence is an amberyze molecule of the invention

Sequence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1306 GAGGAGGAGCCAGAGGA 1322  
DB 1 GAGGAGGAGGAGAGGA 17  
RESULT 380  
ADU93087  
ID ADU93087 standard; DNA; 17 BP.  
XX  
AC ADU93087;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human TERT NCH ribozyme substrate sequence #380.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyze; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
de.  
XX  
OS Homo sapiens.  
XX  
XX WO200116312-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-0173612P.  
PR 29-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197699P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswigen J, Usman N, Blatt L, Beigelman L, Burgin A,  
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX  
PS Example 1; Page 284; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention of  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,  
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 8 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1295 TGGGGGCCCGAGAG 1311  
DB 1 TGGGGGCCCGAGAG 17  
RESULT 381  
ADU93088  
ID ADU93088 standard; DNA; 17 BP.  
XX  
AC ADU93088;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human TERT NCH ribozyme substrate sequence #381.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyze; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW de.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000MO-US023998.  
XX  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
XX 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
XX 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
XX 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
XX 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
XX 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
XX 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.

XX  
PI Mcwiggan J, Uman N, Blat L, Beigelman L, Burgin A,  
PI Kapelsky A, Matulic-Adamic J, Swedler D, Draper K, Chowrira B,  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Spirot BS;  
XX WPI; 2001-244406/25.  
XX  
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX  
PS Example 1; Page 284; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,  
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present  
CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 9 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1296 GGGGGGCCCGAGAG 1312  
DB 1 GGGGGGCCCGAGAG 17  
RESULT 382  
ADU86314  
ID ADU86314 standard; DNA; 17 BP.  
XX  
AC ADU86314;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human TERT hammerhead ribozyme substrate sequence #345.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyze; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW de.  
XX  
OS Homo sapiens.  
XX  
PN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX

30-AUG-2000; 2000MO-US023998.  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A, Chowrira B,  
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Sproat BS;  
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;  
XX WPI; 2001-244406/25.  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX Example 1; Page 274; 717pp; English.  
XX The present invention relates to the use of enzymatic nucleic acid  
PS molecules (e.g. ribozymes) to modulate gene expression. The invention of  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
XX aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,  
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
XX diseases, hepatitis B infections, and hepatitis and hepatocellular  
XX carcinoma. The enzymatic nucleic acid molecules can also be used as  
XX diagnostic tools to examine genetic drift and mutations within diseased  
XX cells and to detect the presence of specific RNA in a cell. The present  
XX sequence represents a substrate/target sequence for a ribozyme used in  
XX the examples of the present invention. Note: Some SEQ ID Nos are repeated  
XX more than once in the specification, but these have different sequences  
XX associated with them.  
XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;  
SQ  
QY Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No.2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
DB 1690 CAGCTTTCTCAAGAG 1706  
1 CAGCTTTCTCAAGAG 17  
AC ADU92547 standard; DNA; 17 BP.  
AC ADU92547;  
XX 10-FEB-2005 (first entry)  
XX Human TERT NCH ribozyme substrate sequence #122.  
DE

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
XX MeAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
XX c-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
XX amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;  
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
XX ds.  
XX Homo sapiens.  
OS  
XX WO200116312-A2.  
XX 08-MAR-2001.  
XX 30-AUG-2000; 2000MO-US023998.  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A,  
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B,  
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;  
XX WPI; 2001-244406/25.  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
PT obesity and heart disease.  
XX Example 1; Page 278; 717pp; English.  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention of  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
XX aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,  
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
XX diseases, hepatitis B infections, and hepatitis and hepatocellular  
XX carcinoma. The enzymatic nucleic acid molecules can also be used as  
XX diagnostic tools to examine genetic drift and mutations within diseased  
XX cells and to detect the presence of specific RNA in a cell. The present  
XX sequence represents a substrate/target sequence for a ribozyme used in  
XX the examples of the present invention. Note: Some SEQ ID Nos are repeated  
XX more than once in the specification, but these have different sequences  
XX associated with them.  
XX Sequence 17 BP; 0 A; 4 C; 9 G; 4 T; 0 U; 0 Other;  
SQ

```
Query Match      0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No.2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      1450 GCAGGTGCGCCGCCAC 1466
      |||||
      17 GCAGCAGCAGCCGCCAC 1
Db

RESULT 384
ADU93086
ID ADU93086 standard; DNA; 17 BP.
XX
AC ADU93086;
XX
DT 10-FEB-2005 (first entry)
DE
XX Human TERT NCH ribozyme substrate sequence #379.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KM de.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A,
PI Karpelsky A, Maculic-Adamc J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sprout BS;
XX
XX WPI; 2001-24406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 1; Page 284; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
```

```
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer; Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX SQ Sequence 17 BP; 2 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
XX
Query Match      0.8*; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No.2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      1294 GTGGGCGGCCGACGAGA 1310
      |||||
      1 GTGGCGGCCGCCGAGCA 17
Db

RESULT 385
ADV62161
ID ADV62161 standard; RNA; 17 BP.
XX
XX ADV62161;
XX
DT 10-FEB-2005 (first entry)
DE
XX HBV amberzyme ribozyme substrate sequence #528.
XX
KM Enzymatic nucleic acid molecule; gene expression; down regulation;
KM protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KM amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
XX
XX Hepatitis B virus.
XX
OS
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
```







KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KM amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
se.  
KM Homo sapiens.  
XX  
XX  
XX  
XX WO200116312-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US023998.  
XX  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
XX 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
XX 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
XX 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
XX 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
XX 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
XX 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswigen J, Uman N, Blatt L, Beigelman L, Burgin A;  
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
XX WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX  
XX Example 4; Page 360; 717pp; English.  
XX  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
XX zinzyme, and/or DNazyme motifs. The method of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,  
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
XX diseases, hepatitis B infections, and hepatitis and hepatocellular  
XX carcinoma. The enzymatic nucleic acid molecules can also be used as  
XX diagnostic tools to examine genetic drift and mutations within diseased  
XX cells and to detect the presence of specific RNA in a cell. The present  
XX sequence represents a substrate/target sequence for a ribozyme used in  
XX the examples of the present invention. Note: Some SEQ ID Nos are repeated  
XX more than once in the specification, but these have different sequences  
XX associated with them.  
XX  
XX Sequence 17 BP; 3 A; 10 C; 2 G; 0 T; 2 U; 0 Other;  
XX  
XX Query Match 0.84; Score 13.8; DB 1; Length 17;  
XX Best Local Similarity 76.5%; Pred. No. 2.8e+02;  
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1346 CCTGACCTGACCTCC 1362  
Db 1 CCCGACACACACCTCC 17  
RESUR 388  
ADU93089  
ID ADU93089 standard; DNA; 17 BP.  
XX  
XX AC ADU93089;  
XX  
XX 10-FEB-2005 (first entry)  
XX  
XX DE Human TERT NCH ribozyme substrate sequence #382.  
XX  
XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KM protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KM c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KM amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
de.  
XX  
XX Homo sapiens.  
XX  
XX WO200116312-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US023998.  
XX  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
XX 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
XX 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
XX 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
XX 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
XX 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
XX 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswigen J, Uman N, Blatt L, Beigelman L, Burgin A;  
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
XX WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX  
XX Example 1; Page 284; 717pp; English.  
XX  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes



PA (AEOM-) AEOMICA INC.  
XX  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMMP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMMP-1.  
XX  
XX Disclosure; SEQ ID NO 2756; 214bp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMMP-1). The protein and polynucleotide sequences of hGDMMP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMMP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMMP-1 nucleic acids in samples, as amplification substrates; to  
CC provide initial substrates for the recombinant engineering of hGDMMP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMMP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMMP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMMP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMMP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMMP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMMP-1, in particular heart  
CC and skeletal muscle disorders. hGDMMP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMMP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
XX Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1196 GCGACTATGAGGGCTG 1212  
Db 1 GCGAGTATGAGAGCTG 17  
RESULT 391  
AB063570  
ID AB063570 standard; DNA; 17 BP.  
XX  
XX AB063570;  
AC  
XX 20-AUG-2002 (first entry)  
XX  
XX  
DE Human KTOM1a portion (AB063232) probe # 283.  
XX  
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytoskeletal;  
XX gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
XX kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200224750-A2.  
XX  
XX  
XX 28-MAR-2002.  
PD  
XX  
XX 21-SEP-2001; 2001WO-US029656.  
PF  
XX  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX 30-JAN-2001; 2001WO-US000661.  
PR  
XX 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.  
PR  
PR 30-JAN-2001; 2001WO-US000664.  
PR  
PR 30-JAN-2001; 2001WO-US000665.  
PR  
PR 30-JAN-2001; 2001WO-US000666.  
PR  
PR 30-JAN-2001; 2001WO-US000667.  
PR  
PR 30-JAN-2001; 2001WO-US000668.  
PR  
PR 30-JAN-2001; 2001WO-US000669.  
PR  
PR 30-JAN-2001; 2001WO-US000670.  
PR  
PR 23-MAY-2001; 2001US-00864761.  
PR  
PR 28-AUG-2001; 2001US-0315676P.  
XX  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Zhang J;  
XX  
XX WPI; 2002-479509/51.  
XX  
XX  
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
PT e.g., liver or bone.  
XX  
XX  
XX Example 2; Page 194; 418bp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the  
CC invention has cytostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (AB063232)  
XX  
XX Sequence 17 BP; 2 A; 5 C; 2 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1402 AGCTTCAGTTCTTCCTC 1418  
Db 1 AGCTTCAGTTCTTCCTC 17  
RESULT 392  
ABV83022/C  
ID ABV83022 standard; DNA; 17 BP.  
XX  
XX ABV83022;  
AC  
XX  
XX 03-JAN-2003 (first entry)  
XX  
XX  
XX Human HTP1 scanning oligonucleotide SEQ ID 4268.  
XX  
XX Human; gene therapy; tumour suppressor; HTP1; chromosome 10p12.1;  
XX human testis expressed Patched like protein; testis; adrenal; liver;  
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;  
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EPI229046-A2.  
XX  
XX  
XX 07-AUG-2002.  
PD  
XX  
XX 28-JAN-2002; 2002EP-00001167.  
PF  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PR  
XX 30-JAN-2001; 2001WO-US000664.  
PR  
XX 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 23-MAY-2001; 2001US-00864761.  
PR 09-OCT-2001; 2001US-0327898P.  
PA (AEOM-) AEOMICA INC.  
XX Zhan J;  
XX WPI; 2002-676582/73.  
DR  
XX  
XX Novel isolated human testis expressed patched like protein (HTPL), useful  
PT for identifying agonist and antagonist and specific binding partners, and  
PT for treating subjects having defects in HTPL.  
PS Example 2; Page 623; 718pp; English.  
XX  
XX The present invention relates to human testis expressed patched like  
CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL  
CC has two isoforms, with a few single base pair differences between the  
CC two. One of the single base pair changes introduces a premature stop  
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
CC shares an overall structure organisation with the patched protein. The  
CC shared structural features strongly imply that HTPL plays a role similar  
CC to that of Patched, and is a potential tumour suppressor. HTPL is  
CC important in regulating male germ cell development, and the HTPL gene was  
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
CC therapy and manufacture of a medicament for treatment or prevention of  
CC such disorder associated with decreased expression or activity of human  
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
CC clinically useful diagnostic markers and potential therapeutic agents for  
CC male infertility and cancer. The present oligonucleotide was used in an  
CC example from the invention  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1089 GGCATGAGCTCCACCA 1105  
DB 17 GGCATGAGCTCCCA 1  
RESULT 393  
ABV90740/C  
ID ABV90740 standard; DNA; 17 BP.  
XX  
AC ABV90740;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1453.  
XX  
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP1239051-A2.  
XX  
XX PN  
XX PD 11-SEP-2002.  
XX  
XX 28-JAN-2002; 2002EP-00001165.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX  
XX 30-JAN-2001; 2001WO-US000664.  
PR

PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 30-MAY-2001; 2001US-00864761.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
PA (AEOM-) AEOMICA INC.  
XX  
XX Shannon M;  
XX WPI; 2002-684061/74.  
DR  
XX  
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
PS Example 2; SEQ ID NO 1453; 60pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoded by altered expression of human POSHL1 including diagnosing and  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1444 CTTTGGCAGGTGCAGC 1460  
DB 17 CTTTGGCAGGTGCAGC 1  
RESULT 394  
ABL31550  
ID ABL31550 standard; DNA; 17 BP.  
XX  
AC ABL31550;  
XX  
DT 21-MAR-2002 (first entry)  
XX  
DE Human HLA genotyping oligonucleotide SEQ ID NO 1039.  
XX  
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
KW immunogenetic; transplantation; genetic disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192572-A1.  
XX  
XX PN  
XX PD 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-JP004662.  
XX  
XX

PR 01-JUN-2000; 2000JP-00164798.  
XX (N1SN ) NISSHINO IND INC.  
PA (SYST-) SYSTEM RES INC.  
XX  
PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
DR WPI; 2002-122074/16.  
XX  
PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when  
transplanting between them.  
XX  
PS Claim 10; Page 290; 345pp; Japanese.  
XX  
CC The invention relates to a typing kit for judging human leukocyte antigen  
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
CC genes e.g. belonging to HLA class I antigens on human genome and  
CC containing gene polymorphisms as alloantigens have been immobilised as  
CC primers for amplification of cleaved nucleic acids relating to gene  
CC polymorphisms. The method is useful for judging HLA genotypes of  
CC individuals by determining immunogenetic differences before transplanting  
CC between them, providing genetic information to decide compatibility of  
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
CC pancreas, langerhans islet in pancreas and cornea, susceptibility  
CC diagnosis of genetic diseases and identifying individuals  
XX  
SQ Sequence 17 BP; 3 A; 5 C; 8 G; 1 T; 0 U; 0 Other;  
Query March 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1299 GGGCCAGGAGGAGC 1315  
Db 1 GGGCCATGAGCGGAGC 17  
RESULT 395  
ABQ76743/C  
ID ABQ76743 standard; DNA; 17 BP.  
XX  
AC ABQ76743;  
XX  
DT 03-MAR-2003 (first entry)  
XX  
DE TNF-associated PCR primer #2.  
XX  
KM Shine-Dalgarno; exogenous gene expression; filamentous blue-green algae;  
KM promoter; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN CN1353189-A.  
XX  
PD 12-JUN-2002.  
XX  
PF 14-NOV-2000; 2000CN-00132268.  
XX  
PR 14-NOV-2000; 2000CN-00132268.  
XX  
PA (PHYT-) INST PHYTOLOGY CHINESE ACAD SCI.  
XX  
PI Shi D, Ran L, Li Y;  
XX  
DR WPI; 2002-751432/82.  
XX  
PT Efficient expression box of filamentous blue-green algae.  
XX  
PS Example; Page 4 (Disclosure); 9pp; Chinese.  
XX  
CC This invention describes a novel, efficient expression box for

CC effectively expressing an exogenous gene in filamentous blue-green algae.  
CC The box includes a promoter, a Shine-Dalgarno (SD) sequence and a target  
CC gene. This sequence represents a PCR primer associated with the  
CC amplification of TNF, described in the disclosure of the invention  
XX  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Query March 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 891 GATCCCGGAGACTCT 907  
Db 17 GATCCCGGAGATTCT 1  
RESULT 396  
ACN01554  
ID ACN01554 standard; RNA; 17 BP.  
XX  
AC ACN01554;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE MNV Inozyme substrate SEQ ID NO 1544.  
XX  
KM MNV; West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN W0200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNV), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 1544; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 6 A; 7 C; 4 G; 0 T; 0 U; 0 Other;



```
XX 22-APR-2004 (first entry)
DT
XX
XX MNV Hammerhead Ribozyme substrate SEQ ID NO 1263.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX
XX 20-OCT-2000; 2000US-0242411P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI
XX
XX WPI; 2002-706994/76.
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS
XX
XX Claim 23; SEQ ID NO 1263; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
SQ Sequence 17 BP; 7 A; 5 C; 1 G; 0 T; 4 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1641 CAAACCAATCACTGAA 1657
DB 1 CAAACCAUUCACUGAA 17
RESULT 400
ACN07407
ID ACN07407 standard; RNA; 17 BP.
XX
XX ACN07407;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7410.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
```

```
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX
XX 20-OCT-2000; 2000US-0242411P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI
XX
XX WPI; 2002-706994/76.
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS
XX
XX Claim 23; SEQ ID NO 7410; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.8e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 897 CGGGGACTCCTGCACC 913
DB 1 CGGGGUCUCUCUAAAC 17
RESULT 401
ACN12112/C
ID ACN12112 standard; RNA; 17 BP.
XX
XX ACN12112;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX MNV minus strand Inozyme substrate SEQ ID NO 12115.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
```

XX 06-SEP-2002.  
 PD ACN07336/C  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (MNV), useful for treating a condition related to MNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PS  
 XX Claim 23; SEQ ID NO 12115; 495bp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
 CC treating a condition related to MNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 CC  
 SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1252 GTGTACCAAGTCAGCCG 1268  
 Db 17 GTGCACAAAGTCAGCAG 1  
 RESULT 402  
 ACN07336/C  
 ID ACN07336 standard; RNA; 17 BP.  
 XX  
 XX ACN07336;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX MNV Amberzyme substrate SEQ ID NO 7339.  
 DE  
 XX MNV, West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;  
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX

PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 DR  
 XX New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (MNV), useful for treating a condition related to MNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 PS  
 XX Claim 23; SEQ ID NO 7339; 495bp; English.  
 XX  
 XX The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
 CC treating a condition related to MNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 CC  
 SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 897 CGGGACTCCTCTGACC 913  
 Db 17 CGGGTCTCCTCTGACC 1  
 RESULT 403  
 ACN09339/C  
 ID ACN09339 standard; RNA; 17 BP.  
 XX  
 XX ACN09339;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 9342.  
 DE  
 XX MNV, West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;  
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyme; ss.  
 XX  
 XX West Nile Virus.  
 OS  
 XX WO200268637-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 19-OCT-2001; 2001WO-US048350.  
 PF  
 XX 20-OCT-2000; 2000US-0242411P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PI Blatt L, Mcswiggen JA;  
 XX WPI; 2002-706994/76.  
 DR



XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNW), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 23; SEQ ID NO 9342; 495bp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNW). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
CC  
XX  
SQ Sequence 17 BP; 0 A; 3 C; 7 G; 0 T; 7 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1322 ACCGCCCAAGGCCACA 1338  
Db 17 ACAGCACCAAGGCCACA 1  
RESULT 404  
ACN13675/c  
ID ACN13675 standard; RNA; 17 BP.  
XX  
XX ACN13675;  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX MNV minus strand DNazyme substrate SEQ ID NO 13678.  
XX  
XX MNV; West Nile Virus; antiinflammatory; cytoprotic; hepatotropic;  
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyne; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.  
XX Blatt L, Mcswigen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNW), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 23; SEQ ID NO 13678; 495bp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNW). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
CC  
XX  
SQ Sequence 17 BP; 5 A; 1 C; 5 G; 0 T; 6 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1640 TCAAACCAATCACTGA 1656  
Db 17 TCAAACCAATTCACCTGA 1  
RESULT 405  
ACN03237  
ID ACN03237 standard; RNA; 17 BP.  
XX  
XX ACN03237;  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX MNV Inozyme substrate SEQ ID NO 3240.  
XX  
XX MNV; West Nile Virus; antiinflammatory; cytoprotic; hepatotropic;  
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyne; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-0242411P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.  
XX Blatt L, Mcswigen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNW), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 23; SEQ ID NO 3240; 495bp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNW). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 5 A; 6 C; 1 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 2.8e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1639 CTCGAACCAATCTACTG 1655  
DB 1 CUCAAACCAUUCACUG 17  
RESULT 406  
ACN15211/C  
ID ACN15211 standard; RNA; 17 BP.  
XX  
XX ACN15211;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX MNV minus strand Amberzyme substrate SEQ ID NO 15214.  
XX  
XX MNV, West Nile Virus; antiinflammatory; cyostatic; hepatotropic;  
XX  
XX vircide; neuroprotective; antibacterial; replication; pancreatitis;  
XX  
XX encephalitis; myocarditis; meningitis; infection; hepatitis;  
XX  
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
XX  
XX Amberzyme; Zinzyme; ss.  
XX  
XX West Nile Virus.  
XX  
XX WO200268637-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 19-OCT-2001; 2001WO-US048350.  
XX  
XX 20-OCT-2000; 2000US-024211P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX (BLAT/) BLATT L.  
XX  
XX (MCSW/) MCSWIGEN J A.  
XX  
XX Blatt L, Mcswigen JA;  
XX  
XX WPI; 2002-706994/76.  
XX  
XX New nucleic acid molecule that modulates replication of West Nile Virus  
XX  
XX (MNV), useful for treating a condition related to MNV infection e.g.  
XX  
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
XX Claim 23; SEQ ID NO 15214; 495bp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
XX  
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
XX  
XX treating a condition related to MNV infection e.g. pancreatitis,  
XX  
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
XX  
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
XX  
XX molecule is selected from the group of ribozymes consisting of  
XX  
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
XX  
XX nucleic acid molecules further comprise at least five ribose residues, at  
XX  
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
XX  
XX least three of the 5' terminal nucleotides and a 3' end modification of a  
XX  
XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
XX  
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
XX  
XX in the specification. The present sequence is that of a nucleic acid  
XX  
XX molecule of the invention

XX  
SQ Sequence 17 BP; 0 A; 4 C; 7 G; 0 T; 6 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1321 GACGGCCCAAGCCAC 1337  
DB 17 GACAGCACCAAGCCAC 1  
RESULT 407  
ACD00505  
ID ACD00505 standard; DNA; 17 BP.  
XX  
XX ACD00505;  
XX  
XX 28-JUL-2003 (first entry)  
XX  
XX G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #978.  
XX  
XX Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
XX  
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cyostatic; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2003031621-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032599.  
XX  
XX 12-OCT-2001; 2001US-032900P.  
XX  
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
XX Zhang J;  
XX  
XX WPI; 2003-381720/36.  
XX  
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
XX  
XX investigating and/or treating disorders associated with aberrant  
XX  
XX expression or activity of GPCR-A-1, such as tumors and cancers.  
XX  
XX Example 2; SEQ ID NO 1002; 156bp; English.  
XX  
XX The invention describes an isolated nucleic acid encoding a G protein  
XX  
XX coupled receptor (GPCR), mutations of which cause cancer, comprising a  
XX  
XX 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
XX  
XX 409 residue amino acid sequence, all given in the specification, with or  
XX  
XX without conservative amino acid substitutions, or complements of the  
XX  
XX sequence of them. The encoding nucleic acid is not more than 100 kbase in  
XX  
XX length. The methods and compositions of the present invention are useful  
XX  
XX for diagnosing, investigating and/or treating disorders associated with  
XX  
XX aberrant expression or activity of GPCR-A-1, such as tumours and cancers.  
XX  
XX This sequence represents an oligonucleotide used to analyse the gene  
XX  
XX encoding human G-protein coupled receptor GPCR-A-1  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 455 CTGCATTCATCACTG 471  
DB 1 CTGCATTCATCACTG 17  
RESULT 408  
ACA99879  
ID ACA99879 standard; DNA; 17 BP.

XX AC A99879;  
XX DT 28-JUL-2003 (first entry)  
XX DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #372.  
XX KM Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
XX KM G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
XX OS Homo sapiens.  
XX PN WO2003031621-A2.  
XX PD 17-APR-2003.  
XX PF 11-OCT-2002; 2002WO-US032599.  
XX PR 12-OCT-2001; 2001US-0329000P.  
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX PI Zhang J;  
XX DR WPI; 2003-381720/36.  
XX DR New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
XX PT investigating and/or treating disorders associated with aberrant  
XX PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX PS Example 2; SEQ ID NO 396; 156bp; English.  
XX CC The invention describes an isolated nucleic acid encoding a G protein  
XX CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
XX CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
XX CC 409 residue amino acid sequence, all given in the specification, with or  
XX CC without conservative amino acid substitutions, or complements of the  
XX CC sequence of them. The encoding nucleic acid is not more than 100 kbase in  
XX CC length. The methods and compositions of the present invention are useful  
XX CC for diagnosing, investigating and/or treating disorders associated with  
XX CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.  
XX CC This sequence represents an oligonucleotide used to analyse the gene  
XX CC encoding human G-protein coupled receptor GPCR-A-1  
XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1536 CTGGGACTTGCAAAAG 1552  
XX Db 1 CTGGGACTGCAAAATAG 17  
XX  
XX RESULT 409  
XX ID ACA99880 standard; DNA; 17 BP.  
XX AC ACA99880;  
XX XX  
XX DT 28-JUL-2003 (first entry)  
XX DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #373.  
XX KM Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
XX KM G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
XX OS Homo sapiens.  
XX PN WO2003031621-A2.  
XX PD 17-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032599.  
XX XX  
XX PR 12-OCT-2001; 2001US-0329000P.  
XX XX  
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX PI Zhang J;  
XX DR WPI; 2003-381720/36.  
XX DR New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
XX PT investigating and/or treating disorders associated with aberrant  
XX PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX PS Example 2; SEQ ID NO 397; 156bp; English.  
XX CC The invention describes an isolated nucleic acid encoding a G protein  
XX CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
XX CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
XX CC 409 residue amino acid sequence, all given in the specification, with or  
XX CC without conservative amino acid substitutions, or complements of the  
XX CC sequence of them. The encoding nucleic acid is not more than 100 kbase in  
XX CC length. The methods and compositions of the present invention are useful  
XX CC for diagnosing, investigating and/or treating disorders associated with  
XX CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.  
XX CC This sequence represents an oligonucleotide used to analyse the gene  
XX CC encoding human G-protein coupled receptor GPCR-A-1  
XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
XX Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1537 TGGGACTTGCAAAAG 1553  
XX Db 1 TGGGACTGCAAAATAG 17  
XX  
XX RESULT 410  
XX ID ABT35050/c  
XX ID ABT35050 standard; DNA; 17 BP.  
XX AC ABT35050;  
XX XX  
XX DT 12-JUN-2003 (first entry)  
XX DE Tumour suppression related human fukutin oligo SEQ ID NO 687.  
XX XX  
XX KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX KM schizophrenia; protein chip; gene therapy; tumour suppression;  
XX KM human fukutin; ds.  
XX OS Homo sapiens.  
XX PN WO2003025175-A2.  
XX PD 27-MAR-2003.  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX PI Telerman A, Amson R, Tuijnder M;  
XX DR WPI; 2003-313353/30.  
XX PT New isolated nucleic acid, useful for treating viral diseases associated  
XX PT with tumors and cell degeneration, also related polypeptides, antibodies



PA (STIN/) STINCHOMB D T.  
PA (MCSW/) MCSWIGGEN J.  
PA (DRAP/) DRAPER K G.  
PI Stinchcomb DT, Mcawiggen J, Draper KG;  
DR WPI; 2003-340953/32.  
XX  
XX Novel enzymatic nucleic acid molecules which down regulate expression of  
PT a sequence encoding a subunit of nuclear factor kappa B useful for  
PT treating cancer, inflammatory disorders and autoimmune diseases.  
XX  
PS Claim 3; Page 32; 72pp; English.  
XX  
XX The invention describes an enzymatic nucleic acid molecule (I) which down  
CC regulates expression of a sequence encoding a subunit of nuclear factor  
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or ambenzyme  
CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
CC cancer and is useful for down-regulating RBL-A activity in a cell, for  
CC treating a patient having a condition associated with the level of RBL-A.  
CC (1) is useful for cleaving RNA comprising a sequence of RBL-A gene, in  
CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
CC antisenase nucleic acid molecules are useful for treating breast, lung,  
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
CC multidrug resistant cancer. The method involves use of other drug  
CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or  
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
CC gemcitabine or radiation therapy. The enzymatic and antisenase nucleic  
CC acid molecules are also useful for treating inflammatory disease such as  
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
CC rejection, gene therapy applications, ischaemia/reperfusion injury  
CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
CC infection. This sequence represents the substrate of a novel enzymatic  
CC nucleic acid molecule  
XX  
SQ Sequence 17 BP; 2 A; 11 C; 3 G; 0 T; 1 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 135 CCCGAGCGCCGAC 151  
DB 1 CCCGAGCGCCGAC 17  
XX  
RESULT 413  
ADA99853  
ID ADA99853 standard; DNA; 17 BP.  
XX  
AC ADA99853;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human MD23 scanning oligonucleotide SEQ ID 842.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX EPI281758-A2.  
PN  
XX 05-FEB-2003.  
PD  
XX 30-JUL-2002; 2002BP-00016874.  
PF  
XX

PR 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
PI  
XX WPI; 2003-423107/40.  
DR  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.  
XX  
XX  
PS Example 8; SEQ ID NO 842; 103pp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 429 CCTGCGCTTCGCGAGG 445  
DB 1 CCTGCGCTTCGCGAGG 17  
XX  
RESULT 414  
ADB03782  
ID ADB03782 standard; DNA; 17 BP.  
XX  
AC ADB03782;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human MD27 scanning oligonucleotide SEQ ID 4768.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX EPI281758-A2.  
PN  
XX 05-FEB-2003.  
PD  
XX 30-JUL-2002; 2002BP-00016874.  
PF  
XX 02-AUG-2001; 2001US-00922181.  
PR  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
PI  
XX WPI; 2003-423107/40.  
DR  
XX

PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of  
PT MD24, MD27 or MD212, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 4768; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
CC  
XX  
SQ Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
DY 684 TCTCTGCTGCGCTTCC 700  
1 TCTCTCTGCGCTTCC 17  
DB  
RESULT 415  
ACD55641  
ID ACD55641 standard; RNA; 17 BP.  
XX  
AC ACD55641;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV amberzyme substrate sequence #151.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.

PA (LEBP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBB/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E,  
XX  
DR WPI; 2003-229207/22.  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 206; 387pp; English.  
PS  
XX The present invention relates to nucleic acid molecules which modulate  
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,  
XX inozymes, zinczymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well  
XX as oligonucleotides that specifically bind the Enhancer I region of HBV  
XX DNA. The nucleic acids may be used to modulate the expression of HBV  
XX genes and HBV viral replication. Also disclosed is a method for screening  
XX compounds and/or potential therapies directed against HBV, and compounds  
XX that modulate the expression and/or replication of HCV. The compounds and  
XX methods of the invention are useful for the treatment of degenerative and  
XX expression states related to cirrhosis, liver failure, and hepatocellular  
XX carcinoma. The present sequence represents a substrate for one of the HBV  
XX ribozyme, inozyme, G-cleaver, zinczyme, DNAzyme or amberzyme sequences  
XX disclosed in the present invention  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 2.8e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DY 1267 CGCTGAGACACCAT 1283  
1 CGCAUGGAGACACCGU 17  
DB  
RESULT 416  
ACD55640  
ID ACD55640 standard; RNA; 17 BP.  
XX  
AC ACD55640;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV amberzyme substrate sequence #150.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVCO/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
XX Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 206; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAszymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNAszyme or amberzyme sequences  
CC disclosed in the present invention  
XX  
XX Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 0.8\*; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 2.8e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1265 GCCGCGCTGGAGACCACC 1261  
Db 1 GUCCGCAUGGAGACCACC 17  
ACD58714/c  
ID ACD58714 standard; RNA; 17 BP.  
XX  
XX ACD58714;  
XX  
XX 24-SEP-2003 (first entry)  
XX  
XX HCV DNAszyme substrate sequence #964.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNAszyme; inozyme; zinzyme;  
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

KW virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX W0200281494-A1.  
XX  
XX  
XX 17-OCT-2002.  
PD  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX  
XX 26-MAR-2001; 2001US-00817879.  
XX  
XX 08-JUN-2001; 2001US-00877478.  
XX  
XX 08-JUN-2001; 2001US-0296876P.  
XX  
XX 24-OCT-2001; 2001US-0335059P.  
XX  
XX 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVCO/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
XX Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 251; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAszymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNAszyme or minus strand DNAszyme sequences disclosed in the present  
CC invention  
XX  
XX Sequence 17 BP; 2 A; 3 C; 7 G; 0 T; 5 U; 0 Other;  
SQ  
Query Match 0.8\*; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1254 GTACAAAGTCAGCGGCC 1270  
Db 17 GTACAAAGTCAGCGGCC 1  
ACD62777  
ID ACC62777 standard; DNA; 17 BP.  
XX  
XX ACC62777;  
XX

DT	01-JUL-2003	(first entry)	
XX			
DE	Murine oligonucleotide associated with tumour suppression, SEQ ID 24.		
XX			
XX	Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;		
KW	tumour suppression; tumour reversion; apoptosis; virus resistance;		
KW	viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;		
XX	schizophrenia; ss.		
XX			
OS	Mus musculus.		
XX			
PN	WO2003025176-A2.		
XX			
PD	27-MAR-2003.		
XX			
PF	17-SEP-2002; 2002MO-IB004210.		
XX			
PR	17-SEP-2001; 2001FR-00011979.		
XX			
PA	(MOLE-) MOLECULAR ENGINES LAB.		
XX			
PI	Teleman A, Amson R, Tuijnder M;		
XX			
DR	WPI, 2003-333167/31.		
XX			
PT	New isolated nucleic acid, useful for treating viral diseases associated		
PT	with tumours and cell degeneration, also related polypeptides, antibodies		
PT	and transfected cells.		
XX			
PS	Disclosure; Page 33; 738pp; French.		
XX			
CC	The present invention relates to murine oligonucleotides (ACC62754-		
CC	ACC66806), which are associated with tumour suppression, tumour		
CC	reversion, apoptosis and virus resistance. The oligonucleotides are		
CC	useful as (1) as probes and primers for detecting, identifying,		
CC	quantifying and/or amplifying nucleic acid, e.g. as one component of a		
CC	gene chip; in vitro as (anti)sense reagents; and (2) for production of		
CC	recombinant polypeptides. The oligonucleotides are useful for preparation		
CC	of pharmaceuticals for prevention and/or treatment of viral diseases that		
CC	are characterised by development of tumours or cell degeneration,		
XX	specifically cancer but also Alzheimer's disease and schizophrenia		
XX			
SEQ	Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;		
	Query Match	0.8%;	Score 13.8; DB 1; Length 17;
	Best local Similarity	88.2%;	Pred. No. 2.8e+02;
	Matches 15; Conservative	0;	Mismatches 2; Indels 0; Gaps 0
QY	891 GATCCCGGGGACTCCT 907		
DB	1 GATCCAGGGGACTCT 17		
RESULT 419			
ACAB9989/c			
ID	ACAB9989 standard; DNA; 17 BP.		
AC	ACAB9989;		
XX			
DT	10-JUL-2003 (first entry)		
XX			
DE	Cardiovascular disease differential gene expression related primer #36.		
XX			
KW	Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;		
KW	myocardial infarction; cardiac; antiarteriosclerotic; antianginal;		
KW	gene therapy; differential gene expression; PCR; primer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003031650-A2.		
XX			
PD	17-APR-2003.		
XX			

```

PE      02-OCT-2002; 2002MO-EP011034.
XX
PR      08-OCT-2001; 2001GB-00024145.
XX
PA      (FARB ) BAYER AG.
PI
PI      Munnes M, Gehrmann M, Wick M, Schmitz G,
XX
DR      WPI; 2003-403106/38.
XX
PT      Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
XX
PT      angina, ischemia, myocardial infarction or arteriosclerosis by detection
XX
PT      of a polynucleotide in a biological sample comprises detecting a
XX
PT      hybridization complex.
XX
PS      Example 3; Page 103; 454pp; English.
XX
CC      The invention describes a method of predicting, diagnosing or prognosing
XX
CC      a cardiovascular disease by detection of a polynucleotide in a biological
XX
CC      sample comprising hybridizing at least one of the polynucleotide to a
XX
CC      nucleic acid material of a biological sample, thus forming a
XX
CC      hybridisation complex, and detecting the hybridisation complex. The
XX
CC      polynucleotides, polypeptides, antisense molecule, antibody and reagent
XX
CC      are useful for preparing compositions for preventing, predicting or
XX
CC      diagnosing, or a medicament for treating a cardiovascular disease, e.g.
XX
CC      arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
XX
CC      This sequence represents a primer used to identify genes differentially
XX
CC      regulated in individuals with cardiovascular disease
XX
SQ      Sequence 17 BP; 5 A; 9 C; 2 G; 1 T; 0 U; 0 Other;
QY      Query Match          0.8%; Score 13.8; DB 1; Length 17;
        Best Local Similarity 88.2%; Pred.No.2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
DB      162 TGCAGAGGGGCGTGTG 178
        17 TGCAGCGTGCGGTTGTG 1
RESULT 420
ADB42998
ID      ADB42998 strand; DNA; 17 BP.
AC
AC      ADB42998;
XX
DT      18-DEC-2003 (revised)
DT      04-DEC-2003 (first entry)
XX
DE      Tumour suppression/reversion associated nucleotide #3321.
XX
KW      cyostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW      primer; probe; tumour suppression; tumour reversion; apoptosis;
KW      virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
PN      WO2003040369-A2.
XX
PD      15-MAY-2003.
XX
PF      17-SEP-2002; 2002WO-IB004219.
XX
PR      17-SEP-2001; 2001FR-00011981.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB.
XX
PI      Telerman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-441574/41.
XX
PT      New nucleic acid encoding human prostate membrane-specific antigen,

```



PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX  
PS Disclosure; Page 420; 771pp; French.  
XX  
CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptides are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules.  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 7 A; 6 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 375 GATCATCTTACGCCACA 391  
Db 1 GATCATCAAGCCACA 17  
|||||  
|  
RESULT 421  
ADP64140/c 0.8%; Score 13.8; DB 1; Length 17;  
ID ADP64140 standard; DNA; 17 BP.  
XX  
AC ADP64140;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human PCCP1 DNA fragment SEQ ID 8-directed probe - SEQ ID 2044.  
XX  
XX chromatin organisation modifier; CHROMO domain; cytosstatic; PCCP1;  
KM prostate cancer candidate protein 1; tumour; gene therapy; vaccine;  
KM human; ss; probe.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO2003050284-A1.  
XX  
PD 19-JUN-2003.  
XX  
PF 22-NOV-2002; 2002WO-US037506.  
XX  
PR 10-DEC-2001; 2001US-0339764P.  
XX  
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
XX Guo J;  
PI  
XX WPI; 2003-532916/50.  
DR  
XX New prostate cancer candidate protein 1 (PCCP1), useful for preparing a  
PT composition for treating or preventing a disorder associated with  
PT decreased or increased expression or activity of PCCP1 e.g., tumor.  
XX  
PS Example 2; SEQ ID NO 2044; 164pp; English.  
XX

CC The invention relates to a novel isolated nucleic acid that encodes a  
CC protein with a chromatin organisation modifier (CHROMO) domain. The  
CC polynucleotide of the invention demonstrates cytostatic activity and may  
CC be useful for preparing a composition for treating or preventing a  
CC disorder associated with decreased or increased expression or activity of  
CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as  
CC during gene therapy and vaccine production procedures. The current  
CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 8-  
CC directed probe of the invention. Note: The current sequence is not shown  
CC within the specification per se but was retrieved from the wipoweb  
CC database.  
XX  
SQ Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 255 CTCCTCTAACACCTCGG 271  
Db 17 CTCCTCTAACACCAAGG 1  
|||||  
|  
RESULT 422  
ADP63951  
ID ADP63951 standard; DNA; 17 BP.  
XX  
AC ADP63951;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human PCCP1 DNA fragment SEQ ID 8-directed probe - SEQ ID 1855.  
XX  
XX chromatin organisation modifier; CHROMO domain; cytosstatic; PCCP1;  
KM prostate cancer candidate protein 1; tumour; gene therapy; vaccine;  
KM human; ss; probe.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO2003050284-A1.  
XX  
PD 19-JUN-2003.  
XX  
PF 22-NOV-2002; 2002WO-US037506.  
XX  
PR 10-DEC-2001; 2001US-0339764P.  
XX  
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
XX Guo J;  
PI  
XX WPI; 2003-532916/50.  
DR  
XX New prostate cancer candidate protein 1 (PCCP1), useful for preparing a  
PT composition for treating or preventing a disorder associated with  
PT decreased or increased expression or activity of PCCP1 e.g., tumor.  
XX  
PS Example 2; SEQ ID NO 1855; 164pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid that encodes a  
CC protein with a chromatin organisation modifier (CHROMO) domain. The  
CC polynucleotide of the invention demonstrates cytostatic activity and may  
CC be useful for preparing a composition for treating or preventing a  
CC disorder associated with decreased or increased expression or activity of  
CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as  
CC during gene therapy and vaccine production procedures. The current  
CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 8-  
CC directed probe of the invention. Note: The current sequence is not shown  
CC within the specification per se but was retrieved from the wipoweb  
CC database.  
XX  
SQ Sequence 17 BP; 0 A; 8 C; 4 G; 5 T; 0 U; 0 Other;  
XX

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 987 CTGCTGAGTGCCTTCC 1003  
 DB 1 CTGCTGAGTGCCTTCC 17

RESULT 423  
 ADF62472  
 ID ADF62472 standard; DNA; 17 BP.  
 AC ADF62472;  
 DT 12-FEB-2004 (first entry)  
 DE Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 376.  
 XX chromatin organisation modifier; CHROMO domain; cytosolic; PCCP1;  
 KM prostate cancer candidate protein 1; tumour; gene therapy; vaccine;  
 KM human; ss; probe.  
 XX Homo sapiens.  
 XX MO2003050284-A1.  
 XX 19-JUN-2003.  
 XX 22-NOV-2002; 2002WO-US037506.  
 XX 10-DEC-2001; 2001US-0339764P.  
 XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.  
 PA Guo J;  
 PI WPI; 2003-532916/50.  
 DR New prostate cancer candidate protein 1 (PCCP1), useful for preparing a  
 PT composition for treating or preventing a disorder associated with  
 PT decreased or increased expression or activity of PCCP1 e.g., tumor.  
 XX Example 2; SEQ ID NO 376; 164bp; English.  
 PS The invention relates to a novel isolated nucleic acid that encodes a  
 CC protein with a chromatin organisation modifier (CHROMO) domain. The  
 CC polynucleotide of the invention demonstrates cytosolic activity and may  
 CC be useful for preparing a composition for treating or preventing a  
 CC disorder associated with decreased or increased expression or activity of  
 CC PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as  
 CC during gene therapy and vaccine production procedures. The current  
 CC sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-  
 CC directed probe of the invention. Note: The current sequence is not shown  
 CC within the specification per se but was retrieved from the Wipoweb  
 CC database.  
 CC  
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 786 TGAGAAAGTGACACA 802  
 DB 1 TGAGAAAGTGACACA 17

RESULT 424  
 ADI51353/C  
 ID ADI51353 standard; DNA; 17 BP.  
 AC ADI51353;

XX 15-APR-2004 (first entry)  
 DT Human tumour suppression/reversion-related DNA sequence SeqID3856.  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KM cytosolic; vinctide; neuroprotective; neurotropic; neuroleptic; probe;  
 KM primer; PCR; gene chip; antisense; viral disease; tumour;  
 KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX Homo sapiens.  
 XX MO2003025177-A2.  
 XX 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004523.  
 XX 17-SEP-2001; 2001PR-00011980.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-313354/30.  
 DR New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX Disclosure; SEQ ID NO 3856; 30bp; French.  
 PS This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytosolic, vinctide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration. The  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publihedpct\_sequences

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 806 GTGTGACTGTGTGATC 822  
 DB 17 GTGTGACTGTGTGATC 1

RESULT 425  
 ACC53250  
 ID ACC53250 standard; DNA; 17 BP.  
 AC ACC53250;  
 DT 27-JUN-2003 (first entry)  
 DE Human tumour suppressor sequence #2017.  
 XX ss; tumour suppressor; antitumour; cytosolic; tumour suppression;  
 KM tumour regression; apoptosis; virus resistance; diagnosis;  
 KM cellular degeneration.

```
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PS
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Tejerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 506; 798bp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 9 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
OY Query Match 0.8%; Score 13.8; DB 1; Length 17;
Db Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1665 GAGCCTGTAAATATAA 1681
Db 1 GATCCTTTAAATAATAA 17
RESULT 426
ACCS3982/C
ID ACCS3982 standard; DNA; 17 BP.
XX AC
XX AC CCS3982;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2749.
XX KM 89; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Tejerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
```

```
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 675; 798bp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
OY Query Match 0.8%; Score 13.8; DB 1; Length 17;
Db Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 806 GTGTGACTGTGCTGATC 822
Db 17 GTGTGCTGTGCAATC 1
RESULT 427
ADL46848
ID ADL46848 standard; RNA; 17 BP.
XX AC
XX AC ADL46848;
XX DT 20-MAY-2004 (first entry)
XX DE Human NOCO receptor inozyme substrate sequence #281.
XX KM antisense oligonucleotide; neurite growth inhibitor; NOCO;
KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KM protein kinase PKR; cerebrovascular accident;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KM restenosis; asthma; Crohn's disease; diabetes; obesity;
KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis;
KM NOCO receptor inozyme; substrate; ds.
XX OS Unidentified.
XX OS
XX PN WO200281628-A2.
XX PD 17-OCT-2002.
XX PF 03-APR-2002; 2002WO-US010512.
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blact L, Chowitra B, Haeblerl P, Mcawiggen J, Fossnaugh K;
XX DR WPI; 2003-058513/05.
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX PS Claim 9; SEQ ID NO 381; 317bp; English.
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOCO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
```

invention are useful for treating: cerebrovascular accident; central nervous system (CNS) injury; spinal cord injury; cancer (e.g. melanoma, lymphoma or glioma); inflammatory disease (e.g. rheumatoid arthritis, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis)). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human NCOO receptor inozyme substrate sequence.

Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 2.8e+02;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1084 TGGCTGGCCATGAGCTC 1100  
Db 1 UGGCUGGCCGAGCCTC 17

RESULT 428

ADL48696/C  
ID ADL48696 standard; RNA; 17 BP.

ADL48696;  
20-MAY-2004 (first entry)  
Human IKK-gamma substrate sequence #1206.

antisense oligonucleotide; neurite growth inhibitor; NCOO;  
prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;  
central nervous system injury; CNS injury; spinal cord injury; cancer;  
melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
restenosis; asthma; Crohn's disease; diabetes; obesity;  
autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;  
substrate; ds.

Unidentified.

WO200281628-A2.

17-OCT-2002.

03-APR-2002; 2002WO-US010512.

05-APR-2001; 2001US-00827395.

28-MAY-2001; 2001US-0294412P.

28-AUG-2001; 2001US-0315315P.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Chowrira B, Haerberli P, Mcswigen J, Fosnaugh K;

WPI; 2003-058513/05.

Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor; prostaglandin D2 receptor; Ikappab kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.  
Claim 59; SEQ ID NO 2229; 317bp; English.

The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NCOO, prostaglandin D2 receptor (PTGDR), Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

invention are useful for treating: cerebrovascular accident; central nervous system (CNS) injury; spinal cord injury; cancer (e.g. melanoma, lymphoma or glioma); inflammatory disease (e.g. rheumatoid arthritis, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis)). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human IKK-gamma substrate sequence.

Sequence 17 BP; 7 A; 1 C; 8 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1402 AGCTTCAGCTTCCTC 1418  
Db 17 AGCTTCCTCTCTCCTC 1

RESULT 429

ADM60211  
ID ADM60211 standard; RNA; 17 BP.

ADM60211;  
03-JUN-2004 (first entry)  
Hepatitis B virus (HBV) RNA target sequence #2345.

Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
viral; hepatotropic; antiinflammatory; cytostatic.

Hepatitis B virus.

US2004054156-A1.

18-MAR-2004.

15-JAN-2003; 2003US-00342902.

14-MAY-1992; 92US-00882712.

07-FEB-1994; 94US-00193627.

08-NOV-1999; 99US-00436430.

20-MAR-2000; 2000US-00531025.

09-AUG-2000; 2000US-00636385.

24-OCT-2000; 2000US-00696347.

08-JUN-2001; 2001US-00877478.

(DRAP/) DRAPER K.

(BLAT/) BLATT L.

(MCSW/) MCSWIGEN J A.

(MORR/) MORRISSEY D.

Draper K, Blatt L, Mcswigen JA, Morrissey D;

WPI; 2004-247781/23.

Novel enzymatic nucleic acid molecule such as DNAszymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.

Disclosure; SEQ ID NO 2345; 122bp; English.

The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a

CC 2'-OH group within the molecule for activity. The nucleic acids are  
CC useful for treating hepatitis B virus infection, hepatitis,  
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
CC combination with other therapies such as lamivudine and interferons. The  
CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
CC mutations within diseased cells, for detecting the presence of HBV RNA in  
CC a cell, for the study of RNA and for down-regulating gene expression of  
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
CC sequence represents an HBV RNA target sequence, used in the scope of the  
CC invention. Note: The sequence data for this patent is also available in  
CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 2.8e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1265 GCGCGCTGGAGACCAACC 1281  
Db 1 GCGCGAUGGAGACCAACC 17  
RESULT 430  
ADM60212  
ID ADM60212 standard; RNA; 17 BP.  
XX  
AC ADM60212;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis B virus (HBV) RNA target sequence #2346.  
XX  
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
KM hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
KM virucide; hepatotropic; antiinflammatory; cytostatic.  
XX  
OS Hepatitis B virus.  
XX  
PN US2004054156-A1.  
XX  
PD 18-MAR-2004.  
XX  
PF 15-JAN-2003; 2003US-00342902.  
XX  
PR 14-MAY-1992; 92US-00882712.  
PR 07-FEB-1994; 94US-00193627.  
PR 08-NOV-1999; 99US-00436430.  
PR 20-MAR-2000; 2000US-00531025.  
PR 09-AUG-2000; 2000US-00636385.  
PR 24-OCT-2000; 2000US-00696347.  
PR 08-JUN-2001; 2001US-00877478.  
XX  
PA (DRAP/) DRAPER K.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
PA (MORR/) MORRISSEY D.  
XX  
PI Draper K, Blatt L, Mcswigen JA, Morrissey D;  
XX  
DR WPI; 2004-247781/23.  
XX  
PT Novel enzymatic nucleic acid molecule such as DNAsymes and inozymes  
XX specifically cleaving RNA derived from hepatitis B virus and comprising  
XX one or more binding arms, useful for treating hepatitis and cirrhosis.  
XX  
PS Disclosure; SEQ ID NO 2346; 122bp; English.  
XX  
CC The invention relates to an enzymatic nucleic acid molecule that  
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and  
CC comprising one or more binding arms, without requiring the presence of a  
2'-OH group within the molecule for activity. The nucleic acids are

CC useful for treating hepatitis B virus infection, hepatitis,  
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
CC combination with other therapies such as lamivudine and interferons. The  
CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
CC mutations within diseased cells, for detecting the presence of HBV RNA in  
CC a cell, for the study of RNA and for down-regulating gene expression of  
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
CC sequence represents an HBV RNA target sequence, used in the scope of the  
CC invention. Note: The sequence data for this patent is also available in  
CC electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 2.8e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1267 GCGCTGGAGACCAACC 1283  
Db 1 GCGAUGGAGACCACCG 17  
RESULT 431  
ACN70772/C  
ID ACN70772 standard; DNA; 17 BP.  
XX  
AC ACN70772;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMPL-1 probe SEQ ID NO:7674.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KM hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
PA (GUY/) GU Y.  
PA (UIY/) UI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
DR WPI; 2004-533378/51.  
XX

PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 7674; Opp; English.  
XX  
CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 8 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2;  
QY 1404 CTTGAGCTTCCTCCCA 1420  
Db 17 CTTGCTCTTCTTCTCCA 1  
RESULT 432  
ACN65854  
ID ACN65854 standard; DNA; 17 BP.  
XX ACN65854;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human GDMPL-1 probe SEQ ID NO:2756.  
XX  
KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
OS Homo sapiens.  
XX  
PN US2004137589-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 26-NOV-2003; 2003US-00723361.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.  
XX  
XX (GUY/) GU Y.  
PA (JUY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
DR WPI; 2004-533378/51.  
XX  
PT Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
PS Disclosure; SEQ ID NO 2756; Opp; English.  
XX  
CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63102  
XX  
SQ Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 2;  
QY 1196 GCGACTATGAGGAGCTG 1212  
Db 1 GCGAGTAGAGGAGCTG 17  
RESULT 433  
ADM29146  
ID ADM29146 standard; DNA; 17 BP.  
XX ADM29146;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Gastric cancer related gene GSTP1 primer SEQ ID NO 79.  
XX  
KW diagnosis; gene expression; stomach tumor; gastrointestinal disease;  
KW neoplasm; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2005001126-A1.  
XX  
PD 06-JAN-2005.  
XX  
PF 25-MAR-2004; 2004WO-KR000677.  
XX  
PR 12-JUN-2003; 2003KR-00038034.  
PR 25-NOV-2003; 2003KR-00084001.  
XX  
XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
XX  
PA Kim N, Kim YS, Lee J, Oh J, Park H, Ahn H, Yoon S, Han Y;  
PI Kim S, Kim J, Byun S, Noh S, Song K, Yoo HS;  
XX  
DR WPI; 2005-075581/08.  
XX  
PT Diagnosing gastric cancer or metastatic gastric cancer comprises  
PT measuring the expression levels of RNA or protein of any of the up-  
PT and/or down-regulated genes in gastric cancers or metastatic gastric  
PT cancer.

XX Example 3; SEQ ID NO 79; 112bp; English.  
PS  
XX The invention describes a method of diagnosing gastric cancer or  
CC metastatic gastric cancer comprising measuring the expression levels of  
CC RNA or protein of at least one gene, e.g. up- and/or down-regulated genes  
CC in gastric cancers or metastatic gastric cancer. Also described are: a  
CC kit, for diagnosing gastric cancer and/or metastatic gastric cancer,  
CC comprising: a sense primer and an anti-sense primer of; a probe  
CC corresponding to; and an antibody that recognizes the protein encoded by  
CC at least one of the cited up- and down-regulated genes; and screening a  
CC suppressor of gastric cancer or metastatic gastric cancer. The methods  
CC and kits are useful for diagnosing gastric cancer or metastatic gastric  
CC cancer. Expression levels for gastric cancer-related marker genes were  
CC identified in the 4 pairs of patient samples with gastric cancer.  
CC tissues/normal tissues taken from 4 patients with gastric cancer.  
CC Competitive RT-PCR was performed to determine the amount of the gene  
CC expression of any of the up- and down-regulated genes in gastric cancer.  
CC In addition, expression level of any of the up- and down-regulated genes  
CC in metastatic gastric cancer was also identified. The amount of  
CC competitive RT-PCR products of up- and down-regulated genes in metastatic  
CC gastric cancer was higher in most tested metastatic cancer tissues than  
CC those of primary cancer tissues. This sequence represents a primer used  
CC in competitive PCR to establish which genes are up and/or down regulated  
CC in gastric and metastatic cancers.  
XX  
SQ Sequence 17 BP, 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 432 GGCTTCGGCGAGGCT 448  
Db 1 GGCTTCGGCTGAGGACT 17  
RESULT 434  
AEB23914  
XX AEB23914 standard; DNA; 17 BP.  
XX  
AC AEB23914;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE HLA-C allele identification-related oligonucleotide probe SeqID55.  
XX  
KM HLA-C; human leukocyte antigen; diagnostic; SNP detection; DNA detection;  
KM transplant rejection; cancer; diabetes; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2005185174-A.  
XX  
PD 14-JUL-2005.  
XX  
PF 25-DEC-2003; 2003JP-00430556.  
XX  
PR 25-DEC-2003; 2003JP-00430556.  
XX  
PA (CANO ) CANON KK.  
XX  
PI Tsukada M;  
XX  
DR WPI; 2005-483348/49.  
XX  
PT Probe set for identifying human leukocyte antigen (HLA)-C allele in test  
PT substance in patients with organ transplant, cancer, diabetes, comprises  
PT probes such as CM.0102, CM.0104, CM.0206, CM.03042, CM.0314, CM.0408,  
PT CM.0603 or CM.070201.  
XX  
PS Claim 2; SEQ ID NO 180; 51bp; Japanese.  
XX

CC This invention relates to a novel probe set for identifying HLA-C (human  
CC leukocyte antigen-C) alleles in a test substance. The invention enables  
CC identification of HLA-C alleles in patients with organ transplant,  
CC cancer, diabetes and other multiple-factor diseases, and thus provides  
CC tailored medical treatment to individual patients. The present sequence  
CC is that of an oligonucleotide probe which is used in the HLA-C probe set  
CC of the present invention.  
XX  
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 138 CAGGCCGACGACAGG 154  
Db 1 CAGGCCGACGACAGG 17  
RESULT 435  
AED8144  
XX AED8144 standard; DNA; 17 BP.  
XX  
AC AED8144;  
XX  
DT 26-JAN-2006 (first entry)  
XX  
DE Human Leukocyte Antigen B allele identification probe, SEQ ID 27.  
XX  
KM HLA; Leukocyte; Antigen; transplant rejection; histocompatibility;  
KM preclinical testing; cancer; cytostatic; diabetes mellitus; antidiabetic;  
KM probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2005185172-A.  
XX  
PD 14-JUL-2005.  
XX  
PF 25-DEC-2003; 2003JP-00430554.  
XX  
PR 25-DEC-2003; 2003JP-00430554.  
XX  
PA (CANO ) CANON KK.  
XX  
PI Tsukada M;  
XX  
DR WPI; 2006-013379/02.  
XX  
PT Probe set for specific identification of an HLA-B allele in a sample,  
PT useful e.g. in matching transplant donors and recipients, and in  
PT determining suitable treatment for patients with conditions such as  
PT cancer and diabetes mellitus.  
XX  
PS Claim 2; SEQ ID NO 27; 152bp; Japanese.  
XX  
XX The invention relates to a novel probe set for the identification of a  
CC Human Leukocyte Antigen (HLA)-B allele in a sample. The invention further  
CC includes a method for identifying an HLA-B allele using the probe set.  
CC The probe set and method are useful for identifying an HLA-B allele in a  
CC sample. The information gained is useful, for example, in matching organ  
CC donors and recipients, and in guiding clinical decisions in the treatment  
CC of diseases such as cancer and diabetes mellitus. This oligo sequence  
CC represents a probe used in the identification of a Human Leukocyte  
CC Antigen B allele of the invention.  
XX  
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 138 CAGGCCGACGACAGG 154

Db 1 GAGGCCGACGACAGG 17

RESULT 436  
AEF42068/c  
ID AEF42068 standard; DNA; 17 BP.

XX AEF42068;

XX 23-MAR-2006 (first entry)

XX Chicken Pycin LightCycler RT-PCR, reverse PCR primer.

XX DNA microarray; PCR; primer; ss; gene expression; malabsorption syndrome;

XX metabolic; gastrointestinal-gen.; diagnosis; gastrointestinal disease.

XX Gallus gallus.

XX MO2006006853-A2.

XX 19-JAN-2006.

XX 08-JUN-2005; 2005WO-NL000494.

XX 09-JUN-2004; 2004EP-00077001.

XX 16-FEB-2005; 2005EP-00075373.

XX (IDLE-) ID-LEHSTAD INST DIERHOUDERIJ EN DIERGEZ.

XX Niwold JA, Rebel JMJ, Smits MA;

XX WPI; 2006-110237/11.

XX New set of genes or gene sequences comprising at least 20 intestinal  
PT genes, and at least 5 enzymes, e.g. caspase, apob, aminopeptidase, etc.,  
PT useful for determining intestinal health, and/or disease of an animal or  
PT a human.

XX Example 1; Page 22; 88pp; English.

XX The invention relates a set of genes or gene sequences comprising at  
XX least 20 genes in table 1, and comprising at least 5 of: Na/glucose  
XX transporter, K/Cl channel, I-PABP, L-PABP, Cytochrome P450, caspase, beta  
XX -2-microglobin, guanylyl, calbindin, phosphatase, aldolase, actin,  
XX metallopeptidase, aminopeptidase, glycosaminotransferase, glutathion S  
XX transferase, maltase/glucosylidase, sucrase/isomaltase, butyrophilin,  
XX apob, and cytochrome C oxidase. Also included are detecting the  
XX presence/absence of an intestinal disease in an animal/human (comprising  
XX measuring, in a sample of the animal or human, expression levels of a set  
XX of genes or gene sequences, or a gene specific fragment of the genes and  
XX comparing the expression levels with a reference value), measuring an  
XX increase of the intestinal health status of an animal/human (comprising  
XX measuring in a series of samples of intestinal tissue of the animal taken  
XX at different timepoints, expression levels of a set of genes or gene  
XX sequences, or a gene specific fragment of the genes and comparing the  
XX expression levels with a reference value), a kit comprising a set of at  
XX least 2 oligonucleotide primers capable of specifically hybridizing to a  
XX set of genes (or a gene specific fragment of the genes) and a kit  
XX containing ingredients to measure protein levels of gene products encoded  
XX by genes. The set of genes or gene sequences are useful for determining  
XX intestinal health, and/or disease of an animal or a human. Expression of  
XX genes in 2 chicken strains (susceptible or resistant to Malabsorption  
XX syndrome, MAS) was studied using the differential display method.  
XX Differentially expressed genes were amplified and sequenced. cDNAs  
XX representing differentially expressed genes were analyzed for their  
XX expression levels using the LightCycler RT-PCR method. The present  
XX sequence is a PCR primer for a chicken cDNA or chicken virus sequence,  
XX used in the LightCycler PCR experiment (Note, these are not RT-PCR  
XX primers, the reverse transcription stage is accomplished using random  
XX hexamers as primers).

XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.8e-02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 122 GAGGACCCCTGAGCCCC 138  
DB 17 GAAAGACCTTGAGCCAC 1

RESULT 437  
AAS19285/c  
ID AAS19285 standard; DNA; 15 BP.

XX AAS19285;

XX 26-MAR-2002 (first entry)

XX Human ASO PCR primer for detecting GPR3 polymorphisms #8.

XX Human; polymorphism; ss; G protein-coupled receptor; GPR3; haplotype;

XX genotyping; adenylate cyclase related disorder; ASO; PCR primer;

XX allele specific oligonucleotide.

XX Homo sapiens.

XX MO200190128-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US016983.

XX 24-MAY-2000; 2000US-0206857P.

XX (GENA-) GENA1SSANCE PHARM INC.

XX Messer C, Sanchis A, Tanguay DA;

XX WPI; 2002-106170/14.

XX Novel isolated human G protein-coupled receptor 3 polynucleotide, useful  
PT for therapeutic purposes, for studying the expression and function of the  
PT polynucleotide, and for expressing the receptor protein.

XX Claim 16; Page 12; 63pp; English.

XX The invention relates to an isolated human G protein-coupled receptor 3,  
XX (GPR3) polynucleotide comprising a sequence which is a polymorphic  
XX variant for a reference sequence for the GPR3 gene or its fragment, or a  
XX polymorphic variant of a reference sequence for a GPR3 cDNA or its  
XX fragment, and the encoded proteins. Also include are method for  
XX genotyping/haplotyping an individual by determining the sequence of both  
XX copies of the individuals GPR3 genes and examining the sequence at the  
XX polymorphic sites included in the specification, identifying an  
XX association between a trait and at least one haplotype or haplotype pair  
XX of the GPR3 gene involves comparing the frequency of the haplotype or  
XX haplotype pair in a population exhibiting the trait with the frequency of  
XX the haplotype or haplotype pair in a reference population, where the  
XX haplotype is selected from haplotypes 1-5 defined in the specification,  
XX where a higher frequency of the haplotype or haplotype pair in the trait  
XX population than in the reference population indicates that the trait is  
XX associated with the haplotype or haplotype pair. The GPR3 polynucleotide  
XX is useful in studying the expression and function of GPR3, and in  
XX expressing GPR3 protein for use in screening for candidate drugs to treat  
XX diseases related to GPR3 activity. GPR3 is useful for studying expression  
XX of the GPR3 isogenes in vivo, for in vivo screening and testing of drugs  
XX targeted against GPR3 protein, and for testing the efficacy of  
XX therapeutic agents and compounds for disorders related to defects in  
XX adenylate cyclase activation, in a biological system. An anti-GPR3  
XX antibody is useful for studying the effect of the variation on the  
XX biological activity of GPR3 as well as on the binding affinity of  
XX candidate drugs targeting GPR3 for the treatment of disorders related to  
XX defects in adenylate cyclase activation. The present sequence is an ASO



CC (allele specific oligonucleotide) PCR primer for detecting GPR3  
CC polymorphisms  
XX  
SQ Sequence 15 BP; 1 A; 3 C; 7 G; 3 T; 0 U; 1 Other;  
Query Match 0.8%; Score 13.6; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.2e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 727 ACCATGCCGACGAG 740  
Db 14 RCCATGCCGACGAG 1  
RESULT 438  
AEE77703/c  
ID AEE77703 standard; DNA; 20 BP.  
XX  
AC AEE77703;  
XX  
DT 09-FEB-2006 (first entry)  
XX  
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1324.  
XX  
KM Diagnosis: therapeutic; neurological disease; psychiatric disorder;  
KM neuropsychologic disorder; dopamine receptor D2; DRD2; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO2005118843-A1.  
XX  
PD 15-DEC-2005.  
XX  
PF 01-JUN-2005; 2005MO-AUD000775.  
XX  
PR 01-JUN-2004; 2004AU-00902919.  
XX  
PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
DR WPI; 2006-047555/05.  
XX  
XX Identifying genetic profile associated with a neurological, psychiatric,  
PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
PS Claim 31; SEQ ID NO 1324; 634bp; English.  
XX  
XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic or psychological diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1046 TGAAGAGTTTATCCAGCAG 1065  
Db 20 TGAAGAGGCGACGACGAG 1  
RESULT 439  
AAX66607  
ID AAX66607 standard; RNA; 15 BP.  
XX  
AC AAX66607;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
DE Human CD40 hammerhead ribozyme target SEQ ID NO:1239.  
XX  
KM Arthritic condition; graft tolerance; immune response; target; cleavage;  
KM hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KM streptolysin; synovial membrane; joint; arthritis; osteoarthritis;  
KM rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX  
OS Homo sapiens.  
XX  
PN W09618736-A2.  
XX  
PD 20-JUN-1996.  
XX  
PF 22-NOV-1995; 95MO-US015516.  
XX  
PR 13-DEC-1994; 94US-00354920.  
XX  
PR 23-DEC-1994; 94US-00363253.  
XX  
PR 23-DEC-1994; 94US-00363254.  
XX  
PR 17-FEB-1995; 95US-00390850.  
XX  
PR 20-APR-1995; 95US-00426124.  
XX  
PR 02-MAY-1995; 95US-00432874.  
XX  
PR 04-MAY-1995; 95US-00434509.  
XX  
PR 07-JUL-1995; 95US-0000951P.  
XX  
PR 07-AUG-1995; 95US-0000974P.  
XX  
PR 07-AUG-1995; 95US-00512861.  
XX  
PR 05-OCT-1995; 95US-00541365.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Belgelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
PI Mcswiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
PI Karpetsky A, Thompson JD, Modak A, Burgin A;  
XX  
DR WPI; 1996-300653/30.  
XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for  
PT the treatment of arthritis, induction of graft tolerance or treatment of  
PT auto-immune diseases.  
XX  
PS Claim 10; Page 204; 307bp; English.  
XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
CC (iii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
CC can inhibit collagenase and streptolysin production in the synovial  
CC membrane of joints for the treatment or prevention of arthritis,  
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
CC be used to treat antigen presenting cells of a donor to induce tolerance  
CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC streptolysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention

XX Sequence 15 BP; 2 A; 4 C; 2 G; 0 T; 7 U; 0 Other;

SO Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 53.3%; Pred. No. 2.3e+02;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1411 TTCCTCTCCAATG 1425  
:::|:|:|:|:|:|:  
Db 1 UUCUUCUCCAUG 15

RESULT 440

AAK66606  
ID AAK66606 standard; RNA, 15 BP.

XX AAK66606;

XX 20-JUN-1999 (first entry)

XX Human CD40 hammerhead ribozyme target SEQ ID NO:3238.

XX Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW streptomycin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.

XX Homo sapiens.

XX WO9618736-A2.

XX 20-JUN-1996.

XX 22-NOV-1995; 95WO-US015516.

XX 13-DEC-1994; 94US-00354920.

XX 23-DEC-1994; 94US-00363253.

XX 17-FEB-1994; 94US-00363254.

XX 20-APR-1995; 95US-00308850.

XX 02-MAY-1995; 95US-00426124.

XX 04-MAY-1995; 95US-00432874.

XX 07-JUL-1995; 95US-0000951P.

XX 07-JUL-1995; 95US-0000974P.

XX 07-AUG-1995; 95US-00512861.

XX 05-OCT-1995; 95US-00541365.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;

XX Mersinggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;

XX Karpelisky A, Thompson UD, Modak A, Burgin A;

XX WPI; 1996-300653/30.

XX Enzymatic nucleic acid molecules having a hammer-head motif - used for

XX the treatment of arthritis, induction of graft tolerance or treatment of

XX auto-immune diseases.

XX Claim 10; Page 204; 307pp; English.

CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC streptomycin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention

SO Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1409 GCTTCCTCCAATG 1423  
||:|:|:|:|:|:  
Db 1 GCUUCUUCUCCAUG 15

RESULT 441

AAF49867/C  
ID AAF49867 standard; DNA, 15 BP.

XX AAF49867;

XX 30-MAR-2001 (first entry)

XX IGF-I oligonucleotide #827.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cycostatic; dermatological; cardiac; vitreous; ophthalmological; keloid;  
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; psoriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; seboderthosa; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
XX inhibits or reduces growth factor mediated cell proliferation and/or  
XX inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
XX skin disorders. The method comprises contacting the skin with an  
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
XX inhibiting or reducing growth factor mediated cell proliferation,  
XX inflammation and/or other disorders. The present sequence is an  
XX oligonucleotide which can be used to design the antisense  
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-  
XX F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichtyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
 SO

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 GCGGCGAGCGCGCA 23  
 Db 15 GCGGCGAGCGCGCA 1

RESULT 442  
 AAF45173/c  
 ID AAF45173 standard; DNA, 15 BP.  
 XX AAF45173;  
 AC  
 XX 30-MAR-2001 (first entry)  
 DT  
 XX IGFBP2 oligonucleotide #12.  
 DE  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytosaric; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichtyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PI  
 XX Wright CJ, Werther GA, Edmondson SR;  
 DR WPI; 2001-041421/05.  
 XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PT  
 XX Example 6; Page 34; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichtyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 0 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 CC Sequence 15 BP; 6 A; 0 C; 9 G; 0 T; 0 U; 0 Other;  
 SO

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1008 CTTCTCTCTCTGCC 1022  
 Db 15 CTTCTCTCTCTGCC 1

RESULT 443  
 AAF49642/c  
 ID AAF49642 standard; DNA, 15 BP.  
 XX AAF49642;  
 AC  
 XX 30-MAR-2001 (first entry)  
 DT  
 XX IGF-I oligonucleotide #602.  
 DE  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytosaric; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichtyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PI  
 XX Wright CJ, Werther GA, Edmondson SR;  
 DR WPI; 2001-041421/05.  
 XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PT  
 XX Example 8; Page 64; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichtyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1406 TCAGCTTCTCTCCA 1420  
 |||  
 15 TCAGCTTCTCTCCA 1

## RESULT 444

AAF52680/c  
 ID AAF52680 standard; DNA; 15 BP.

AC AAF52680;

DT 30-MAR-2001 (first entry)

DE IGF-1 oligonucleotide #3640.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000WO-AU000693.

PR 21-JUN-1999; 99US-0140345P.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

XX Example 8; Page 84; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

SQ Sequence 15 BP; 0 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1315 CCAGAGACGGCCCC 1329  
 |||  
 15 CCAGAGACGACCCCC 1

## RESULT 445

AAF52481  
 ID AAF52481 standard; DNA; 15 BP.

AC AAF52481;

DT 30-MAR-2001 (first entry)

DE IGF-1 oligonucleotide #3441.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000WO-AU000693.

PR 21-JUN-1999; 99US-0140345P.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

XX Example 8; Page 83; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

SQ Sequence 15 BP; 4 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 719 CCAGAGACCAATGC 733  
 |||  
 1 CCAGAGACCACTGC 15

Db 1 CCAGAGACCACTGC 15

```
RESULT 446
AAF45224/c
ID AAF45224 standard; DNA, 15 BP.
XX
XX
AC AAF45224;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP2 oligonucleotide #63.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; rubra;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, rubra, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
ID AAF45223 standard; DNA, 15 BP.
XX
XX AAF45223;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP2 oligonucleotide #62.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; rubra;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, rubra, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 15 GCGGCGAGCGGCGCA 29
DB 15 GCGGCGAGCGGCGCA 1
15 GCGGCGAGCGGCGCA 1
```

```
RESULT 448
AEB53643
ID AEB53643 standard; DNA, 15 BP.
XX
XX AEB53643;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP2 oligonucleotide #62.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cyostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; rubra;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 6; Page 34; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, rubra, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Levitt RC;  
XX  
XX WPI; 1995-215278/28.  
XX  
XX Kit for automated genotyping contg. pairs of PCR primers - designed to  
PT amplify polymorphic nucleotide repeat sequences, arranged in sets each  
PT with a characteristic fluorescence label, useful e.g. in detection of  
PT disease related genetic rearrangement.  
XX  
PS Disclosure; Fig 7G-2; 104pp; English.  
XX  
XX The method aims to provide a collection of highly reproducible  
CC microsatellite marker sequences (MMS) at approx. 10-50 cM intervals  
CC throughout the human genome which can be detectably labelled. The MMS are  
CC polymorphic, simple sequence repeats and can be used in automated  
CC genotyping. esp. fluorescence-based. The primers correspond to the unique  
CC DNA sequence surrounding each marker, and PCR is used to detect each  
CC polymorphism. When the MMS show considerable polymorphism (ie. a  
CC difference in the number of repeats) between individuals, the markers can  
CC be particularly informative. The MMS can be ideal for linkage studies.  
CC Kits comprise at least 4 groups, of at least 3 sets, each comprising  
CC labelled primers for PCR amplification of the DNA. Group 7 primer pairs  
CC are shown in AAg95687-734. The published size range of the D18S66 allele  
CC is 244-262 bp, and the degree of heterozygosity in the population is  
CC about 86%  
XX  
XX Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 922 GAGCAAGTCTCTGCC 936  
DB 2 GAGCAAGTCTCTGCC 16  
XX  
XX RESULT 451  
ADCC84377/c  
ID ADCC84377 standard; DNA; 16 BP.  
XX  
XX ADCC84377;  
XX  
XX 01-JAN-2004 (first entry)  
XX  
XX Human papillomavirus type MM7 detection oligonucleotide #11.  
XX  
XX probe; human papilloma virus; HPV; detection; identification; ss.  
XX  
XX Human papillomavirus.  
XX  
XX EP1302550-A1.  
XX  
XX 16-APR-2003.  
XX  
XX 10-OCT-2001; 2001EP-00123379.  
XX  
XX 10-OCT-2001; 2001EP-00123379.  
XX  
XX (KING-) KING CAR FOOD IND CO LTD.  
XX  
XX Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Fan C,  
PI Hsu H, Shih C, Yeh C, Kao Y, Pan C, Chan P;  
XX  
XX WPI; 2003-432396/41.  
XX  
XX Detector for identifying human papilloma virus subtypes, comprises  
PT carrier having two parts carrying first and second oligonucleotides that  
PT respectively hybridize with DNA contained in first and second subtypes of  
PT the virus.  
XX

PS Claim 4; SEQ ID NO 607; 221pp; English.  
XX  
XX The invention comprises oligonucleotides for detecting and identifying  
CC subtypes of human papilloma virus (HPV) contained in a sample. The  
CC oligonucleotides of the invention are useful for simultaneously detecting  
CC and identifying subtypes of HPVs. The present DNA sequence represents an  
CC HPV detection oligonucleotide of the invention.  
XX  
XX Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 601 TACATGGCCATCATA 615  
DB 16 TACATGGCCATCATA 2  
XX  
XX RESULT 452  
ADF44279/c  
ID ADF44279 standard; DNA; 16 BP.  
XX  
XX ADF44279;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX HPV MM7 detecting probe MM711.  
XX  
XX detection; human papillomavirus; HPV subtype; probe; ss.  
XX  
XX Human papillomavirus.  
XX  
XX JP2002360271-A.  
XX  
XX 17-DEC-2002.  
XX  
XX 28-NOV-2001; 2001JP-00362595.  
XX  
XX 04-MAY-2001; 2001TW-00110785.  
XX  
XX (KING-) KING CAR FOOD IND CO LTD.  
XX  
XX WPI; 2003-600935/57.  
XX  
XX A detecting apparatus and a detecting method for identifying the subtypes  
PT of many species of human papilloma viruses at the same time and a  
PT composition for the detection.  
XX  
XX Claim 1; SEQ ID NO 636; 166pp; Japanese.  
XX  
XX This invention describes a novel detecting apparatus for identifying the  
CC subtypes of human papillomaviruses (HPV) contained in a sample which  
CC comprises a carrier which can load sample, a first oligonucleotide loaded  
CC on first part of the carrier and a second oligonucleotide loaded on  
CC second part of carrier, in which first and second oligonucleotides  
CC hybridize with the DNA of the first and the second HPV subtype and can  
CC identify HPV subtype contained in sample at the same time. ADF43644-  
CC ADF44289 represent oligonucleotide probes used in the method of the  
CC invention.  
XX  
XX Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 601 TACATGGCCATCATA 615  
DB 16 TACATGGCCATCATA 2  
XX  
XX RESULT 453

```

ADU76209
ID ADU76209 standard; DNA; 16 BP.
XX
XX ADU76209;
AC
XX 10-FEB-2005 (first entry)
XX
XX V segment TCR beta primer SEQ ID NO 225.
XX
XX DE
XX ss; primer; genetic marker; neoplasia; cytostatic; leukemia.
XX
XX Synthetic.
XX
XX WO2004101815-A1.
XX
XX 25-NOV-2004.
XX
XX 13-MAY-2004; 2004WO-AU000625.
XX
XX 13-MAY-2003; 2003AU-00902299.
XX
XX (MONO-) MONOQUANT PTY LTD.
XX
XX Morley AA, Brisco M, Sykes P;
XX
XX WPI; 2004-821897/81.
XX
XX Analyzing a marker nucleic acid region of a clonal population of cells
XX that is flanked on one or both sides by members of distinct repeated
XX sequences by identifying nucleic acid sequence regions flanking the
XX marker nucleic acid region.
XX
XX Example 3; SEQ ID NO 225; 99pp; English.
XX
XX The invention relates to a method of analyzing a marker nucleic acid
XX region of a clonal population of cells that is flanked on one or both
XX sides by members of a family of distinct repeated sequences comprises
XX identifying one or more of the nucleic acid sequence regions flanking the
XX marker nucleic acid region. The method is useful in diagnosing and/or
XX monitoring a mammalian disease condition, the condition is a neoplastic
XX condition, e.g. malignant or non-malignant neoplastic condition. The
XX condition is an immunodeficiency and the screening is directed to
XX detecting specific immune cell expansion. The condition is an immune
XX response and the screening is directed to detecting specific immune cell
XX expansion. The method is useful for analyzing a marker nucleic acid
XX region of a clonal population of cells that is flanked on one or both
XX sides by members of distinct repeated sequences. The present sequence
XX represents a V segment TCR beta primer.
XX
XX Sequence 16 BP; 4 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 2.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1324 GGGCCCAAGGCCCA 1338
XX |||||
XX 2 GGCTCCAAGGCCCA 16
XX
XX RESULT 454
XX ABB56195/c
XX ID ABB56195 standard; DNA; 16 BP.
XX
XX ABB56195;
XX
XX 20-OCT-2005 (first entry)
XX
XX HPV MM7 probe SEQ ID NO 419.
XX
XX human papilloma virus; probe; ss; diagnosis; DNA microarray; biochip.
XX
XX Human papillomavirus.
XX

```

```

XX
XX US2005175989-A1.
XX
XX 11-AUG-2005.
XX
XX 23-JUN-2003; 2003US-00601497.
XX
XX 20-JUN-2001; 2001US-00885799.
XX
XX (LINC/) LIN C.
XX (LINR/) LIN R.
XX (YOUNC/) YOU C.
XX (YANC/) YAN C.
XX (LEEB/) LEE B.
XX (LEEH/) LEE H.
XX (LINY/) LIN Y.
XX (PANC/) PAN C.
XX (HSUH/) HSU H.
XX (SHIH/) SHIH C.
XX (YEH/) YEH C.
XX (KAOY/) KAO Y.
XX (PANC/) PAN C.
XX (CHAN/) CHAN P.
XX
XX Lin C, Lin R, You C, Yan C, Lee B, Lee H, Lin Y, Fan C, Hsu H;
XX Shih C, Yeh C, Kao Y, Pan C, Chan P;
XX
XX WPI; 2005-553735/56.
XX
XX Detector for detecting and simultaneously diagnosing subtype of human
XX papilloma viruses (HPV) e.g. HPV 6, HPV 11 or HPV 16, has carrier,
XX several micro-dots immobilized on carrier and oligonucleotide sequences
XX contained in each micro-dot.
XX
XX Claim 15; SEQ ID NO 419; 105pp; English.
XX
XX The invention relates to a detector (I) for detecting and simultaneously
XX diagnosing one or more subtypes of human papilloma viruses (HPV)
XX contained in a biological sample. (I) is useful for detecting and
XX simultaneously diagnosing one or more subtypes of HPV contained in a
XX biological sample. (I) enables rapid and reliable detection of HPV
XX subtype in a biological sample. The present sequence represents a human
XX papilloma virus subtype probe.
XX
XX Sequence 16 BP; 3 A; 2 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 2.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 601 TACATGGCCATCATTA 615
XX |||||
XX 16 TACAAGGCCATCATTA 2
XX
XX RESULT 455
XX ABF73244/c
XX ID ABF73244 standard; DNA; 13 BP.
XX
XX ABF73244;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 173241 for detecting SNP TSC0043153.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX

```



PD 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 173241; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1603 ATTCTCCCTATC 1615  
Db 13 ATTCTCCCTATC 1  
RESULT 456  
ABH37834/C  
ID ABH37834 standard; DNA; 13 BP.  
XX  
XX ABH37834;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 237811 for detecting SNP TSC0058003.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT

PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 237811; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1593 AAAATCTCAATT 1605  
Db 13 AAAATCTCAATT 1  
RESULT 457  
ABC89691  
ID ABC89691 standard; DNA; 13 BP.  
XX  
XX ABC89691;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 89708 for detecting SNP TSC0022491.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 89708; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1592 AAAAAATCTCAAT 1604  
1 AAAAAATCTCAAT 13

RESULT 458  
ABH06065  
ID ABH06065 standard; DNA; 13 BP.

AC ABH06065;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 206042 for detecting SNP TSC0007438.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPig-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 206042; 29pp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1591 CAAAAATCTCAA 1603  
1 CAAAAATCTCAA 13

Db 1 CAAAAATCTCAA 13

RESULT 459

ABF59772  
ID ABF59772 standard; DNA; 13 BP.

AC ABF59772;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 159769 for detecting SNP TSC0040218.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPig-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 159769; 29pp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 781 ATTATGAGAAAG 793  
1 ATTATGAGAAAG 13

RESULT 460

ABF29162/c  
ID ABF29162 standard; DNA; 13 BP.

AC ABF29162;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 129159 for detecting SNP TSC0032336.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX OS  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 129159; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 608 CCATCATATCATCC 620  
Db 13 CCATCATATCATCC 1  
RESULT 461  
ABC98834/C  
ID ABC98834 standard; DNA; 13 BP.  
XX  
XX ABC98834;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 98851 for detecting SNP TSC0024561.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.

XX  
XX (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 98852; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1639 CTCACCAACCAATC 1651  
Db 13 CTCACCAACCAATC 1  
RESULT 462  
ABC98835  
ID ABC98835 standard; DNA; 13 BP.  
XX  
XX ABC98835;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 98852 for detecting SNP TSC0024561.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 98852; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

CC XX Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

SO Query Match 0.7%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTAAACCAATC 1651  
Db 1 CTTAAACCAATC 13

RESULT 463  
ABC77569  
ID ABC77569 standard; DNA; 13 BP.  
XX ABC77569;  
AC  
XX  
XX 21-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 77586 for detecting SNP TSC0019760.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 77586; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

QY 247 CCNAACATCTCCA 259  
Db 1 CCNAACATCTCCA 13

RESULT 464  
ABF98357/C  
ID ABF98357 standard; DNA; 13 BP.  
XX ABF98357;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 198354 for detecting SNP TSC0004656.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is PT designed to detect single-nucleotide polymorphisms and cytosine PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 198354; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) CC and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. ABC00010 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC represent the oligomers described in the invention. NOTE: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

CC XX Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;

SO Query Match 0.7%; Score 13; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 GATTTATGAGAA 792  
Db 13 GATTTATGAGAA 1

RESULT 465  
ABC89690/C

ID ABC89690 standard; DNA; 13 BP.  
XX  
AC ABC89690;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 89707 for detecting SNP TSC0022491.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 89707; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP). The  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1592 AAAAATCTCAAT 1604  
DB 13 AAAAATCTCAAT 1  
XX  
RESULT 466  
ABC77568/c  
ID ABC77568 standard; DNA; 13 BP.  
XX  
AC ABC77568;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 77585 for detecting SNP TSC0019760.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX

XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 77585; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP). The  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 247 CCAACATCTCCA 259  
DB 13 CCAACATCTCCA 1  
XX  
RESULT 467  
ABC10989/c  
ID ABC10989 standard; DNA; 13 BP.  
XX  
AC ABC10989;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 10980 for detecting SNP TSC0002720.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX

DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 10980; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 3 C; 1 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;  
XX  
QY 38 AGAAGCGTTTATA 50  
Db 13 AGAAGCGTTTATA 1  
XX  
RESULT 468  
ABH06064/C  
ID ABH06064 standard; DNA; 13 BP.  
XX  
AC ABH06064;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 206041 for detecting SNP TSC0007438.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 206041; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;  
XX  
QY 1591 CAAAAATCTCAA 1603  
Db 13 CAAAAATCTCAA 1  
XX  
RESULT 469  
ABF99773/C  
ID ABF99773 standard; DNA; 13 BP.  
XX  
AC ABF99773;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 159770 for detecting SNP TSC0040218.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 159770; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

QY 781 ATTATGGAAG 793  
DB 13 ATTATGGAAG 1  
RESULT 470  
ABH37835  
ID ABH37835 standard; DNA, 13 BP.  
AC ABH37835;  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
DE Oligonucleotide SEQ ID NO 237812 for detecting SNP TSC0058003.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 237812; 29bp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABR9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1593 AAAATCTCAATT 1605  
DB 1 AAAATCTCAATT 13  
RESULT 471  
ABC4325  
ID ABC4325 standard; DNA, 13 BP.  
AC ABC4325;  
XX  
XX 20-FEB-2002 (first entry)  
DT

XX  
DE Oligonucleotide SEQ ID NO 34342 for detecting SNP TSC0010966.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 34342; 29bp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABR9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1594 AAAATCTCAATTC 1606  
DB 1 AAAATCTCAATTC 13  
RESULT 472  
ABC10988  
ID ABC10988 standard; DNA, 13 BP.  
AC ABC10988;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
XX  
DE Oligonucleotide SEQ ID NO 10979 for detecting SNP TSC0002720.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX

PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPiG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 10979; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 5 A; 1 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 38 AGAAGCGTTTATA 50  
Db 1 AGAAGCGTTTATA 13  
XX  
XX RESULT 473  
XX ABF29163  
XX ID ABF29163 standard; DNA; 13 BP.  
XX  
XX ABF29163;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 129160 for detecting SNP TSC0032336.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPiG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX  
XX Claim 1; SEQ ID NO 129160; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 608 CCATCATACATCC 620  
Db 1 CCATCATACATCC 13  
XX  
XX RESULT 474  
XX ABF98356  
XX ID ABF98356 standard; DNA; 13 BP.  
XX  
XX ABF98356;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 198353 for detecting SNP TSC0004656.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPiG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 198353; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but



CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 780 GATTATGAGAAA 792  
 DB 1 GATTATGAGAAA 13  
 RESULT 475  
 ABC34324/c  
 XX ABC34324 standard; DNA; 13 BP.  
 AC ABC34324;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 34341 for detecting SNP TSC0010966.  
 XX  
 XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 34341; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1594 AAAATCTCAATTC 1606  
 DB 13 AAAATCTCAATTC 1

RESULT 476  
 ABF73245  
 ID ABF73245 standard; DNA; 13 BP.  
 XX  
 AC ABF73245;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 173242 for detecting SNP TSC0043153.  
 XX  
 XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 173242; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1603 ATTCTTCCTATC 1615  
 DB 1 ATTCTTCCTATC 13  
 RESULT 477  
 AAT33386  
 ID AAT33386 standard; cDNA; 15 BP.  
 XX  
 AC AAT33386;  
 XX  
 DT 16-MAY-1997 (first entry)  
 XX  
 DE Human vascular endothelial growth factor antisense oligonucleotide.  
 XX  
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;  
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;

KW degeneration; expression inhibitor; ss.  
 XX Synthetic.  
 OS  
 XX WO627006-A2.  
 PN  
 XX  
 PD 06-SEP-1996.  
 XX  
 XX 29-FEB-1996; 96WO-US002840.  
 PF  
 XX 02-MAR-1995; 95US-00398945.  
 PR  
 PR 08-DEC-1995; 95US-00569926.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 XX Robinson GS;  
 PT WPI; 1996-412773/41.  
 DR  
 XX Human vascular endothelial growth factor anti:sense oligo:nucleotide -  
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced  
 PT neovascularisation and angiogenesis associated disease states.  
 PT  
 PS Claim 17; Page 51; 92pp; English.  
 XX  
 XX AAT3371-T33431 are antisense oligonucleotides used to inhibit the  
 CC expression of human vascular endothelial growth factor (VEGF). The  
 CC synthetic oligonucleotides contain phosphorothioate linkages and  
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the  
 CC expression of VEGF is useful in the treatment of hypoxia induced  
 CC neovascularisation and angiogenesis associated disease states.  
 CC retinopathy of prematurity, diabetic retinopathy and age related macular  
 CC degeneration  
 CC  
 SQ Sequence 15 BP; 0 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1011 CTTCTCTCTGCCC 1023  
 Db 1 CTTCTCTCTGCCC 13  
 RESULT 478  
 AAT48401  
 ID AAT48401 standard; DNA; 15 BP.  
 XX  
 AC AAT48401;  
 XX  
 DT 11-MAR-1997 (first entry)  
 XX  
 DE Oligonucleotide H-8A specific for human VEGF nucleic acid.  
 XX  
 XX Vascular endothelial growth factor; inhibition; decrease; antisense;  
 KW neovascularisation; retinopathy; age-related macular degeneration;  
 KW diabetes; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9623065-A2.  
 PN  
 XX 01-AUG-1996.  
 PD  
 XX 26-JAN-1996; 96WO-US001189.  
 PF  
 XX 26-JAN-1995; 95US-00378860.  
 PR  
 XX (HYBR-) HYBRIDON INC.  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX Robinson GS, Smith LEH;  
 PI

XX  
 DR WPI; 1996-362689/36.  
 XX  
 XX Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -  
 PT for treatment of retinopathies and age-related macular degeneration.  
 PT  
 XX Disclosure; Page 12; 66pp; English.  
 PS  
 XX Neovascularisation can be reduced by blocking vascular endothelial growth  
 CC factor (VEGF) expression using a synthetic oligonucleotide specific for  
 CC VEGF. Inhibiting neovascularisation is useful for treatment of  
 CC retinopathy of prematurity, diabetic retinopathy and age-related macular  
 CC degeneration. The present sequence is an example of a suitable  
 CC oligonucleotide specific for human VEGF  
 CC  
 SQ Sequence 15 BP; 0 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1011 CTTCTCTCTGCCC 1023  
 Db 1 CTTCTCTCTGCCC 13  
 RESULT 479  
 AAX33621/C  
 ID AAX33621 standard; DNA; 15 BP.  
 XX  
 AC AAX33621;  
 XX  
 DT 25-JUN-1999 (first entry)  
 XX  
 DE Thrombin inhibitor SEQ ID NO. 9.  
 XX  
 XX Thrombin inhibitor; molecular design; exon shuffling; DNA library;  
 KW function improvement; high functional fit evolution; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9911818-A1.  
 PN  
 XX 11-MAR-1999.  
 PD  
 XX 28-AUG-1998; 98WO-JP003854.  
 PF  
 XX 28-AUG-1997; 97JP-00249679.  
 PR  
 XX (KARU/) KARUBE I.  
 PA  
 XX Karube I, Okabe Y, Sumikura K;  
 PI  
 DR WPI; 1999-228983/19.  
 XX  
 PT Molecular design by exon shuffling within a library of DNA sequences.  
 XX  
 PS Example 2; Page 15; 42pp; Japanese.  
 XX  
 XX This sequence represents a thrombin inhibitor that was used in an example  
 CC of the process of the invention. The process is for molecular design, and  
 CC is carried out by shuffling exons within a library of similar DNA  
 CC sequences, followed by ranking of the products of reshuffling by their  
 CC fit to the desired functionality, and repeating the shuffling and ranking  
 CC until a product of the desired functionality is obtained. A similar  
 CC process may be carried out using polypeptide sequences. The technique can  
 CC be used for the improvement of function, and devising of new functions,  
 CC of polypeptides and nucleic acids, for a broad range of uses such as  
 CC drugs and foodstuffs. Evolution of high functional fit is rapid compared  
 CC to the use of conventional genetic evolution algorithms  
 CC  
 SQ Sequence 15 BP; 3 A; 1 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1014 CCTCCTGCCCCAC 1026  
 |||||  
 DB 14 CCTCCTGCCCCAC 2

RESULT 480  
 ID ABRK5500/c  
 XX ABRK5500 standard; DNA; 15 BP.  
 AC ABRK5500;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #36.  
 XX  
 KM Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;  
 KM neonatal pertussis; whooping cough; haplotyping; primer;  
 KM allele-specific oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216654-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 27-AUG-2001; 2001WO-US026675.  
 XX  
 PR 25-AUG-2000; 2000US-0228262P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 PI Anastasio AB, Bieglecki KM, Klieem SE, Koshy B, Kumar AM;  
 XX WPI; 2002-292071/33.  
 DR  
 PT Novel genetic variants of selectin L lymphocyte adhesion molecule 1  
 PT (SELL) gene useful for therapeutic purposes and for expressing SELL  
 PT protein useful in identifying drugs to treat whooping cough.  
 XX  
 XX Claim 17; Page 14; 137pp; English.

The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence which is a polymorphic variant of a reference  
 CC sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL  
 CC polypeptide is useful for screening for drugs targeting the polypeptide.  
 CC Oligonucleotides derived from (I) are used to target SELL and a haplotype  
 CC or haplotype pair of SELL gene. These are useful in developing diagnostic  
 CC tests and therapeutic treatments for neonatal pertussis (whooping cough).  
 CC (1) is useful for studying the expression and function of SELL and  
 CC expressing SELL protein for use in screening for candidate drugs to treat  
 CC diseases related to SELL activity. The polymorphism and haplotype data  
 CC are useful for validating whether SELL is a suitable target for drugs to  
 CC treat whooping cough, screening for such drugs and reducing bias in  
 CC clinical trials of such drugs. Establishing the SELL haplotype or  
 CC haplotype pair of an individual is useful for improving the efficiency  
 CC and reliability of several steps in the discovery and development of  
 CC drugs for treating diseases associated with SELL activity e.g. neonatal  
 CC pertussis (whooping cough). The haplotyping method is useful to validate  
 CC SELL as a candidate target for treating a specific condition or disease  
 CC predicted to be associated with SELL activity. The method is also useful  
 CC in screening for compounds targeting SELL to treat a specific condition  
 CC or disease predicted to be associated with SELL activity, e.g. detecting  
 CC which of the SELL haplotypes or haplotype pairs present in individual  
 CC members of a population with the specific disease of interest enables one  
 CC to screen for compounds that display the highest desired agonist or  
 CC antagonist activity for each of the most frequent SELL isoforms present  
 CC in the disease population. A polymorphic variant of SELL is useful in  
 CC studying the effect of the variation on the biological activity of SELL,  
 CC on the binding affinity of candidate drugs targeting SELL for the

CC treatment of neonatal pertussis (whooping cough) and in assays to measure  
 CC the binding affinities of one or more candidate drugs targeting the SELL  
 CC protein. ABRK5465-ABRK5559 represent SELL gene allele-specific  
 CC oligonucleotides of the invention  
 XX  
 S0 Sequence 15 BP; 3 A; 1 C; 8 G; 2 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1278 CACCATCTCCCACT 1292  
 ||:|||||  
 DB 15 CCCCATCTCCCACT 1

RESULT 481  
 ID ABRK95827  
 XX ABRK95827 standard; DNA; 15 BP.  
 AC ABRK95827;  
 XX  
 DT 24-SEP-2002 (first entry)  
 XX  
 DE Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #67.  
 XX  
 KM Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;  
 KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;  
 KM amino acid transporter disorder; single nucleotide polymorphism; SNP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200244198-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 29-NOV-2001; 2001WO-US044781.  
 XX  
 PR 30-NOV-2000; 2000US-0250254P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;  
 XX WPI; 2002-519580/55.  
 DR  
 PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral  
 PT Amino Acid Transporter), Member 4 isoforms, for improving efficiency and  
 PT reliability in drug development for treating cancers.  
 XX  
 XX Claim 15; Page 16; 139pp; English.

The invention relates to an isolated polynucleotide (I) comprising a  
 CC first nucleotide sequence which comprises solute carrier family 1  
 CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isoforms  
 CC (II) and an isolated polypeptide (III) comprising an amino acid sequence  
 CC which is a polymorphic variant of a reference sequence for SLC1A4  
 CC protein. Also described are methods for: (1) haplotyping or genotyping  
 CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4  
 CC gene of an individual; (3) identifying an association between a trait and  
 CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful  
 CC in screening for drugs targeting (III) that are useful for treating  
 CC cancer, neurological diseases and amino acid transporter disorders. The  
 CC methods are useful for improving the efficiency and reliability of  
 CC several steps in the discovery and development of drugs for treating  
 CC diseases associated with SLC1A4 activity. The haplotyping method is also  
 CC used by the pharmaceutical research scientist to validate SLC1A4 as a  
 CC candidate target for treating a specific condition or disease predicted  
 CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases  
 CC and amino acid transporter disorders, and in the design of clinical  
 CC trials for treating a specific condition of disease associated with  
 CC SLC1A4 activity. The methods are also useful for screening compounds  
 CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic.

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4  
 CC gene allele-specific oligonucleotides, primer extension oligonucleotides  
 CC and related PCR primers used to identify single nucleotide polymorphisms  
 CC (SNP) of the gene

XX Sequence 15 BP; 0 A; 7 C; 2 G; 5 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 1; Mismatches 0; Gaps 0;

YY 686 TCCTGCTGCGCTTC 700  
 1 TCCTGCTGCGCTTC 15

# RESULT 482

ABK95804  
 ID ABK95804 standard; DNA; 15 BP.

AC ABK95804;

DT 24-SEP-2002 (first entry)

DE Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #44.

XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;  
 KM glutamate/neutral amino acid transporter; neurological disease; PCR; ss;  
 KM amino acid transporter disorder; single nucleotide polymorphism; SNP.

OS Homo sapiens.

PN WO200244198-A2.

PD 06-JUN-2002.

PF 29-NOV-2001; 2001WO-US044781.

PR 30-NOV-2000; 2000US-0250254P.

XX (GENA-) GENAISSANCE PHARM INC.

PA Bieglecki KM, Kazemi A, Russo DP, Sauker EA;

PI Bieglecki KM, Kazemi A, Russo DP, Sauker EA;

DR WPI; 2002-519580/55.

XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral

PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency and

PT reliability in drug development for treating cancers.

XX Claim 15; Page 15; 139pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising a

CC first nucleotide sequence which comprises solute carrier family 1

CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (I) and an isolated polypeptide (II) comprising an amino acid sequence

CC which is a polymorphic variant of a reference sequence for SLC1A4

CC protein. Also described are methods for: (1) haplotyping or genotyping

CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4

CC gene of an individual; (3) identifying an association between a trait and

CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful

CC in screening for drugs targeting (III) that are useful for treating

CC cancer, neurological diseases and amino acid transporter disorders. The

CC methods are useful for improving the efficiency and reliability of

CC several steps in the discovery and development of drugs for treating

CC diseases associated with SLC1A4 activity. The haplotyping method is also

CC used by the pharmaceutical research scientist to validate SLC1A4 as a

CC candidate target for treating a specific condition or disease predicted

CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases

CC and amino acid transporter disorders, and in the design of clinical

CC trials for treating a specific condition of disease associated with

CC SLC1A4 activity. The methods are also useful for screening compounds

CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4  
 CC gene allele-specific oligonucleotides, primer extension oligonucleotides  
 CC and related PCR primers used to identify single nucleotide polymorphisms  
 CC (SNP) of the gene

XX Sequence 15 BP; 1 A; 7 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 0.7%; Score 13; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

YY 428 ACCTGACCTTCGCG 442  
 1 ACCTGACCTTCGCG 15

# RESULT 483

ABK16925  
 ID ABK16925 standard; DNA; 15 BP.

AC ABK16925;

DT 26-MAR-2002 (first entry)

DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) probe #5.

XX Pyridoxal kinase; pyridoxine; vitamin B6;

KM PDXK autoimmune polyglandular disease type 1; transgenic animal;

KM gene therapy; allele specific oligonucleotide; ASO; probe; ss.

OS Homo sapiens.

PN WO200190125-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016909.

PR 24-MAY-2000; 2000US-0206664P.

XX (GENA-) GENAISSANCE PHARM INC.

PA Chew A, Duda A, Koshy B;

PI WPI; 2002-106169/14.

XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polynTs, useful

PT for therapeutic purposes, for studying the expression and function of the

PT polynT, and for expressing pyridoxal protein.

XX Claim 17; Page 13; 135pp; English.

XX The invention describes an isolated human pyridoxal (pyridoxine, vitamin

CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in

CC studying the expression and function of PDXK, and in expressing PDXK

CC protein for use in screening for candidate drugs to treat PDXK related

CC diseases and for therapeutic purposes. A transgenic animal is useful for

CC studying expression of the PDXK isogenes in vivo, for in vivo screening the

CC efficacy of therapeutic agents and compounds for autoimmune polyglandular

CC disease type 1. The polypeptide is useful for studying the effect of the

CC variation on the biological activity of PDXK and the binding affinity of the

CC candidate drugs targeting PDXK for the treatment of autoimmune

CC polyglandular disease type 1. Genotyping and haplotyping is useful for

CC improving the efficacy and reliability of several steps in the discovery

CC and development of drugs for treating diseases associated with PDXK

CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK

CC as a candidate agent for treating a specific condition or disease

CC predicted to be associated with PDXK activity, and in the design of

CC clinical trials of candidate drugs. This sequence is one of 20 (see

CC ABK16921-ABK16940) allele specific oligonucleotide (ASO) probe used for

CC detecting PDXK gene polymorphisms, described in the method of the

CC invention

XX  
SQ Sequence 15 BP; 0 A; 7 C; 1 G; 6 T; 0 U; 1 Other;  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 106 CCTCTGCTGCTTT 120  
DB 1 CCTCTGCTGCTTT 15  
RESULT 484  
ABN80579  
ID ABN80579 standard; DNA, 15 BP.  
AC ABN80579;  
XX  
XX 19-JUL-2002 (first entry)  
XX  
DE Human P450(cytochrome) oxidoreductase allele specific PCR primer #19.  
XX  
XX Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;  
XX single nucleotide polymorphism; flavoprotein; enzyme; PCR; primer; ss.  
XX Homo sapiens.  
XX MO200226768-A2.  
XX PN  
XX PD  
XX 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001MO-US030877.  
XX PF  
XX 29-SEP-2000; 2000US-0236449P.  
XX PR  
XX (GENA-) GENAISSANCE PHARM INC.  
XX PA  
XX Kazemi A, Kliehm SE, Lanz EM, Messer C, Tanguay DA,  
XX WPI; 2002-394236/42.  
XX DR  
XX  
XX New genetic variants comprising haplotypes of the P450 (cytochrome)  
XX PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug  
XX PT screening protocols for compounds targeting POR.  
XX  
XX  
XX Claim 14; Page 14; 141pp; English.  
XX PS  
XX The present invention provides the protein, gene and cDNA sequences of  
XX CC human P450(cytochrome) oxidoreductase POR, and single nucleotide  
XX CC polymorphisms (SNPs) identified therein. The sequences can be used to  
XX CC haplotype the POR gene of an individual, and to establish whether POR is  
XX CC a suitable target for drugs to treat cancer and disorders associated with  
XX CC impaired protein synthesis in cells. The present sequence is an allele  
XX CC specific primer for the coding sequences of the invention  
XX  
XX Sequence 15 BP; 5 A; 3 C; 5 G; 1 T; 0 U; 1 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 30 GTGCATCCAGAGCG 44  
DB 1 GTGCATCCAGAGSG 15  
RESULT 485  
ABK92616/C  
ID ABK92616 standard; DNA, 15 BP.  
XX  
XX ABK92616;  
XX  
XX 20-AUG-2002 (first entry)  
DT

XX  
DE ASO primer #14 to detect human ADORA3 gene polymorphisms.  
XX  
XX Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;  
XX KW chromosome 1p21-p13; adenosine A3 receptor; genotyping;  
XX KW pathophysiological heart condition; myocardial ischaemia;  
XX KW chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX MO200236610-A2.  
XX PN  
XX 10-MAY-2002.  
XX PD  
XX 31-OCT-2001; 2001MO-US045718.  
XX PF  
XX 31-OCT-2000; 2000US-0244626P.  
XX PR  
XX (GENA-) GENAISSANCE PHARM INC.  
XX PA  
XX Gilson CR, Kazemi A, Koshy B, Monroe G,  
XX WPI; 2002-489998/52.  
XX DR  
XX  
XX Novel genetic variants of the adenosine A3 receptor, useful  
XX PT therapeutically and in screening for drugs to treat diseases related to  
XX PT ADORA3 activity e.g., myocardial ischemia and chronic heart failure.  
XX  
XX Claim 15; Page 14; 82pp; English.  
XX PS  
XX The present invention relates to novel single nucleotide polymorphisms  
XX CC (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on  
XX CC chromosome 1p21-p13, and methods for haplotyping and/or genotyping the  
XX CC ADORA3 gene. The methods of the invention make use of allele-specific  
XX CC oligonucleotides (ASOs) as probes and primers and/or primer-extension  
XX CC oligonucleotides for detecting the ADORA3 gene polymorphisms. The  
XX CC polymorphisms and screened compounds are useful for the treatment of  
XX CC diseases associated with ADORA3 activity, such as pathophysiological  
XX CC conditions of the heart e.g. myocardial ischaemia and chronic heart  
XX CC failure. ABK92603-ABK92628 represent ASO primers for detecting human  
XX CC ADORA3 gene polymorphisms  
XX  
XX Sequence 15 BP; 2 A; 7 C; 1 G; 4 T; 0 U; 1 Other;  
SQ  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1205 AGGGCTGGAATGA 1219  
DB 15 AGGGCTGGAAGTGA 1  
RESULT 486  
ABL52021/C  
ID ABL52021 standard; DNA, 15 BP.  
XX  
XX ABL52021;  
XX  
XX 11-JUL-2002 (first entry)  
XX  
XX Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:69.  
XX DE  
XX Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;  
XX KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;  
XX KW single nucleotide polymorphism; antiinflammatory; neuroleptic;  
XX KW haplotyping; genotyping; respiratory inflammatory disease;  
XX KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX Key Location/Qualifiers  
XX FH misc\_feature 14  
XX FT



XX 05-APR-2000; 2000US-0194362P.  
PR (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;  
PI WPI; 2002-041281/05.  
XX  
XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose  
PT and treat disorders associated with its abnormal expression or function  
XX such as coronary artery disease.  
XX  
PS Claim 16; Page 15; 71pp; English.  
XX  
XX The invention relates to haplotyping the human apolipoprotein A-IV  
CC (APOA4) gene of an individual, comprising determining if the individual  
CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the  
CC specification. Also disclosed are genotyping oligonucleotides (or allele  
CC specific oligonucleotides, ASO) as well as methods for correlating a  
CC particular haplotype pair with a trait e.g. obesity, in a population. The  
CC APOA4 gene is located on chromosome 11q23-qter. The methods of the  
CC invention are useful to diagnose and develop treatment for disorders  
CC associated with abnormal APOA4 expression or function, for example  
CC coronary heart disease and atherosclerosis. The APOA4 isogenes and  
CC screened compounds are useful for the treatment of disorders associated  
CC with abnormal APOA4 expression or function such as coronary artery  
CC disease. The present sequence is an APOA4 allele specific  
CC oligonucleotide, ASO, probe used to detect an APOA4 polymorphism  
XX  
SQ Sequence 15 BP; 4 A; 3 C; 6 G; 1 T; 0 U; 1 Other;  
  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 828 CCTCCCTGCTGCT 842  
Db 15 CCTCCCTGCTGCT 1  
  
RESULT 489  
ABK81517/c  
ID ABK81517 standard; DNA; 15 BP.  
XX  
AC ABK81517;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Human CASP5 gene allele-specific oligonucleotide sequencing primer #38.  
XX  
KW Human; caspase 5; apoptosis-related cysteine protease; CASP5; primer; ss;  
KW haplotyping; haplotype pair; cancer; single nucleotide polymorphism;  
KW hereditary nonpolyposis colorectal cancer; gastrointestinal tumour;  
KW endometrial tumour; chromosome 11q22.2-q22.3; sequencing.  
XX  
OS Homo sapiens.  
XX  
PN WO200226769-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 01-OCT-2001; 2001WO-US030878.  
XX  
PR 29-SEP-2000; 2000US-0236568P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kliem SE, Russo DP;  
XX  
XX WPI; 2002-435191/46.  
XX  
PT Novel caspase 5 apoptosis-related cysteine protease, useful

PT therapeutically and in screening for drugs targeting protease  
PT polypeptide.  
XX  
XX Claim 14; Page 15; 115pp; English.  
XX  
XX The invention relates to single nucleotide polymorphisms in the gene  
CC encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)  
CC polypeptide. A method for haplotyping the CASP5 gene in an individual  
CC comprises identifying the nucleotide at one or more polymorphic sites and  
CC determining whether one of the copies of the gene is defined by one of  
CC the CASP5 haplotypes given in the specification or whether both copies  
CC are defined by a haplotype pair. This method is useful in genotyping,  
CC whereby all possible haplotype pairs can be assigned to specific  
CC genotypes. An association between a trait and a haplotype or haplotype  
CC pair of the CASP5 gene can be identified by comparing the frequency of  
CC the haplotype or haplotype pair in a population exhibiting the trait with  
CC the frequency of the haplotype or haplotype pair in a reference  
CC population, where a higher haplotype frequency in the trait population  
CC indicates the trait is associated with the haplotype or haplotype pair.  
CC CASP5 and its corresponding DNA are used for studying the expression and  
CC function of CASP5, for use in screening for candidate drugs to treat  
CC diseases related to CASP5 activity, such as cancer (e.g. hereditary  
CC nonpolyposis colorectal cancer, gastrointestinal tumours and endometrial  
CC tumours). Sequences ABK81480-ABK81519 represent allele-specific  
CC oligonucleotide sequencing primers used to detect CASP5 gene  
CC polymorphisms  
XX  
SQ Sequence 15 BP; 4 A; 5 C; 2 G; 3 T; 0 U; 1 Other;  
  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 467 CAGTGTGTAAGTTC 481  
Db 15 CAGTGTGTAAGTTC 1  
  
RESULT 490  
ABA97329  
ID ABA97329 standard; DNA; 15 BP.  
XX  
AC ABA97329;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE CCR5 allele-specific primer for detecting polymorphisms SEQ ID 13.  
XX  
KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;  
KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;  
KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;  
KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;  
KW allele specific oligonucleotide; ASO; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200177125-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 04-APR-2001; 2001WO-US010708.  
XX  
PR 05-APR-2000; 2000US-0194361P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kliem SE, Koshy B;  
XX  
XX WPI; 2002-041282/05.  
XX  
XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful  
PT to diagnose and treat diseases associated with its abnormal expression or  
PT function, including human immunodeficiency virus-1 infection.

XX Claim 16; Page 13; 61pp; English.  
PS  
XX The present sequence is that of an allele-specific primer used to assay a  
CC polymorphism in the human chemokine (C-C motif) receptor 5 (CCR5) gene of  
CC the invention. The specification describes haplotyping the CCR5 gene of  
CC an individual by determining if the individual has one of the CCR5  
CC haplotypes or haplotype pairs fully defined in the specification. The  
CC specification also describes an isolated polynucleotide comprising a  
CC nucleotide sequence which is a polymorphic variant of the reference CCR5  
CC gene sequence (see AB97318) and comprises an isogene defined by a  
CC haplotype described in the specification and its encoded polypeptide. The  
CC methods of the invention are useful to diagnose and develop treatment for  
CC diseases associated with abnormal expression or function of the gene. The  
CC CCR5 isogenes and the screened compounds are useful for treating human  
CC immunodeficiency virus (HIV)-1 infection and the progression to acquired  
CC immunodeficiency syndrome (AIDS). The invention has antiviral  
CC applications. The specification describes genotyping the CCR5 gene of an  
CC individual; predicting a haplotype pair for the CCR5 gene of an  
CC individual; identifying an association between a trait and a haplotype or  
CC haplotype pair of the CCR5 gene. The specification describes a  
CC composition comprising a genotyping oligonucleotide for detecting a CCR5  
CC polymorphism; a recombinant non-human organism transformed with CCR5  
CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;  
CC an isolated antibody specific for the CCR5 polypeptide and a method for  
CC screening drugs targeting the CCR5 polypeptide  
XX  
SQ Sequence 15 BP; 8 A; 2 C; 1 G; 3 T; 0 U; 1 Other;  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Gy 1666 AGCCTGTAATAATAA 1680  
Db 1 AGCCTAATAATAA 15  
RESULT 491  
ABJ36318  
ID ABJ36318 standard; DNA; 15 BP.  
XX  
AC ABJ36318;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human lysosomal acid phosphatase 2 (ACP2) allele-specific probe 20.  
XX  
KW Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;  
KW lysosome-specific enzyme; orthophosphoric monoester hydrolasis;  
KW Hodgkin's disease; HD; acid phosphatase deficiency;  
KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;  
KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;  
KW single nucleotide polymorphism.  
XX  
OS Homo sapiens.  
XX  
PN WO200194362-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 07-JUN-2001; 2001WO-US018457.  
XX  
PR 07-JUN-2000; 2000US-0210047P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kliehm SE, Messer C, Tangway DA;  
XX  
DR WPI; 2002-154563/20.  
XX  
PT Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene  
PT useful in studying expression and function of the protein, and for

PT screening drugs to treat diseases e.g. Hodgkin's disease.  
XX  
PS Claim 17; Page 14; 109pp; English.  
XX  
XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)  
CC nucleic acid and protein sequences. Specifically, the invention relates  
CC to the discovery of 22 novel polymorphic sites within the ACP2 gene. The  
CC invention also comprises methods for haplotyping and genotyping the ACP2  
CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a  
CC lysosomal-specific enzyme that catalyzes the hydrolysis of  
CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and  
CC protein are pharmaceutically important in the treatment of Hodgkin's  
CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene  
CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.  
CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing  
CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's  
CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are  
CC useful for ACP2 genotyping, which can also be used to develop diagnostic  
CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of  
CC the invention are useful in the production of a transgenic animal which  
CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are  
CC useful in the production of allele-specific oligonucleotides designed to  
CC genotype each of the ACP2 polymorphisms. Nucleic acids ABJ36299-ABJ36320  
CC represent claimed ACP2 allele-specific probes. Nucleic acids ABJ36321-  
CC ABJ36364 represent claimed ACP2 allele-specific PCR primers. Nucleic  
CC acids ABJ36365-ABJ36408 represent claimed ACP2 primer-extension  
CC oligonucleotides  
XX  
SQ Sequence 15 BP; 1 A; 8 C; 0 G; 5 T; 0 U; 1 Other;  
Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Gy 1005 CATCTCTCTCTCTCT 1019  
Db 1 CATCTCTCTCTCTCT 15  
RESULT 492  
AAL39772  
ID AAL39772 standard; DNA; 15 BP.  
XX  
AC AAL39772;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE SMOH polymorphism detecting primer SEQ ID No 87.  
XX  
KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;  
KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;  
KW gene therapy; antisense gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200229004-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 04-OCT-2001; 2001WO-US031304.  
XX  
PR 04-OCT-2000; 2000US-0237871P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;  
XX  
DR WPI; 2002-519113/55.  
XX  
PT New genetic variants of smoothened Drosophila homolog (SMOH) gene useful  
PT for therapeutic purposes and for expressing SMOH protein useful in  
PT identifying drugs to treat basal cell carcinomas.  
XX





polymorphic sites comprising a substitute haplotype for any one of haplotypes 101-194, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position of each polymorphic site corresponds to the following nucleotide position in the 32577-bp sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6), 2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194 (PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944 (PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618 (PS42). INDEPENDENT CLAIMS are also included for: determining whether an individual has a statin response marker I or a statin response marker II; selecting a statin therapy to provide an optimal High Density Lipoprotein Cholesterol (HDL) response in an individual; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; predicting an individual's High Density Lipoprotein Cholesterol (HDL) response to treatment with a statin; manufacturing a drug product; seeking regulatory approval for marketing a pharmaceutical formulation for treating a disease or condition in a population partially or wholly comprised by having a statin response marker I; marketing a drug product comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; an isolated polynucleotide comprising a first nucleotide sequence which comprises an integrin, beta 3 (ITGB3) isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered haplotype, where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 25559-26029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence, except where substituted by the sequence of alleles for the ITGB3 isogene, the sequence of alleles for the polymorphic sites whose correspondingly numbered haplotype at the polymorphic sites whose nucleotide positions in the 32577-bp sequence and a second nucleotide sequence which is complementary to the first nucleotide sequence; a recombinant nonhuman organism transformed or transfected with the isolated polynucleotide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment of an integrin, beta 3 (ITGB3) isogene, where the fragment comprises one or more polymorphisms consisting of thymine at PS 1, guanine at PS2, cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11, thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18, thymine at PS 19, guanine at PS21, guanine at PS22, cytosine at PS23, thymine at PS24, thymine at PS25, adenine at PS26, adenine at PS27, cytosine at PS29, adenine at PS30, cytosine at PS31, guanine at PS38, adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38, cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42, guanine at PS43 and guanine at PS44; a genome anthology for the integrin, beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence except where substituted by the sequence of alleles for the correspondingly numbered haplotype at the sequence of alleles for the integrin, beta 3 (ITGB3) gene of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3) gene of an individual; assigning a haplotype pair for the integrin, beta 3 (ITGB3) gene to an individual; reducing the potential for bias in a clinical trial of a candidate drug for treating a disease or condition predicted to be associated with ITGB3 activity; an isolated polypeptide comprising a ITGB3 protein variant consisting of protein variants A, B, C, D, E, F and G and comprising 788-amino acid sequence, except where substituted by the corresponding sequence of amino acids whose positions and alleles are given in the specification; an isolated monoclonal antibody specific for and immunoreactive with the selected ITGB3 protein variant comprising the isolated polypeptide; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; an isolated fragment of an ITGB3 protein variant, where the fragment is at least 6 amino acids in length and comprises one or more variant amino acids consisting of methionine at a position corresponding to amino acid position 66, methionine at a position corresponding to amino acid position 445, and glutamine at a position corresponding to amino acid position 515 the 788-amino acid sequence; screening for drugs targeting

the selected ITGB3 protein variant comprising the isolated polypeptide; screening for compounds targeting the ITGB3 protein to treat a condition or disease predicted to be associated with ITGB3 activity; validating the ITGB3 protein as a candidate target for treating a medical condition predicted to be associated with ITGB3 activity; and an isolated oligonucleotide designed for detecting a polymorphism in the integrin, beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44, where the oligonucleotide contains or is located one to several nucleotides downstream of the selected PS, where the oligonucleotide has a length of about 15 to about 100 nucleotides. Preferred Kit: The kit further comprises a manual with instructions for performing one or more reactions on a human nucleic acid sample to identify the allele(s) present in the individual at each polymorphic site in the set of polymorphic sites and determining if the individual has a statin response marker I or a statin response marker II based on the identified allele(s). The set of oligonucleotides is designated for identifying both alleles at each polymorphic site of the selected set of polymorphic sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42; PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of PS 18 PS3, PS12 or PS42. The individual is Caucasian. The linkage disequilibrium between the linked haplotype and any one of haplotypes 101-194, 201-463 or 501-515 has  $r^2 \geq 0.2$  consisting of at least 0.75, at least 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of the oligonucleotides in the set of oligonucleotides is an allele-specific oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp. The set of polymorphic sites is PS3, PS12, and PS42 and the set of oligonucleotides comprises first, second and third allele-specific oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp sequence, or its complement, and S in the 15-bp sequence is guanine; the second ASO probe comprises 15-bp sequence, or its complement, and Y in the 15-bp sequence is cytosine; the third ASO probe comprises 15 bp, or its complement, and Y in the 15-bp sequence is cytosine. Preferred Article: The article of manufacture comprises a pharmaceutical formulation and at least one indicium identifying a population for whom the pharmaceutical formulation is indicated, where the pharmaceutical formulation comprises a statin as at least one active ingredient and the identified population is partially or wholly defined by having a statin response marker I, where a trial population to the pharmaceutical marker I exhibits a better HDL response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. It also comprises packaging material, where the formulation contained within the packaging material, where the pharmaceutical formulation comprises a statin as at least one separate active ingredient, and the packaging material formulation is indicated for a which states that the pharmaceutical formulation is indicated for a population partly or wholly defined by having a statin response marker I, where a trial population having the statin response marker exhibits a better HDL response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific oligonucleotide that specifically hybridizes to an allele of the ITGB3 gene at a region containing the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for haplotyping the integrin, beta 3 (ITGB3) gene of all individual, comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of two or more polymorphic sites. Preferred Method: Determining whether an individual has a statin response marker I or a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, then the individual has a statin response marker I if the individual has at least one copy of the selected haplotype and a statin response marker II if the individual has zero copy of the selected haplotype and the individual has a statin response marker I if the individual has one copy of the selected haplotype and a statin response marker I if the individual has two copies of the selected haplotype. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites comprising the selected haplotype and using the results of the genotyping step to identify, for the set of polymorphic sites the haplotype pair present in the individual. The determining step comprises consulting a data repository that provides information on the copy number present in the individual for the selected haplotype. The data repository is the

CC individual's medical records or a medical data card. Assigning an  
CC individual to a first or second statin response marker group comprises  
CC determining the copy number in the individual or a haplotype and  
CC assigning the individual to the first statin response marker group if the  
CC individual has at least one copy of the selected haplotype and to the  
CC second statin response marker group if the individual has zero copy of  
CC the selected haplotype; and assigning the individual to the first statin  
CC response marker group if the individual has zero or one copy of the  
CC selected haplotype and to the second statin response marker group if the  
CC individual has two copies of the selected haplotype. The determining step  
CC comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 2.7e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1273 GAGACCACTATCTCC 1287  
1 GAGACCACTACTTC 15

RESULT 495  
ADS88857  
ID ADS88857 standard; DNA; 16 BP.

AC ADS88857;  
XX  
XX 16-DEC-2004 (first entry)

DE Primer for second strand synthesis of a random 7 residue peptide DNA.

XX adeno-associated virus; AAV; capsid protein; VP1, VP2, VP3; gene therapy;  
KM coronary artery endothelial cell; coronary heart disease;  
KM cardiovascular disease; infectious disease; primer; ss.

XX Synthetic.

XX WO2004083441-A2.

XX 30-SEP-2004.

XX 19-MAR-2004; 2004WO-EP002923.

XX 19-MAR-2003; 2003US-0455594P.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX (UYFR-) UNIV FREIBURG ALBERT-LUDWIGS.

PI Kleinschmidt J, Mueller O, Trepel M, Kaul F, Leder C;

XX WPI; 2004-691059/67.

XX Producing a repertoire of random peptides on the surface of adeno-  
PT associated virus (AAV) particles, useful for gene therapy, comprises  
PT expressing in a recombinant host cell nucleic acids encoding a diverse  
PT population of peptides.

XX Example 1; Page 18; 36pp; English.

XX The specification describes a method for producing a repertoire of random  
CC peptides on the surface of adeno-associated virus (AAV) particles. The  
CC method comprises expressing in a recombinant host cell nucleic acids  
CC encoding a diverse population of peptides, where each peptide is  
CC expressed as a fusion with an AAV capsid protein of an AAV particle which  
CC displays at its surface the diverse population of peptides, and the AAV  
CC particle have the ability to replicate provided by genetic information  
CC packaged with it and a helper vector providing the adenovirus helper  
CC functions. The capsid protein is VP1, VP2, or VP3 protein. The method is  
CC useful for producing a repertoire of random peptides on the surface of  
CC AAV particles. The method is useful in gene therapy, where the AAV  
CC vectors obtained are useful for treating diseases associated with a  
CC dysfunction of human coronary artery endothelial cells, e.g. coronary  
CC heart disease or cardiovascular diseases. They are also useful for

CC treating infectious diseases. The present primer was used for second  
CC strand synthesis of an oligonucleotide that encodes a random 7 residue  
CC peptide insert at position 3967 in the AAV genome. It was used to  
CC generate random peptide libraries in the plasmid level.

SQ Sequence 16 BP; 1 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1261 GTCAGCCGCTGG 1273  
4 GTCAGCCGCTGG 16

RESULT 496  
ADN12185  
ID ADN12185 standard; DNA; 30 BP.

XX ADN12185;

XX 01-JUL-2004 (first entry)

DE Tachykinin receptor NK1 amplifying primer NK13' (nested).

XX Tachykinin; vascular disease; platelet aggregation; vulnery;  
KM thrombolytic; neurokinin; thrombosis; wound healing; PCR; primer; NK1;  
KM NK3; tachykinin receptor; ss.

XX Synthetic.

XX WO2004030695-A1.

XX 15-APR-2004.

XX 06-OCT-2003; 2003WO-GB004335.

XX 04-OCT-2002; 2002GB-00023077.

XX (UYRE-) UNIV READING.

PI Gibbins JM, Lowry PJ, Graham GJ, Page NM;

XX WPI; 2004-330076/30.

XX Use of tachykinin antagonist or agonist for treating diseases mediated by  
PT binding of tachykinin ligand to its platelet associated receptor and  
PT failure of platelet having tachykinin receptor to aggregate normally in  
PT presence of tachykinin.

XX Disclosure; Page 21; 46pp; English.

XX The invention relates to the use of a tachykinin antagonist in the  
CC manufacture of a medicament for treating e.g. a disease mediated by  
CC binding of a tachykinin ligand to its platelet associated receptor. A  
CC method of identifying an antagonist or agonist of tachykinin having a  
CC platelet associated tachykinin receptor involves contacting a compound to  
CC be evaluated with platelets expressing the tachykinin receptor in the  
CC presence of the tachykinin and monitoring for an increase or decrease of  
CC platelet aggregation. The agonist is useful in the manufacture of a  
CC medicament in bulk quantities for treating a disease or conditions  
CC mediated by binding of a tachykinin ligand to its platelet-associated  
CC receptor (e.g. thrombosis), and by a failure of or a reduced ability of  
CC platelet having a tachykinin receptor to aggregate normally in the  
CC presence of the tachykinin; antagonizing or stimulating the effect of  
CC tachykinin on platelet associated tachykinin receptor; and stimulating  
CC platelet aggregation (e.g. wound healing). Sequences ADN12182-ADN12193  
CC represent PCR primers for amplifying tachykinin receptors NK1, NK2 and  
CC NK3.

XX Sequence 30 BP; 7 A; 8 C; 14 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 13; DB 1; Length 30;  
 Best Local Similarity 65.5%; Pred. No. 6.8e+02;  
 Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 11 CACCGCGGAGCGGCGAGTGCATCCAG 39  
 1 CCTGTGGGGAAGCCAGCAGAGAGCCAG 29

Db

RESULT 497  
 AAT76484/c  
 ID AAT76484 standard; DNA; 16 BP.  
 AC AAT76484;  
 XX  
 XX 16-SEP-1997 (first entry)  
 DT  
 XX Endothelial nitric oxide antisense oligonucleotide.  
 XX  
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;  
 KM chronic obstructive pulmonary disease; bronchitis; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9640162-A1.  
 PN  
 XX 19-DEC-1996.  
 PD  
 XX 06-JUN-1996; 96WO-US009306.  
 PF  
 XX 07-JUN-1995; 95US-00474497.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW, Metzger WJ;  
 PI  
 XX WPI, 1997-051871/05.  
 DR  
 XX  
 XX Treatment of airway diseases such as asthma - by topically applying  
 PT adenosine-free antisense oligonucleotide to airway epithelium of  
 PT subject.  
 PT  
 XX Example 5; Page 42; 71pp; English.  
 PS  
 XX A method for treating airway disease in a subject has been produced,  
 CC which involves the topical administration of an essentially adenosine  
 CC free antisense oligonucleotide (ON) to the airway epithelium of the  
 CC subject. The present sequence is an antisense oligonucleotide specific  
 CC for endothelial nitric oxide. The method can be used to treat airway  
 CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary  
 CC disease, bronchitis and other airway diseases characterised by an  
 CC inflammatory response. By eliminating adenosine from the antisense ON,  
 CC its liberation upon antisense degradation is prevented, thereby  
 CC preventing adenosine-induced bronchoconstriction in patients with hyper-  
 CC reactive airways  
 CC  
 CC Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
 SQ

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 636 GTGAGCCAGCCAGCC 651  
 16 GGCGCCAGCCAGCC 1

RESULT 498  
 AAV70488/c  
 ID AAV70488 standard; DNA; 16 BP.  
 AC AAV70488;  
 XX  
 XX

DT 08-APR-1999 (first entry)  
 XX Control probe hybridising to HCV variants.  
 DE  
 XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; probe;  
 KM bridging oligonucleotide; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_base 1  
 FT /tag= a  
 FT /note= "labeled with fluorescein"  
 FT  
 XX WO9850403-A1.  
 PN  
 XX 12-NOV-1998.  
 PD  
 XX 05-MAY-1998; 98WO-US003194.  
 PF  
 XX 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 PR  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 PI  
 XX WPI, 1998-610317/51.  
 DR  
 XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 PT  
 XX Example 8; Page 129; 279pp; English.  
 PS  
 XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. The present  
 CC sequence represents a control probe that can hybridise to all HCV  
 CC variants  
 CC  
 CC Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1436 CCACAGGCGCTTTGGC 1451  
 16 CCACAGGCGCTTTGGC 1

```

RESULT 499
AAZ09807/C
ID AAZ09807 standard; DNA; 16 BP.
XX
XX
AC AAZ09807;
XX
XX
DT 26-NOV-1999 (first entry)
XX
XX
DE p53 exon 8 PCR primer 1.
XX
XX
KM Primer extension; primer; preamplification; 3'-5' exonuclease activity;
XX
XX
PEP-PCR; mutation analysis; microsatellite analysis; DNA polymerase; p53;
XX
XX
OS Synthetic.
XX
XX
PN DE19813317-A1.
XX
XX
PD 30-SEP-1999.
XX
XX
PE 26-MAR-1998; 98DE-01013317.
XX
XX
PR 26-MAR-1998; 98DE-01013317.
XX
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
XX
PI Rueschhoff J, Dietmaier W;
XX
XX
DR WPI; 1999-541759/46.
XX
XX
PT Nucleic acid amplification involving primer extension preamplification,
XX
XX
PT especially for whole genome amplification.
XX
XX
PS Example 6; Page 7; 24pp; German.
XX
XX
XX
This invention describes a novel method for the amplification of nucleic
XX
XX
acid fragments from a sample in two or three thermal cycling reactions
XX
XX
using random primers in the first reaction and specific primers in the
XX
XX
second reaction is new and comprises using a mixture of at least two DNA
XX
XX
polymerases, at least one of which has 3'-5' exonuclease activity. The
XX
XX
process is useful for whole genome amplification by primer extension
XX
XX
preamplification polymerase chain reaction (PEP-PCR). DNA amplified by
XX
XX
the process can be used for mutation analysis, as a template for
XX
XX
sequencing reactions, or for microsatellite analysis. The use of a
XX
XX
mixture of DNA polymerases, including at least one with proofreading
XX
XX
ability, results in increased sensitivity, such that cell-specific
XX
XX
amplification products can be generated with a probability of more than
XX
XX
90% from samples containing no more than 100 cells, preferably no more
XX
XX
than 5-10 cells. AAZ09799-209815 represent PCR primers used in the method
XX
XX
of the invention
XX
XX
XX
Sequence 16 BP; 5 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX
XX
Query Match 0.7%; Score 12.8; DB 1; Length 16;
XX
XX
Best Local Similarity 87.5%; Pred.No. 3.3e+02;
XX
XX
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
XX
XX
Oy 1061 AGCAGGTCTACTCTGC 1076
XX
XX
| | | | | | | | | |
XX
XX
Db 16 ATCAGGTCTACTCTGC 1
XX
XX
XX
RESULT 500
AAZ54320
ID AAZ54320 standard; DNA; 16 BP.
XX
XX
AC AAZ54320;
XX
XX
DT 05-JUL-1999 (first entry)
XX
XX
DE Inducible nitric oxide synthase antisense oligonucleotide.
XX

```

KM	Antisense oligonucleotide; multiple target; antisense treatment;
KM	impaired respiration; inflammation; lung disease;
KM	pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM	acute asthma; allergy; asthma; impeded respiration;
KM	respiratory distress syndrome; pain; cystic fibrosis;
KM	pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM	chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM	colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM	hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX	prostate cancer; ss.
XX	
OS	Synthetic.
XX	
PN	WO913886-A1.
XX	
PD	25-MAR-1999.
XX	
XX	17-SEP-1998; 98WO-US019419.
PF	17-SEP-1997; 97US-0059160P.
PR	09-JUN-1998; 98US-00093972.
XX	
XX	(UYEC-) UNIV EAST CAROLINA.
PA	
PI	Nyce JW;
XX	
XX	
DR	WPI, 1999-229400/19.
XX	
PT	New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT	vasoconstriction.
XX	
XX	Disclosure; Page 62; 120pp; English.
PS	
XX	
CC	The specification describes antisense oligonucleotides (AA52869-X55271)
CC	directed against at least 2 mRNAs selected from target gene, coding and
CC	non-coding regions of RNAs corresponding to target genes, gene initiation
CC	codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC	-end and the juxta-section between coding and non-coding regions and all
CC	segments of RNAs encoding proteins associated with one or more diseases,
CC	conditions or mixtures. The antisense oligonucleotides may be derived
CC	from sequences AA55272-74. These multiple target oligonucleotides
CC	(specifically AA55180-271) can be used for the antisense treatment of
CC	diseases and conditions. Typical diseases and conditions are those
CC	associated with impaired respiration and inflammation, including lung
CC	diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC	acute asthma, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC	pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC	disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC	colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC	hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC	well as all types of cancers which may metastasize or have metastasized
CC	to the lungs, including breast and prostate cancer
XX	
SQ	Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
QY	
Db	Query Match 0.7%; Score 12.8; DB 1; Length 16; Best Local Similarity 87.5%; Pred. No. 3.3e+02; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	537 CTTCTTCCCATCGCC 552       1 CTTCTTCCCGCTCTC 16
RESULT 501	
AA54275/c	
ID	AA54275 standard; DNA; 16 BP.
XX	
AC	AA54275;
XX	
DT	05-JUL-1999 (first entry)
XX	

DE Endothelial nitric oxide synthase antisense oligonucleotide.  
XX  
XX Antisense oligonucleotide; multiple target; antisense treatment;  
XX impaired respiration; inflammation; lung disease;  
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
XX acute asthma; allergy; asthma; impeded respiration;  
XX respiratory distress syndrome; pain; cystic fibrosis;  
XX pulmonary hypertension; pulmonary disease; emphysema;  
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
XX prostate cancer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYce JW;  
XX  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX  
XX Disclosure; Page 61; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AAx52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
XX end and the juxta-section between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AAx55272-74. These multiple target oligonucleotides  
XX (specifically AAx5180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 636 GTCAAGCCAGCCAGCC 651  
DB 16 GGCAGCCAGCCAGCC 1  
RESULT 502  
AAx54321  
ID AAx54321 standard; DNA; 16 BP.  
XX  
XX AAx54321;  
XX

DT 05-JUN-1999 (first entry)  
XX  
XX Inducible nitric oxide synthase antisense oligonucleotide.  
DE  
XX Antisense oligonucleotide; multiple target; antisense treatment;  
XX impaired respiration; inflammation; lung disease;  
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
XX acute asthma; allergy; asthma; impeded respiration;  
XX respiratory distress syndrome; pain; cystic fibrosis;  
XX pulmonary hypertension; pulmonary disease; emphysema;  
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
XX prostate cancer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYce JW;  
XX  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX  
XX Disclosure; Page 62; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AAx52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
XX end and the juxta-section between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AAx55272-74. These multiple target oligonucleotides  
XX (specifically AAx5180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 537 CTTCTTCCGATCGCC 552  
DB 1 CTTCTTCCGATCGCC 16  
RESULT 503  
AAx3719/c  
ID AAx3719 standard; DNA; 16 BP.  
XX  
XX AAx3719;  
XX

AC AAA3719;  
XX  
XX 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:1408.  
XX  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorochiata; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO20009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers.  
XX  
XX Claim 18; Page 440; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets  
XX nucleic acids involved in bronchoconstriction, allergies, and/or  
XX inflammation. The ON can have antiinflammatory, antiallergic,  
XX antiasthmatic, cytostatic and analgesic activities. The compositions are  
XX useful for the treatment of diseases associated with inflammation,  
XX impaired airways, including lung disease and diseases whose secondary  
XX effects afflict the lungs of a subject. They can be used for treating  
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
XX impaired respiration, respiratory distress syndrome, pain, cystic  
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
XX pulmonary disease (COPD), and cancers such as leukaemia, lymphomas,  
XX carcinomas, and cancers which may metastasise to the lungs, including  
XX breast and prostate cancer. The reduction of the adenosine content of the  
XX ONs reduces side effects. The A-containing ONs break down with the  
XX release of deoxyadenosine which activates adenosine receptors causing  
XX bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the  
XX nucleotide sequences given in the sequence listing from the present  
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
XX AAA33992) are specifically claimed ONs from the present invention. N.B.  
XX Sequences given in the disclosure of the present invention do not match  
XX up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing  
XX  
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 504  
AAA3764  
ID AAA3764 standard; DNA; 16 BP.  
XX  
XX AAA3764;  
XX  
XX 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:1453.  
XX  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorochiata; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO20009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers.  
XX  
XX Claim 18; Page 446; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets  
XX nucleic acids involved in bronchoconstriction, allergies, and/or  
XX inflammation. The ON can have antiinflammatory, antiallergic,  
XX antiasthmatic, cytostatic and analgesic activities. The compositions are  
XX useful for the treatment of diseases associated with inflammation,  
XX impaired airways, including lung disease and diseases whose secondary  
XX effects afflict the lungs of a subject. They can be used for treating  
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
XX impaired respiration, respiratory distress syndrome, pain, cystic  
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
XX pulmonary disease (COPD), and cancers such as leukaemia, lymphomas,  
XX carcinomas, and cancers which may metastasise to the lungs, including  
XX breast and prostate cancer. The reduction of the adenosine content of the  
XX ONs reduces side effects. The A-containing ONs break down with the  
XX release of deoxyadenosine which activates adenosine receptors causing  
XX bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the  
XX nucleotide sequences given in the sequence listing from the present  
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
XX AAA33992) are specifically claimed ONs from the present invention. N.B.  
XX Sequences given in the disclosure of the present invention do not match  
XX up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing  
XX  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.8; DB 1; Length 16;



Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTTCTTCCCATCGCC 552  
1 CTTCTTCCCATCGCC 16

RESULT 505

AAA33765  
ID AAA33765 standard; DNA; 16 BP.

AC AAA33765;

DT 28-JUN-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:1454.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
XX phosphorohistate; impaired respiration; inflammation; allergy;  
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
XX antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX NYCE JW;

DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or  
PT cancers.

PS Claim 18; Page 446; 1343pp; English.

XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1660 (AAA3233 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTTCTTCCCATCGCC 552  
1 CTTCTTCCCATCGCC 16

RESULT 506

AAZ97920/c  
ID AAZ97920 standard; DNA; 16 BP.

AC AAZ97920;

DT 15-SEP-2003 (revised)

DT 26-APR-2000 (first entry)

XX HIV-1 protease gene probe SEQ ID NO:410.  
XX Human immunodeficiency virus; HIV; protease; probe; detection;  
XX drug selected mutation; hybridisation; genotyping; infection;  
XX drug resistance; ss.

XX Human immunodeficiency virus 1.

OS WO9967428-A2.

XX 29-DEC-1999.

XX 22-JUN-1999; 99WO-EP004317.

XX 24-JUN-1998; 98EP-00870143.

XX (INNO-) INNOGENETICS NV.

XX Stuyver I;

DR WPI; 2000-147219/13.

XX Detection of drug-selected mutations in the HIV protease gene used to  
PT treat HIV infections.

PS Claim 3; Page 43; 76pp; English.

XX The present invention describes the detection of drug-selected mutations  
CC in the HIV protease gene. The method of detection allows the simultaneous  
CC characterisation of a range of codons involved in drug resistance using  
CC sets of probes optimised to function together in a reverse-hybridisation  
CC assay. AAZ97517 to AAZ97997 represent specifically claimed probes for use  
CC in the assay, and AAZ97479 to AAZ97501 represent specifically claimed HIV  
CC protease gene polymorphic nucleotide sequences. AAZ97502 to AAZ97515, and  
CC AAZ98004 to AAZ98007, represent PCR primers for the HIV protease gene.  
CC and AAZ97516 represents an HIV protease probe used in an example from the  
CC present invention. The method, probes and primers can be used for the  
CC detection of drug-selected mutations in the HIV protease gene. The method  
CC allows the simultaneous characterisation of a range of codons involved in  
CC drug resistance. The method may also be used for HIV protease genotyping  
CC assays. The probes are able to discriminate between wild type and mutated  
CC protease sequences. The method allows rapid and reliable detection of  
CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS  
CC field)

XX Sequence 16 BP; 5 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



OY 1586 TGAGTCAAAAATCTC 1601  
 |||||  
 DB 16 TGAGTCACCAAAATTC 1

RESULT 507  
 AAF19886  
 ID AAF19886 standard; DNA, 16 BP.  
 XX  
 AC AAF19886;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human inducible nitric oxide synthase polynucleotide fragment #1453.  
 XX  
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KM human; airway disorder; bronchoconstriction; lung inflammation;  
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KM cancer; ss.

XX Homo sapiens.  
 OS  
 XX WO200062736-A2.  
 XX  
 XX 26-OCT-2000.  
 PD  
 XX 24-MAR-2000; 2000WO-US008020.  
 PF  
 XX 06-APR-1999; 99US-0127958P.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 PA NYce JW;  
 PI  
 XX WPI; 2000-679539/66.  
 DR  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX  
 XX Claim 14; Page 256; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome

CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 CC  
 XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 537 CTTCTTCCCATGCC 552  
 |||||  
 DB 1 CTTCTTCCCATGCC 16

RESULT 508  
 AAF19887  
 ID AAF19887 standard; DNA, 16 BP.  
 XX  
 AC AAF19887;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human inducible nitric oxide synthase polynucleotide fragment #1454.  
 XX  
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KM human; airway disorder; bronchoconstriction; lung inflammation;  
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KM cancer; ss.

XX Homo sapiens.  
 OS  
 XX WO200062736-A2.  
 XX  
 XX 26-OCT-2000.  
 PD  
 XX 24-MAR-2000; 2000WO-US008020.  
 PF  
 XX 06-APR-1999; 99US-0127958P.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 PA NYce JW;  
 PI  
 XX WPI; 2000-679539/66.  
 DR  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX  
 XX Claim 14; Page 256; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,

CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS), and peripheral nervous and non-nervous system peptide  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasocactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impaired respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAR18434 to AAR21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention  
XX  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
SQ

Query Match	12.8%	Score	12.8	DB	1	length	16
Best Local Similarity	87.5%	Pred. No.	3.3e+02				
Matches	14	Conservative	2	Mismatches	0	Indels	0
						Gaps	0

OY	537	CTTCTTCCCATCGCC	55
Db	1	CTTCTTCCCGTCTCC	16

RESULT 509  
AAFI19841/C  
ID AAFI19841 standard; DNA; 16 BP.

AC	AAFI19841;
XX	
DT	14-MAR-2001 (first entry)

XX Human endothelial nitric oxide synthase polynucleotide fragment #1408.  
DE

XX Low adenosine antisense oligonucleotide; phosphorothiolate; allergy;  
KM human; airway disorder; bronchoconstriction; lung inflammation;  
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KM immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;  
KM respiratory obstruction; pulmonary; obstruction; impeded respiration;  
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KM cancer; ss.

Homo sapiens

PN WO2000062736-A2.

PD 26-OCT-2000.

XX  
PF 24-MAR-2000: 2000WO-US008020.

XX  
06-APR-1999 9911S-0127958P.

XX  
 (XXXX) UNIT PAGE CARBON.TNA

PA (NYCE/) NYCE J W.

NYce JW;  
PI

XX WPI: 2000-679539/66.  
DR

XX Low adenosine (A) content oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.

PS Claim 14; Page 251; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, CNS and peripheral nervous and non-nervous system peptides, transmitters, defensins, growth factors, vasoactive peptides and chemokines, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AP19434 to AP21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Seq	Sequence	16 BP;	0 A;	5 C;	7 G;	4 T;	0 U;	0 Other;
Query Match	0.7%;	Score 12.8;	DB 1;	Length 16;				

QY	636	GTGAGCCACAGGCCACC	651
Db	16	GGCAGCCACAGGCCACC	1

RESULT 510  
ADU94873/c  
ID ADU94873 standard; RNA; 16 BP.

ADU94873; AC

AA  
DT 10-FEB-2005 (first entry)

XX Human TERT G-cleaver ribozyme substrate sequence #233

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KM protein-cysteine-phosphatase-1b; PTP-1b; methionine aminopeptidase;  
KM MeAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KM C-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver  
KM amaryzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KM ss.

OS Homo sapiens.

XX  
PN  
WQ200116312-A2

XX  
XX  
00 MAR 2001[illegible]

XX 2

PR 31-AUG-1999; 99US-00406643  
PR 27-SEP-1999;



CY 1296 GGGGGCCCGAGGAG 1311  
 |||||  
 Db 1 GGGGGCCCGAGGAG 16  
 |||||  
 RESULT 512  
 ID ADU94557  
 ADU94557 standard; RNA; 16 BP.  
 AC ADU94557;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Human TERT G-cleaver ribozyme substrate sequence #72.  
 XX  
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTP-1B; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erbB2; neu; phospholamban; PLN; presentin-1; ps-1; presentin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116312-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 30-AUG-2000; 2000WO-US023998.  
 XX  
 PR 31-AUG-1999; 99US-0151713P.  
 PR 27-SEP-1999; 99US-00406643.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.  
 PR 29-DEC-1999; 99US-0173612P.  
 PR 30-DEC-1999; 99US-00476387.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswigen J, Usman N, Blatt L, Beigelman L, Burgin A,  
 PI Karpetsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B,  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig U, Sproat BS,  
 XX  
 DR WPI; 2001-244406/25.  
 XX  
 PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 XX  
 PS Example 1; Page 301; 717P; English.  
 XX  
 CC The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTP-1B), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presentin-1 (ps-1),  
 CC presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,

zinczyme, and/or DNAzyme motifs. The methods of the invention are useful  
for treating cancer, in particular breast cancer; Alzheimer's disease,  
diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
diseases, hepatitis B infections, and hepatitis and hepatocellular  
carcinoma. The enzymatic nucleic acid molecules can also be used as  
diagnostic tools to examine genetic drift and mutations within diseased  
cells and to detect the presence of specific RNA in a cell. The present  
invention represents a substrate/target sequence for a ribozyme used in  
the examples of the present invention. Note: Some SEQ ID Nos are repeated  
more than once in the specification, but these have different sequences  
associated with them.

Query Match           0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity     62.5% ; Pred. No. 3.3e+02;  
Matches      10; Conservative       4; Mismatches       2; Indels          0; Gaps          0;

OY                   680 TGGCCTTCCTGCTGCAC 695  
                     ::|:| | |:||: ||  
Db                   1 UGUUUCACUGCUUGC 16

RESULT 513  
IDBLA6099/C  
ABLA6099 standard; DNA; 16 BP.  
  
XX ABLA6099;  
AC  
XX  
XX  
DT 26-APR-2002 (first entry)  
XX  
XX  
DE Control probe SEQ ID NO:66.  
XS  
KS Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM characterisation; identification; nucleic acid structure; diagnosis;  
KW PCR primer; probe; ss.  
KK  
OS Synthetic.  
XS  
PN WO200198537-A2.  
PD  
XD 27-DEC-2001.  
PP  
XP 15-JUN-2001; 2001WO-US019401.  
XF  
XZ 17-JUN-2001; 2000US-0212308P.  
PR 15-JUN-2001; 2001US-00212308.  
PS  
XA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XT Lyamichev V, Allawi H, Dong F, Nerl BP, Venier IT;  
F1  
WIPI; 2002-049698/06.  
DR  
XX  
XX Example 8; Page 158; 409pp; English.  
PS  
XX  
XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABH46367 represent  
CC sequences used in the exemplification of the present invention  
CX

SO Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1436 CCACAGGCGCTTGGC 1451  
Db 16 CCACAGGCGCTTGGC 1  
RESULT 514  
ABS97178/c  
ID ABS97178 standard; DNA; 16 BP.  
AC ABS97178;  
XX  
XX 23-DEC-2002 (first entry)  
DT  
XX  
DE Human CYP4501A2 Exon 7 sequencing primer #2.  
XX  
XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF;  
KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KM epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NMNT;  
KM NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;  
KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor; uPA;  
KM multidrug resistance associated protein 3; cancer; prostate;  
KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5;  
KM altered drug metabolism; cardiovascular function; colorectal tumour;  
KM central nervous system; pulmonary; immunological; sequencing.  
XX  
XX Homo sapiens.  
OS  
XX ABL31409  
XX ID ABL31409 standard; DNA; 16 BP.  
XX AC ABL31409;  
XX  
XX 25-JUL-2002.  
PD  
XX 28-NOV-2001; 2001WO-US044838.  
PF  
XX 28-NOV-2000; 2000US-00724389.  
PR  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
PI  
XX WPI; 2002-698522/75.  
DR  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes  
PT e.g. cytochrome p450 and cathepsin s useful as genetic linkage markers  
PT for locating, identifying and characterizing the genes responsible for  
PT disorder-related traits.  
XX  
XX Example 2; Page 101; 714pp; English.  
PS  
XX  
XX This invention relates to the sequence of an isolated nucleic acid  
CC molecule comprising at least one base variation from that of a known  
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
CC cytochrome P450 02B1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating  
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl  
CC transferase (NMNT), NADPH quinone oxidoreductase 2 (NQO2),  
CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1  
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
CC The polymorphisms in the human genes cited in the invention are useful as  
CC genetic linkage markers for locating and characterizing the genes that  
CC are responsible for specific traits within the genome and eventually  
CC identifying the genes responsible for a variety of disorder-related  
CC traits as a result of their e.g., overexpression, constitutive  
CC expression, mutation or underexpression, which may be used in diagnosing  
CC and/or treating the disorders. The nucleic acid molecules comprising the  
CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
CC ARNT, EPHX2, GST12, NMNT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
CC used to screen for altered cardiovascular function, in COX2 for altered  
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
CC nervous system function, in FLAP and HNMT for altered pulmonary,  
CC immunological or haematological function, in KLK2 for altered serine  
CC protease activity in the prostate, in LTF for altered immunological or  
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
CC peripheral nervous system function. The present sequence represents a  
CC sequencing primer used to sequence the polymorphic genes of the invention  
XX  
XX  
SO Sequence 16 BP; 4 A; 4 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 374 GGATCATCTTAGCCCA 389  
Db 16 GGATCATCTTAGCCCA 1  
RESULT 515  
ABL31409  
ID ABL31409 standard; DNA; 16 BP.  
XX  
XX ABL31409;  
XX  
XX 21-MAR-2002 (first entry)  
DT  
XX  
XX Human HLA genotyping oligonucleotide SEQ ID NO 898.  
DE  
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
KM immunogenetic; transplantation; genetic disease; ss.  
KM  
XX  
XX Homo sapiens.  
OS  
XX W0200192572-A1.  
XX  
XX 06-DEC-2001.  
PD  
XX 01-JUN-2001; 2001WO-JP004662.  
PF  
XX 01-JUN-2000; 2000JP-00164798.  
PR  
XX  
XX (NITSN ) NISSHINBO IND INC.  
XX (SYST-) SYSTEM RES INC.  
XX  
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
PI  
XX WPI; 2002-122074/16.  
DR  
XX  
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when  
PT transplanting between them.  
XX  
XX Claim 10; Page 263; 345pp; Japanese.  
PS  
XX

CC The invention relates to a typing kit for judging human leukocyte antigen  
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
CC genes e.g. belonging to HLA class I antigens on human genome and  
CC containing gene polymorphisms as alloantigens have been immobilised as  
CC primers for amplification of cleaved nucleic acids relating to gene  
CC polymorphisms. The method is useful for judging HLA genotypes of  
CC individuals by determining immunogenetic differences before transplanting  
CC between them, providing genetic information to decide compatibility of  
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility  
CC diagnosis of genetic diseases and identifying individuals  
XX  
SQ Sequence 16 BP; 3 A; 0 C; 9 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 170 GGGGTTGTGTACAGAT 185  
Db 1 GGGGTTGTGTACAGAT 16  
RESULT 516  
ABL31307  
ID ABL31307 standard; DNA; 16 BP.  
XX  
AC ABL31307;  
XX  
DT 21-MAR-2002 (first entry)  
XX  
DE Human HLA genotyping oligonucleotide SEQ ID NO 796.  
XX  
KM Human, human leukocyte antigen; HLA; genotype; polymorphism;  
KM immunogenetic; transplantation; genetic disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192572-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 01-JUN-2001; 2001WO-IP004662.  
XX  
PR 01-JUN-2000; 2000JP-00164798.  
XX  
PA (NISON) NISSHINBO IND INC.  
PA (SYST-) SYSTEM RES INC.  
XX  
PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
XX  
DR WPI; 2002-122074/16.  
PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when  
PT transplanting between them.  
XX  
PS Claim 10; Page 244; 345pp; Japanese.  
XX  
XX The invention relates to a typing kit for judging human leukocyte antigen  
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
CC genes e.g. belonging to HLA class I antigens on human genome and  
CC containing gene polymorphisms as alloantigens have been immobilised as  
CC primers for amplification of cleaved nucleic acids relating to gene  
CC polymorphisms. The method is useful for judging HLA genotypes of  
CC individuals by determining immunogenetic differences before transplanting  
CC between them, providing genetic information to decide compatibility of  
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility  
CC diagnosis of genetic diseases and identifying individuals  
XX

SQ Sequence 16 BP; 3 A; 0 C; 9 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 170 GGGGTTGTGTACAGAT 185  
Db 1 GGGGTTGTGTACAGAT 16  
RESULT 517  
AAL56914  
ID AAL56914 standard; DNA; 16 BP.  
XX  
AC AAL56914;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human hypoxia-inducible factor-1 alpha antisense oligo #10.  
XX  
KM HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;  
KM pre-eclampsia; cytosolic; gynaecological; antiinflammatory; nootropic;  
KM neuroprotective; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003085110-A2.  
XX  
PD 16-OCT-2003.  
XX  
PF 04-APR-2003; 2003WO-IB001758.  
XX  
PR 05-APR-2002; 2002US-0370126P.  
XX  
PA (CURE-) CUREON AS.  
XX  
PI Thru CA, Hog AM, Kristjansen PEG;  
XX  
DR WPI; 2003-812728/76.  
XX  
PF New oligonucleotide that modulates hypoxia-inducible factor-1alpha,  
PT useful for treating e.g. cancer or Alzheimer's disease.  
XX  
PS Claim 1; Page 41; 0pp; English.  
XX  
XX The present invention relates to compounds capable of modulating hypoxia-  
CC inducible factor-1alpha (HIF1a). The compounds are used to treat patients  
CC with, or at risk of developing, cancer (e.g. of breast, prostate,  
CC pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's  
CC disease, for modulating angiogenesis, proliferation of erythrocytes and  
CC other cells, iron, glucose and energy metabolism, pH regulation, tissue  
CC invasion, apoptosis, multiple drug resistance, cellular stress responses,  
CC and matrix metabolism, especially apoptosis where modulation is  
CC sensitivity to an apoptotic stimulus, particularly a chemotherapeutic  
CC agent and for inhibiting proliferation of cells (especially cancer cells)  
CC in vitro. The present sequence is an antisense oligonucleotide against  
CC HIF1alpha identified in the exemplification of the invention  
XX  
SQ Sequence 16 BP; 4 A; 4 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 73 CAAAAGAGTGTGCTGCC 88  
Db 1 CGAAGAGAGTGTGCTGCC 16  
RESULT 518  
ABZ95580  
ID ABZ95580 standard; DNA; 16 BP.

XX AC AB295580;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human inducible nitric oxide synthase antisense fragment no.1444.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
XX  
XX Homo sapiens.  
XX OS  
XX PN MO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX PS Disclosure; SEQ ID NO 10822; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an  
XX antiinflammatory steroid in a subject, for reducing or depleting levels  
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 12.8; DB 1; Length 16;  
XX Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 537 CTTCTTCCATCGCC 552  
Db | ||||| |||||  
1 CTTCTTCCCGCTCC 16

XX AC AB295535;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human endothelial nitric oxide synthase antisense fragment no.1399.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
XX  
XX Homo sapiens.  
XX OS  
XX PN MO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX PS Disclosure; SEQ ID NO 10777; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an  
XX antiinflammatory steroid in a subject, for reducing or depleting levels  
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 12.8; DB 1; Length 16;  
XX Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 636 GTGAGCCAGCCACC 651  
Db | ||||| |||||  
16 GCGAGCCAGCCAGCC 1

RESULT 519  
AB295535/C  
ID AB295535 standard; DNA; 16 BP.

RESULT 520  
AB295581  
ID AB295581 standard; DNA; 16 BP.



XX	ABZ95581;
AC	17-OCT-2003 (first entry)
DT	
XX	
DE	Human inducible nitric oxide synthase antisense fragment no.1445.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
KM	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	antichemetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KX	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX	lung inflammation; respiratory disease; ds.
OS	Homo sapiens.
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX	Miller S, Tang L, Shahabuddin S;
DR	WPI, 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	disclosure; SEQ ID NO 10823; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SO	Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
QY	Query March 0.7%; Score 12.8; DB 1; Length 16;
DG	Best Local Similarity 87.5%; Pred. No. 3.3e+02;
MATCHES	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	537 CTTCTTTCATCGGC 552       
DB	1 CTTCTTTCGGGTGCC 16 
RESULT 521	
ABD19740	
ID ABD19740 standard; DNA; 16 BP.	

XX AB019740;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
DE Human inducible nitric oxide synthase DNA fragment 1445.  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; antiallergic; antiinflammatory; antialstatic;  
XX analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; de.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200285309-A2.  
PN  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX  
XX 24-APR-2001; 2001US-0266036P.  
PR  
XX  
XX (EPIC-) EPIGENESIS PHARM INC.  
PA  
XX  
XX Myce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S,  
PI  
XX  
XX WPI; 2003-093058/08.  
DR  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing, less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX  
XX Claim 15; SEQ ID NO 10823; 763pp; English.  
PS  
XX  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC bronchoconstriction, respiratory tract inflammation, (A) or (A) receptors,  
CC reducing adenosine sensitivity, levels of adenosine. The  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antistatic,  
CC analgesic, hypotensive, immunosuppressive and cyostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction and/or lung  
CC inflammation, condition such as pulmonary vasoconstriction,  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertransformation, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidine present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;



Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 537 CTTCTTCCCATGCC 552  
1 CTTCTTCCCATGCC 16

Db

RESULT 522  
ABD19685/c  
ID ABD19685 standard; DNA; 16 BP.  
XX  
XX AC ABD19685;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
XX Human endothelial nitric oxide synthase fragment 1399.  
DE  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KM analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;  
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KM pulmonary transplantation rejection; ds.  
XX  
XX Homo sapiens.  
OS  
XX MO200285309-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIC-) EPIGENESIS PHARM INC.  
PA  
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI: 2003-093058/08.  
DR  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 10777; 763bp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
XX Sequence 16 BP; 0 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 636 GTCAGCCAGCCACC 651  
16 GGCAGCCAGCCAGCCACC 1

Db

RESULT 523  
ABD19739  
ID ABD19739 standard; DNA; 16 BP.  
XX  
XX AC ABD19739;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
XX Human inducible nitric oxide synthase DNA fragment 1444.  
DE  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KM analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;  
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KM pulmonary transplantation rejection; ds.  
XX  
XX Homo sapiens.  
OS  
XX MO200285309-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIC-) EPIGENESIS PHARM INC.  
PA  
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI: 2003-093058/08.  
DR  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 10822; 763bp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cyostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or surfactant hypoproduction are associated  
CC inflammation allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infectious, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX Sequence 16 BP; 0 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 537 CTCTCTTCCATGCGC 552  
Db 1 CTCTCTTCCGCTCTCC 16

RESULT 524  
ADK82289/c  
ID ADK82289 standard; DNA; 16 BP.

XX ADK82289;

AC 03-JUN-2004 (first entry)

XX Nucleic acid analysis method associated probe seqid 66.

XX nucleic acid analysis; hepatitis C virus;  
XX non-contiguous single-stranded region; NCSR; cleavage structure;  
XX clinical; diagnostic; microorganism detection;  
XX microorganism identification; probe; ss.

XX Synthetic.

XX US6709815-B1.

XX 23-MAR-2004.

XX 18-JUL-2000; 2000US-00402618.

XX 05-MAY-1997; 97US-00851568.

XX 19-SEP-1997; 97US-00934097.

XX 03-MAR-1998; 98US-00034205.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

XX Anderson TA, Dahlberg JE;

XX Analyzing nucleic acids, comprises mixing target nucleic acid such as

XX hepatitis C virus nucleic acid, bridging oligonucleotide, second

XX oligonucleotide and cleavage agent to form cleavage structure.

XX Example 8; SEQ ID NO 66; 143bp; English.

CC The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a probe associated  
CC with the nucleic acid analysis method of the invention.

XX Sequence 16 BP; 3 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451  
Db 16 CCACAGGCGCTTGGC 1

RESULT 525  
AD015394/c  
ID AD015394 standard; DNA; 16 BP.

XX AD015394;

XX 01-JUL-2004 (first entry)

XX Glutathione S-transferase omega 2 (GSTO2) primer/probe #16.

XX Alzheimer's disease; Parkinson's disease; chromosome 10q24.32; D4S1652;  
XX D10S1239; D10S1237; D1S2134; D8S1128; D8S373; D1S200; D5S1462; D5S1453;  
XX D6S2439; D6S2427; D6S1017; D1S800; D1S8285; D17S1303; D18S877;  
XX D20S851; D20S604; D2S6883; glutathione-S-transferase omega-1; GSTO1;  
XX glutathione-S-transferase omega-2; GSTO2; Alzheimer's disease;  
XX Parkinson's disease; primer; probe; ss.

XX Homo sapiens.

XX US2004014109-A1.

XX 22-JAN-2004.

XX 23-MAY-2003; 2003US-00444347.

XX 23-MAY-2002; 2002US-0382880P.

XX 16-JUL-2002; 2002US-0396223P.

XX 25-NOV-2002; 2002US-0428876P.

XX (PERI/) PERICAK-VANCE M A.

XX (VANC/) VANCE J M.

XX (HAIN/) HAINES J L.

XX (GILB/) GILBERT J.

XX (LITY/) LI Y.

XX Perleak-Vance MA, Vance JM, Haines JL, Gilbert J, Li Y;

XX MPI; 2004-121564/12.

XX Screening or diagnosing a subject for Alzheimer's disease and/or

XX Parkinson's disease, comprises detecting the presence or absence of

XX markers, genes or enzymes linked to Alzheimer's disease and/or

XX Parkinson's disease.

XX Example; Page 12; 20pp; English.

XX The invention describes a method of screening or diagnosing a subject for

XX Alzheimer's disease and/or Parkinson's disease comprising detecting the

XX presence or absence of at least one or more markers, genes or enzymes

XX linked to Alzheimer's disease and/or Parkinson's disease. The marker,



Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 CTCTGCTGCGCTTCC 700  
|||||  
1 CTCTGCTGCGCGCTTC 16

## RESULT 528

AD062809  
ID AD062809 standard; DNA; 16 BP.

AC AD062809;

DT 07-OCT-2004 (first entry)

DE Aptamer-related DNA sequence #2.

KW aptamer; authentication; ss.

XX Synthetic.

OS JP004196753-A.

PN 15-JUL-2004.

PD 20-DEC-2002; 2002JP-00370729.

PF 20-DEC-2002; 2002JP-00370729.

PR 20-DEC-2002; 2002JP-00370729.

XX (KANF) KANEKA CORP.

XX WPI; 2004-503927/48.

DR Novel nucleic acid having a stable structure, useful for authentication

XX for conforming organisms, person or goods.

PT Example 2; SEQ ID NO 4; 9pp; Japanese.

XX The invention comprises an aptamer (e.g. DNA aptamer, peptide nucleic

CC acid or 2 type DNA). The aptamer of the invention is useful for

CC authentication, for producing a plasmid that is transduced into a

CC microorganism, or for recognising a compound (e.g. sulfo rhodamine B),

CC which in turn is useful for authentication. The present DNA sequence was

CC used in an example of the invention.

XX Sequence 16 BP; 0 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

SEQ Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 685 CTCTGCTGCGCTTCC 700  
|||||  
1 CTCTGCTGCGCGCTTC 16

DB 18-NOV-2004 (first entry)

DE Oligonucleotide of the invention SEQ ID NO:1910.

XX ss; cell proliferative disorder; breast; methylation; cyrostatic;

KW gene therapy; single nucleotide polymorphism; SNP.

XX Unidentified.

PN WO2004035803-A2.

XX 29-APR-2004.

PD 01-OCT-2003; 2003WO-EP010881.

PF 01-OCT-2003; 2003WO-EP010881.

PR 01-OCT-2002; 2002DE-01045779.

PR 07-JAN-2003; 2003DE-01000096.

PR 17-APR-2003; 2003DE-01017955.

XX (EPIG-) EPIGENOMICS AG.

PA Peckens J, Harbeck N, Koenig T, Maier S, Martens J, Model F,

PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;

XX WPI; 2004-348468/32.

DR Predicting responsiveness of a subject with breast cell proliferative

XX disorder, useful for treating or differentiating breast cell

PT proliferative disorders comprises analyzing methylation pattern of a

PT genomic DNA from the subject.

XX Disclosure; SEQ ID NO 1910; 104pp; English.

PS The invention relates to a novel method for predicting the responsiveness

CC of a subject with a cell proliferative disorder of the breast tissues to

CC a therapy comprising analysing the methylation pattern of a target

CC nucleic acid by contacting at least one of the target nucleic acids in a

CC biological sample obtained from the subject prior to or during treatment.

CC The method of the invention has cyrostatic activity, and may have a use

CC in gene therapy. The set of oligonucleotides comprising at least two of

CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The

CC methods, nucleic acid, oligonucleotide, and kit are useful for the

CC treatment, characterisation, classification and/or differentiation, of

CC breast cell proliferative disorders. The method is also useful for

CC predicting the responsiveness of a subject with a cell proliferative

CC disorder of the breast tissues to a therapy. The present sequence is used

CC in the exemplification of the invention.

XX Sequence 16 BP; 7 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

SEQ Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1001 TCCACATCTTCTCTCT 1016  
|||||  
16 TCCACTTCTTCATCCT 1

DB 16 TCCACTTCTTCATCCT 1

RESULT 530  
ADY03782/C  
ID ADY03782 standard; DNA; 16 BP.

AC ADY03782;

DT 05-MAY-2005 (first entry)

DE Hepatitis C virus-specific antisense oligo - SEQ ID 44.

XX viral infections; virus; hepatitis C virus infection; hepatitis E virus infection;

KW coronavirus infection; flavivirus infection; hepatitis E virus infection;

KW gene silencing; antisense oligonucleotide; ss.

XX Hepatitis C virus.

OS WO2005013905-A2.

PN 17-FEB-2005.

XX 06-AUG-2004; 2004WO-US025401.

PF Unidentified.

PR 07-AUG-2003; 2003US-0493990P.  
XX  
PA (AVIB-) AVI BIOPHARMA INC.  
XX  
PI Iversen PL;  
XX  
DR WPI; 2005-172937/18.  
XX  
PT New oligonucleotide analog, compound having a single-stranded, positive-sense RNA genome, useful for inhibiting replication in mammalian host cells of an RNA virus.  
PT  
PS Example 1; SEQ ID NO 44; 81bp; English.  
XX  
CC The invention comprises oligonucleotides which are designed to inhibit the replication of an RNA virus in a mammalian cell. The oligonucleotides of the invention are useful for the treatment of Picornaviridae, CC  
CC Caliciviridae, Togaviridae, Coronaviridae, Flaviviridae and Hepatitis B virus infection. The present DNA sequence represents an oligonucleotide of the invention which is designed to inhibit the replication of a virus. CC  
XX  
SQ Sequence 16 BP; 2 A; 7 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1076 CCATCANGTGCTGCGC 1091  
Db 16 CCATCAGGGGCTGCGC 1  
RESULT 531  
AEA50577  
ID AEA50577 standard; DNA; 16 BP.  
XX  
AC AEA50577;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE Human nucleic acid PCR primer #200.  
XX  
XX SNP detection; cardiovascular disease; myocardial infarction;  
KM cerebrovascular ischemia; atherosclerosis; cerebrovascular disease;  
KM unstable angina; coronary artery disease; congenital heart defect;  
KM congestive heart failure; PCR; primer; ss; cardiovascular-gen.;  
KM cerebroprotective; cardiac; vasotropic; antiarteriosclerotic;  
KM antianginal.  
XX  
OS Homo sapiens.  
XX  
PN WO2005056837-A2.  
XX  
PD 23-JUN-2005.  
XX  
PF 24-NOV-2004; 2004WO-US039576.  
XX  
PR 26-NOV-2003; 2003US-0524882P.  
PR 06-MAY-2004; 2004US-0568219P.  
PA (APPL-) APPLERA CORP.  
PI Gargill M, Jakoubova O, Devlin JJ, Tsuchihashi Z, Shaw P,  
PI Ploughman LM, Zerba KE, Koustubh R, Kirchgessner T;  
XX  
DR WPI; 2005-467032/47.  
XX  
PT Novel isolated nucleic acid molecule, useful for identifying individual who has altered risk for developing cardiovascular disorder or altered likelihood of responding to statin treatment.  
PT  
PS Claim 21; SEQ ID NO 85290; 200pp; English.  
XX

CC The invention relates to an isolated nucleic acid molecule comprising 8 CC  
CC or more contiguous nucleotides, where one of the nucleotides is a single CC  
CC nucleotide polymorphism (SNP). The invention also relates to a method of CC  
CC identifying an individual who has an altered risk for developing a CC  
CC cardiovascular disease or an altered likelihood of responding to statin CC  
CC treatment, involving detecting a SNP in the individual's nucleic acids, CC  
CC where the presence of the SNP is correlated with an altered risk for CC  
CC developing a cardiovascular disease or responding to statin treatment, CC  
CC and a method of treating a cardiovascular disease in an individual CC  
CC involving administering to the individual an effective amount of statin CC  
CC based on the individual's likelihood of responding to statin treatment as CC  
CC predicted by the alleles present at one or more SNP sites. The nucleic CC  
CC acids and the related polypeptides are useful for identifying an agent CC  
CC useful for therapeutically or prophylactically treating cardiovascular CC  
CC diseases which involves contacting a nucleic acid with a candidate agent CC  
CC under conditions suitable to allow formation of a binding complex between CC  
CC the nucleic acid and the candidate agent and detecting formation of the CC  
CC binding complex, where the presence of the complex identifies the agent. CC  
CC The cardiovascular disease is an acute coronary event chosen from CC  
CC myocardial infarction, stroke, atherosclerosis, cerebrovascular disease, CC  
CC unstable angina, coronary artery disease, congenital heart defect and CC  
CC congestive heart failure. This sequence represents a PCR primer used in CC  
CC genotyping of nucleic acid molecules of the invention.  
XX  
SQ Sequence 16 BP; 1 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 673 TGGTCCCTGGCTCC 688  
Db 1 TGGTACTGCTCTCC 16  
RESULT 532  
AEB52878  
ID AEB52878 standard; DNA; 16 BP.  
XX  
AC AEB52878;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human leukocyte antigen-A DNA probe, SEQ ID 498.  
XX  
XX human leukocyte antigen; HLA; probe; transplant rejection; cancer;  
KM cytosolic; diabetes; antidiabetic; multifactorial genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2005185176-A.  
XX  
PD 14-JUL-2005.  
XX  
PF 25-DEC-2003; 2003JP-00430558.  
XX  
PR 25-DEC-2003; 2003JP-00430558.  
PA (CANO ) CANON KK.  
PI Tsukada M;  
XX  
DR WPI; 2005-515775/53.  
XX  
PT Probe set for identifying human leukocyte antigen (HLA)-DP allele in PT  
PT patients with organ transplant, cancer or diabetes enabling tailored PT  
PT medical treatment.  
XX  
PS Claim 2; SEQ ID NO 498; 90pp; Japanese.  
XX  
XX The invention relates to a novel probe set for identifying a human CC  
CC leukocyte antigen-A (HLA-A) allele in a test substance. The probe set CC  
CC comprises several probes chosen from the fully defined nucleic acid

CC sequences (SEQ ID No: 251-431 and SEQ ID No: 455-631) as given in the  
CC specification. The novel probe set can identify HLA-A alleles in patients  
CC with organ transplants, cancer, diabetes and other multiple-factor  
CC diseases, and enables tailored medical treatment to individual patients.  
CC This oligo sequence represents a human leukocyte antigen-A DNA probe of  
CC the invention.  
CC  
CC  
SQ Sequence 16 BP; 3 A; 4 C; 8 G; 1 T; 0 U; 0 Other;  
XX  
XX  
Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1299 GGGCCACGAGGAGGAG 1314  
DB 1 GGGCCATGAGGCGAG 16  
GGCCATGAGGCGAG  
RESULT 533  
ABF46499  
ID ABF46499 standard; DNA; 13 BP.  
XX  
XX ABF46499;  
AC  
XX  
XX 21-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 146496 for detecting SNP TSC0036939.  
DE  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 146496; 29bp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
CC  
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 1 Other;  
XX  
XX  
Query Match 0.7%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 2.2e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX

QY 238 GACCTCTCCCCA 250  
DB 1 RACCTCTCCCCA 13  
GACCTCTCCCCA  
RESULT 534  
ABH39848/C  
ID ABH39848 standard; DNA; 13 BP.  
XX  
XX ABH39848;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide SEQ ID NO 239825 for detecting SNP TSC0058496.  
DE  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX  
XX Claim 1; SEQ ID NO 239825; 29bp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
CC  
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;  
XX  
XX  
Query Match 0.7%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 2.2e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1107 GTACACCCCATC 1119  
DB 13 RTACACCCCATC 1  
GTACACCCCATC  
RESULT 535  
ABH39849  
ID ABH39849 standard; DNA; 13 BP.  
XX  
XX ABH39849;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX

DE Oligonucleotide SEQ ID NO 239826 for detecting SNP TSC0058496.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 239826; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;  
XX  
XX Query Match 0.7%; Score 12.6; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 2.2e+02;  
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1107 GTACACCCCATC 1119  
DB 1 RTACACCCCATC 13  
RESULT 536  
ABF46498/c  
ID ABF46498 standard; DNA; 13 BP.  
XX  
XX ABR46498;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 146495 for detecting SNP TSC0036939.  
DE  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX

XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 146495; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 1 Other;  
XX  
XX Query Match 0.7%; Score 12.6; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 2.2e+02;  
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 238 GACCTCTCCCAA 250  
DB 13 RACCTCTCCCAA 1  
RESULT 537  
ABA98358  
ID ABA98358 standard; DNA; 15 BP.  
XX  
XX ABA98358;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX SCN2B gene polymorphisms ASO primer #2.  
DE  
XX  
XX Human; sodium channel voltage gated type 2 beta polypeptide; SCN2B; ds;  
XX gene therapy; neuroprotective; demyelinating disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200179547-A1.  
XX  
XX 25-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US010743.  
XX  
XX 13-APR-2000; 2000US-0196597P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Chew A, Choi JY, Koshy B;  
XX  
XX WPI; 2002-075072/10.  
XX  
XX New polynucleotide containing polymorphisms in the human sodium channel  
XX voltage gated type 2 beta polypeptide (SCN2B) gene, for developing drugs  
XX for treating demyelinating diseases.  
XX  
XX Claim 15; Page 13; 63pp; English.

XX This invention relates to an isolated polynucleotide which is a  
CC polymorphic variant of a reference sequence for sodium channel voltage  
CC gated type 2 beta polypeptide (SCN2B) gene. The methods have  
CC applicability in developing diagnostic tests and therapeutic treatments  
CC for demyelinating diseases. The protein is useful for studying the  
CC expression and function of SCN2B and expressing SCN2B protein for use in  
CC screening for candidate drugs to treat diseases related to SCN2B  
CC activity. The polymorphism and haplotype data are useful for validating  
CC whether SCN2B is a suitable target for drugs to treat demyelinating  
CC diseases, screening for such drugs and reducing bias in clinical trials.  
CC The haplotyping method is useful to validate SCN2B as a candidate target  
CC for treating a specific condition or disease predicted to be associated  
CC with SCN2B activity. A recombinant non-human organism transformed or  
CC transfected with the polypeptide is useful for studying expression of the  
CC SCN2B isogenes in vivo, for in vivo screening and testing of drugs  
CC against SCN2B protein and for testing the efficacy of therapeutic agents  
CC and compounds for demyelinating diseases in a biological system. This  
CC sequence is used during the detection of polymorphisms of the SCN2B gene

XX SQ Sequence 15 BP; 2 A; 3 C; 8 G; 1 T; 0 U; 1 Other;  
Query Match 0.7%; Score 12.6; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 3.1e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 GGGCAGCGCGGCA 29  
DB 2 GGGCAGCGCGGCA 14

RESULT 538  
ABK27519/C  
ID ABK27519 standard; DNA; 15 BP.

XX AC ABK27519;

XX DT 09-APR-2002 (first entry)

XX DE Human CTLA4 gene allele-specific oligonucleotide probe #2.

XX KW Human; cytotoxic T-lymphocyte-associated protein 4; CTLA4; haplotyping;  
KW haplotype pair; single nucleotide polymorphism; autoimmune disorder; ss;  
KW genotyping; gene therapy; drug screening; antisense gene therapy; primer;  
KW immunosuppressive; sequencing; PCR; probe.

XX OS Homo sapiens.

XX PN WO200190122-A2.

XX PD 29-NOV-2001.

XX PF 23-MAY-2001; 2001WO-US016905.

XX PR 23-MAY-2000; 2000US-0206353P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Chew A, Choi JY, Messer C;

XX DR WPI, 2002-089914/12.

XX PT New genetic variants of human cytotoxic T-lymphocyte-associated protein  
XX 4, CTLA4 gene for studying expression, function of the gene and  
XX PT expressing CTLA4 protein useful in identifying drugs to treat autoimmune  
XX disorder.

XX PS Claim 17; Page 12; 62pp; English.

XX CC The invention relates to single nucleotide polymorphisms in the gene  
XX encoding the human cytotoxic T-lymphocyte-associated protein 4 or CTLA4  
XX protein. A method for haplotyping the CTLA4 gene in an individual  
XX comprises identifying the nucleotide at one or more polymorphic sites and

CC determining whether one of the copies of the gene is defined by one of  
CC the CTLA4 haplotypes given in the specification or whether both copies  
CC are defined by a haplotype pair. This method is useful in genotyping,  
CC whereby all possible haplotype pairs can be assigned to specific  
CC genotypes. An association between a trait and a haplotype or haplotype  
CC pair of the CTLA4 gene can be identified by comparing the frequency of  
CC the haplotype or haplotype pair in a population exhibiting the trait with  
CC the frequency of the haplotype or haplotype pair in a reference  
CC population, where a higher haplotype frequency in the trait population  
CC indicates the trait is associated with the haplotype or haplotype pair.  
CC CTLA4 and its corresponding DNA are used for studying the expression and  
CC function of CTLA4, for use in screening for candidate drugs to treat  
CC diseases related to CTLA4 activity, such as autoimmune disorders. The  
CC sequences are also useful for studying the effect of variation on the  
CC biological activity of CTLA4 as well as on the binding affinity of  
CC candidate drugs targeting CTLA4. Sequences ABK27518-ABK27549 represent  
CC allele-specific oligonucleotide probes, sequencing primers and PCR  
CC primers used to detect CTLA4 gene polymorphisms

XX SQ Sequence 15 BP; 4 A; 3 C; 5 G; 2 T; 0 U; 1 Other;  
Query Match 0.7%; Score 12.6; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 3.1e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1464 CACTGCTTTGAC 1476  
DB 15 CACTGCTTTGAC 3

RESULT 539  
ABK70728  
ID ABK70728 standard; DNA; 15 BP.

XX AC ABK70728;

XX DT 15-JUL-2002 (first entry)

XX DE ASO primer #9 to detect human SCY8 gene polymorphisms.

XX KW Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;  
KW small inducible cytokine subfamily A member 8; SCY8; anti-HIV;  
KW haplotyping; genotyping; inflammatory disease; HIV infection; ASO; ss;  
KW human immunodeficiency virus; allele-specific oligonucleotide; primer.

XX OS Homo sapiens.

XX PN WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US029332.

XX PR 15-SEP-2000; 2000US-0232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX DR WPI, 2002-371973/40.

XX PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),  
XX Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving  
XX efficiency and reliability in drug development for treating diseases.

XX PS Claim 16; Page 13; 84pp; English.

XX CC The present invention relates to novel single nucleotide polymorphisms  
XX (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),  
XX member 8 (monocyte chemotactic protein) (SCY8) gene located on  
XX chromosome 17, and methods for haplotyping and/or genotyping the SCY8  
XX gene. The methods of the invention make use of allele-specific  
XX oligonucleotides (ASOs) as probes and primers and/or primer-extension



CC oligonucleotides for detecting the SCY8 gene polymorphisms. The  
CC polynucleotides and screened compounds are useful for the treatment of  
CC diseases associated with SCY8A activity, such as inflammatory diseases  
CC and human immunodeficiency virus (HIV) infection. ABK70720-ABK70743  
CC represent ASO primers for detecting human SCY8A gene polymorphisms  
XX

SO Sequence 15 BP; 3 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 3.1e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 726 GACCATGCCACG 738  
DB 2 GACCATGCCACG 14

RESULT 540  
AAH99963  
ID AAH99963 standard; DNA; 15 BP.  
XX  
AC AAH99963;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE ASO primer for detecting CXCR4 polymorphisms # 5.  
XX  
XX Human Chemokine receptor 4; CXCR4; human; ss; chromosome 2q21; HIV-1;  
KM PCR primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200179229-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 13-APR-2001; 2001WO-US012268.  
XX  
PR 13-APR-2000; 2000US-0197025P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Chew A, Choi JY, Koshy B;  
XX  
XX WPI; 2002-075062/10.  
XX  
PT Isolated human chemokine receptor 4 polynucleotide, useful for studying  
PT expression and function of chemokine receptor 4 and for treating human  
PT immunodeficiency virus-1.  
XX  
XX Disclosure; Page 13; 54pp; English.  
PS  
XX The invention relates to an isolated chemokine receptor 4 (CXCR4)  
CC polynucleotide which is useful for studying expression and function of  
CC chemokine receptor 4 and for the treatment of viruses, including HIV-1.  
CC Methods associated with chemokine receptor 4 are useful for improving the  
CC efficacy and reliability of several steps in the discovery and  
CC development of drugs for treating diseases associated with CXCR4  
CC activity, e.g., human immunodeficiency virus-1 infection. They can  
CC validate CXCR4 as a candidate agent for treating a specific condition or  
CC disease predicted to be associated with CXCR4 activity, and in the design  
CC of clinical trials of candidate drugs for treating a specific condition  
CC or disease predicted to be associated with CXCR4 activity. CXCR4  
CC polynucleotides are useful for therapeutic purposes such as to treat HIV-  
CC 1 infection and also are useful for studying expression of the CXCR4  
CC isogenes in vivo. This sequence represents a ASO primer used to detect  
CC CXCR4 gene polymorphisms  
XX  
XX  
SO Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 3.1e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1068 CTACCTGCCATC 1080  
DB 2 CTACCTGCCATC 14

RESULT 541  
AAQ30786  
ID AAQ30786 standard; DNA; 20 BP.  
XX  
AC AAQ30786;  
XX  
DT 25-MAR-2003 (revised)  
DT 22-MAR-1993 (first entry)  
XX  
DE PCR primer hsp35a2 to amplify human NK1R 5' N-terminal region.  
XX  
XX Neurokinin-1 receptor short form; arthritis; Substance P;  
KM polymerase chain reaction; rat NK1R; ss.  
XX  
OS Synthetic.  
XX  
PN EP514207-A2.  
XX  
PD 19-NOV-1992.  
XX  
PF 15-MAY-1992; 92BP-00304432.  
XX  
PR 17-MAY-1991; 91US-00701930.  
PR 17-MAY-1991; 91US-00701935.  
PR 17-MAY-1991; 91US-00701937.  
XX  
PA (MERI) MERCK & CO INC.  
XX  
PI Strader CD, Fong TM;  
XX  
XX WPI; 1992-384034/47.  
XX  
XX New human neurokinin-1 receptor short form protein - useful for  
PT identifying and determining substance P antagonists in arthritic  
PT patients.  
XX  
PS Example 1; Page 8; 36pp; English.  
XX  
XX The core region of human NK1R 5' was isolated by PCR and sequenced (see  
CC AAQ30774-Q30778). The antisense primers hsp35a5, hsp35a1, hsp35a2,  
CC hsp36a1 and hsp36a2 (AAQ30784-Q30788) were synthesised based on the human  
CC core sequence. Human glioblastoma mRNA and each of these primers were  
CC used in first strand cDNA synthesis to produce the template for a primary  
CC PCR amplification. Primer hsp35a5 was used with 2 rat sense primers hsp31  
CC and hsp31h (AAQ30779 and AAQ30780) for the primary amplification. The PCR  
CC product was then used as template for secondary PCR with the same rat  
CC primers and the human antisense primer hsp35a4 (AAQ30783). The secondary  
CC PCR product was the template for tertiary PCR amplification, again using  
CC the same rat sense primers but with human antisense primer hsp31a1  
CC (AAQ30782). The amplified DNA fragment hybridised to hsp35a2 (AAQ30781),  
CC indicating it is not a non-specific by-product. The DNA was sequenced and  
CC found to encode the human NK1R 5' N-terminal region and also contains a  
CC 5' UTR. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SO Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 861 CGTAGTGGATCAGACTA 879  
DB 1 CATAGTGTGATTCCTCACTA 19

RESULT 542  
AAQ29675

ID AAQ29675 standard; DNA; 20 BP.  
XX  
XX AAQ29675;  
AC  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAR-1993 (first entry)  
XX  
XX hepr5a2 primer 793-774.  
DE  
XX Human; neurokinin-1 receptor; NK1R; membrane receptor; substance P;  
XX neurotransmitter; polymerase chain reaction; PCR; rat NK1R; primer;  
XX amplify; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP510878-A1.  
XX  
XX 28-OCT-1992.  
XX  
XX 16-APR-1992; 92EP-00303457.  
XX  
XX 25-APR-1991; 91US-00691197.  
XX 25-APR-1991; 91US-00691198.  
XX 25-APR-1991; 91US-00691200.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Fong TM, Strader CD;  
PI  
XX WPI; 1992-359073/44.  
XX  
XX New recombinant human neurokinin-1 receptor - used to detect and evaluate  
PT substances that bind to substance P receptor, and to determine substance  
PT P in body fluid of arthritis patients.  
XX  
XX Disclosure; Page 8; 35pp; English.  
XX  
XX The sequences given in AAQ29670-82, AAQ29783 and AAQ29746-48 are primers  
XX CC which were used in the isolation of fragments of the human neurokinin-1  
XX CC receptor (NK1R) cDNA. Human NK1R is a membrane receptor for the  
XX CC neurotransmitter substance P. The primers were designed using regions of  
XX CC the human NK1R cDNA and also regions of the rat NK1R which were thought  
XX CC to be similar to human regions. Part of the human cDNA sequence was  
XX CC derived by amplification using these primers. The remaining part of human  
XX CC NK1R cDNA was obtained from a human cDNA library utilising portions of  
XX CC PCR generated fragments as probes. See also AAQ29749. (Updated on 25-MAR-  
XX CC 2003 to correct PN field.)  
XX  
XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 861 CGTAGTGGGATACACCTA 879  
DB 1 CATAGTGTGATTCCTACTA 19  
RESULT 543  
ABK63893/c  
ID ABK63893 standard; DNA; 20 BP.  
XX  
XX ABK63893;  
AC  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX  
XX Neurokinin 1 receptor (NK-1) antisense oligonucleotide #38.  
DE  
XX  
XX Human; neurokinin receptor-1; NK-1; dermatological disorder;  
XX immune disorder; autoimmune disorder; cardiovascular disorder;  
XX vascular disorder; airway disorder; neuropathic disorder; pain;  
XX psychiatric disorder; central nervous system disorder; inflammation;

KW respiratory condition; ophthalmic condition; intestinal condition;  
KW demyelinating disease; small cell lung cancer; depression;  
KW hypersensitivity disorder; allergy; vasospastic disease; alcoholism;  
KW neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;  
KW neuro-pathological disorder; stress; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200213799-A2.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-1B001510.  
XX  
XX 18-AUG-2000; 2000US-0226086P.  
XX  
XX (UYMC-) UNITV MCGILL.  
XX  
XX Henry JL, Cahill CM, Yashpal K;  
PI  
XX WPI; 2002-241935/29.  
XX  
XX  
XX Treating pathological condition involving neurokinin receptor-1, e.g.  
PT pain or inflammation, by administering oligonucleotide or a non-  
PT nucleotide disruptor compound which modulate NK-1 receptor biosynthetic  
PT pathway.  
XX  
XX Example 18; Page 65; 100pp; English.  
XX  
XX The invention relates to a method of treating a pathological condition  
XX CC characterised partially by involvement of neurokinin receptor-1 (NK-1)  
XX CC receptor, especially treating, attenuating or preventing pain or  
XX CC inflammatory condition. The method comprises administering to a mammal, a  
XX CC compound chosen from an oligonucleotide, its analogue, and a disruptor  
XX CC which interferes with function or production of NK-1 receptors. The  
XX CC method is useful for treating a pathological condition characterised by  
XX CC involvement of NK-1 receptor such as dermatological, immune, autoimmune,  
XX CC cardiovascular, vascular disorders (e.g. migraine), airway, neuropathic,  
XX CC psychiatric and central nervous system disorders (e.g. anxiety,  
XX CC psychosis, schizophrenia), gut inflammation, arthritis, and central or  
XX CC peripheral aspects of chronic or acute pain, and for treating,  
XX CC attenuating or preventing pain or inflammation such as peripheral,  
XX CC chronic, acute pain or inflammation, neuropathic pain, inflammation or  
XX CC pain relating to psychiatric disorders and central nervous system  
XX CC disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia  
XX CC in a mammal, in particular human. NK-1 receptor related disorders,  
XX CC diseases, or pathological conditions treatable by this method include  
XX CC respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic  
XX CC conditions (e.g. conjunctivitis), cutaneous/dermatological conditions  
XX CC (allergic dermatitis), intestinal conditions (stroke), chronic  
XX CC Crohn's disease), cardiovascular conditions (stroke), chronic  
XX CC gastrointestinal tract inflammation, and inflammatory diseases such as  
XX CC inflammatory bowel diseases. Other disorders and diseases include  
XX CC cardiovascular pathologies including stroke, chronic inflammatory  
XX CC diseases such as rheumatoid arthritis, demyelinating diseases such as  
XX CC multiple sclerosis, small cell lung cancer, depression, hypersensitivity  
XX CC disorders such as allergies and poison ivy, vasospastic diseases such as  
XX CC angina, addiction disorders such as alcoholism, neurodegenerative  
XX CC disorders such as acquired immune deficiency syndrome (AIDS) related  
XX CC dementia, epilepsy, Alzheimer's disease, and other neuro-pathological  
XX CC disorders such as peripheral neuropathy, oedema, stress related and  
XX CC somatic disorders, and osteoarthritis. Antisense oligonucleotides  
XX CC effectively treat chronic conditions and other pathological states  
XX CC without the co-administration of substance P, and reduce the number of  
XX CC activated receptors while not reducing the number of quiescent NK-1  
XX CC receptors. Receptors not chronically stimulated are less affected,  
XX CC reducing side effects of treatment. ABK63834-ABK63906 represent NK-1  
XX CC receptor coding sequences and oligonucleotides of the invention  
XX  
XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;

CC	inflammatory bowel diseases. Other disorders and diseases include
CC	cardiovascular pathologies including stroke, chronic inflammatory
CC	diseases such as rheumatoid arthritis, demyelinating diseases such as
CC	multiple sclerosis, small cell lung cancer, depression, hypersensitivity
CC	disorders such as allergies and poison ivy, vasospastic diseases such as
CC	angina, addiction disorders such as alcoholism, neurodegenerative
CC	disorders such as acquired immune deficiency syndrome (AIDS) related
CC	dementia, epilepsy, Alzheimer's disease, and other neuro-pathological
CC	disorders such as peripheral neuropathy, edema, stress related and
CC	somatic disorders, and osteoarthritis. Antisense oligonucleotides
CC	effectively treat chronic conditions and other pathological states
CC	without the co-administration of substance P, and reduce the number of
CC	activated receptors while not reducing the number of quiescent NK-1
CC	receptors. Receptors not chronically stimulated are less affected,
CC	reducing side effects of treatment. ABR63894-ABR63906 represent NK-1
CC	receptor coding sequences and oligonucleotides of the invention
XX	
SQ	Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	0.7%; Score 12.6; DB 1; Length 20;
Best Local Similarity	78.9%; Pred. No. 5,5e+02;
Matches 15; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
DY	861 CGTAGTGGGAATCACCCTTA 879                     Db 20 CATAGTGTAATCCCACCTTA 2
RESULT 545	
ABK63855	
ID	ABK63855 standard; DNA; 20 BP.
XX	
AC	ABK63855;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	Neurokinin 1 receptor (NK-1) sense oligonucleotide #6.
XX	
KW	Human; neurokinin receptor-1; NK-1; dermatological disorder;
KW	immune disorder; autoimmune disorder; cardiovascular disorder;
KW	vascular disorder; airway disorder; neuromathic disorder; pain;
KW	psychiatric disorder; central nervous system disorder; inflammation;
KM	respiratory condition; ophthalmic condition; intestinal condition;
KM	demyelinating disease; small cell lung cancer; depression;
KM	hypersensitivity disorder; allergy; vasospastic disease; alcoholism;
KW	neurodegenerative disorder; acquired immune deficiency syndrome; AIDS;
KW	neuro-pathological disorder; stress; antisense; primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200213799-A2.
XX	
PD	21-FEB-2002.
XX	
PP	17-AUG-2001; 2001WO-IBO01510.
XX	
PR	18-AUG-2000; 2000US-0226086P.
XX	
PA	(UYMC-) UNIV MCGILL.
XX	
PI	Henry JL, Cahill CM, Yashpal K;
XX	
DR	WPI; 2002-241835/29.
XX	
PT	Treating pathological condition involving neurokinin receptor-1, e.g.
XX	pain or inflammation, by administering oligonucleotide or a non-
PT	nucleotide disruptor compound which modulate NK-1 receptor biosynthetic
XX	pathway.
XX	
PS	Claim 24; Page 20; 100pp; English.
XX	
CC	The invention relates to a method of treating a pathological condition
CC	characterised partially by involvement of neurokinin receptor-1 (NK-1)
CC	

receptor, especially treating, attenuating or preventing pain or inflammatory condition. The method comprises administering to a mammal, a compound chosen from an oligonucleotide, its analogue, and a disruptor which interferes with function or production of NK-1 receptors. The method is useful for treating a pathological condition characterised by involvement of NK-1 receptor such as dermatological, immune, autoimmune, cardiovascular, vascular disorders (e.g. migraine), allergy, neuropathic, psychiatric and central nervous system disorders (e.g. anxiety, psychosis, schizophrenia), gut inflammation, arthritis, and central or peripheral aspects of chronic or acute pain, and for treating, attenuating or preventing pain or inflammation such as peripheral, chronic, acute pain or inflammation, neuropathic pain, inflammation or pain relating to psychiatric disorders and central nervous system disorders, including hyperalgesia, allodynia, neuralgia and dysesthesia in a mammal, in particular human. NK-1 receptor related disorders, diseases, or pathological conditions treatable by this method include respiratory conditions (e.g. asthma, allergic rhinitis), ophthalmic conditions (e.g. conjunctivitis), cutaneous/dermatological conditions (allergic dermatitis), intestinal conditions (e.g. ulcerative colitis and Crohn's disease), cardiovascular conditions (stroke), chronic gastrointestinal tract inflammation, and inflammatory diseases such as inflammatory bowel diseases. Other disorders and diseases include cardiovascular pathologies including stroke, chronic inflammatory diseases such as rheumatoid arthritis, demyelinating diseases such as multiple sclerosis, small cell lung cancer, depression, hypersensitivity disorders such as allergies and poison ivy, vasospastic diseases such as angina, addition disorders such as alcoholism, neurodegenerative disorders such as acquired immune deficiency syndrome (AIDS) related dementia, epilepsy, Alzheimer's disease, and other neuro-pathological disorders such as peripheral neuropathy, edema, stress related and somatic disorders, and osteoarthritis. Antisense oligonucleotides effectively treat chronic conditions and other pathological states without the co-administration of substance P, and reduce the number of activated receptors while not reducing the number of quiescent NK-1 receptors. Receptors not chronically stimulated are less affected, reducing side effects of treatment. ABK63834-ABK63906 represent NK-1 receptor coding sequences and oligonucleotides of the invention

Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

861 CGTAGTGGGATCAGACTA 879  
1 CATAGTGTGATTCACACTA 19

RESULT 546  
AEE77702/C  
ID AEE77702 standard; DNA; 20 BP.  
AC AEE77702;  
DT 09-FEB-2006 (first entry)  
XX  
XX  
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1323.  
XX  
XX  
KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
XX neuropsychological disorder; dopamine receptor D2; DRD2; ss.  
XX Homo sapiens.  
XX OS  
XX PN WO2005118843-A1.  
XX  
XX PD 15-DEC-2005.  
XX  
XX PF 01-JUN-2005; 2005WO-AU000775.  
XX  
XX PR 01-JUN-2004; 2004AU-00902919.  
XX  
XX PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
WPI; 2006-047555/05.  
Identifying genetic profile associated with a neurological, psychiatric,  
or psychological condition, comprises screening individuals for a  
polymorphism in a genetic locus comprising the dopamine receptor D2  
(DRD2) gene.  
Claim 31; SEQ ID NO 1323; 634bp; English.

The invention relates to a method of identifying a genetic profile associated with a neurological, psychiatric or psychological condition, phenotype or state including a sub-threshold neurological, psychiatric or psychological condition, phenotype or state in an individual, comprising screening individuals for a polymorphism in a genetic locus comprising the dopamine receptor D2 (DRD2) gene. The invention also relates to a genetic mutation providing a genetic marker for a neurological, psychiatric, or psychological condition, state or phenotype in an individual, where the presence of a 957C polymorphism is indicative of a predisposition to developing a neurological, psychiatric or psychological condition, phenotype or state. The compositions and methods are useful for identifying a genetic profile associated with a neurological, psychiatric or psychological condition. The method enables clinicians to make a genetic-based diagnosis and can thereby implement treatment or preventative or symptom-ameliorating protocols to reduce the adverse consequences of the condition. This sequence represents a human dopamine receptor D2 (DRD2) DNA oligonucleotide used in the scope of the invention.

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1047 GAAGAAGTTTATCCAGCAG 1065  
20 GAAGAAGGCGACCCAGCAG 2

RESULT 547  
AEE77704/C  
ID AEE77704 standard; DNA; 20 BP.  
AC AEE77704;  
DT 09-FEB-2006 (first entry)  
XX  
XX  
DE Human dopamine receptor D2 (DRD2) DNA oligonucleotide SEQ ID NO:1325.  
XX  
XX  
KW Diagnosis; therapeutic; neurological disease; psychiatric disorder;  
XX neuropsychological disorder; dopamine receptor D2; DRD2; ss.  
XX Homo sapiens.  
XX OS  
XX PN WO2005118843-A1.  
XX  
XX PD 15-DEC-2005.  
XX  
XX PF 01-JUN-2005; 2005WO-AU000775.  
XX  
XX PR 01-JUN-2004; 2004AU-00902919.  
XX  
XX PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
XX  
XX PI Morris CP, Van Daal A, Swagell CD, Lawford BR, Young RM;  
XX  
XX DR WPI; 2006-047555/05.  
XX  
XX PT Identifying genetic profile associated with a neurological, psychiatric,

PT or psychological condition, comprises screening individuals for a  
PT polymorphism in a genetic locus comprising the dopamine receptor D2  
PT (DRD2) gene.  
PS Claim 31; SEQ ID NO 1325; 634bp; English.  
XX  
XX  
XX The invention relates to a method of identifying a genetic profile  
CC associated with a neurological, psychiatric or psychological condition,  
CC phenotype or state, including a sub-threshold neurological, psychiatric or  
CC psychological condition, phenotype or state in an individual, comprising  
CC screening individuals for a polymorphism in a genetic locus comprising  
CC the dopamine receptor D2 (DRD2) gene. The invention also relates to a  
CC genetic mutation providing a genetic marker for a neurological,  
CC psychiatric, or psychological condition, state or phenotype in an  
CC individual, where the presence of a 957C polymorphism is indicative of a  
CC predisposition to developing a neurological, psychiatric or psychological  
CC condition, phenotype or state. The compositions and methods are useful  
CC for identifying a genetic profile associated with a neurological,  
CC psychiatric or psychological condition. The method enables clinicians to  
CC make a genetic-based diagnosis of a neurological, psychiatric or  
CC psychological condition and can thereby implement treatment or  
CC preventative or symptom-ameliorating protocols to reduce the adverse  
CC consequences of the condition. This sequence represents a human dopamine  
CC receptor D2 (DRD2) DNA oligonucleotide used in the scope of the  
CC invention.  
XX  
SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1046 TGAAGAGTTATTCACGA 1064  
DB 19 TGAAGAGGCGACGCCACA 1  
|||||  
|  
RESULT 548  
ABZ58817  
ID ABZ58817 standard; DNA; 14 BP.  
XX  
AC ABZ58817;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Nucleotide sequence of oligonucleotide Sse8387I-PvuII-Sse8387I.  
XX  
KM Gene delivery; adeno-associated virus; AAV; therapeutic protein; muscle;  
KM acid alpha-glucosidase; type II glycogen storage disease; cytosolic;  
KM Pompe's disease; cardiomyopathy; ss.  
XX  
OS Synthetic.  
XX  
PN WO9726337-A1.  
XX  
PD 24-JUL-1997.  
XX  
PF 17-JAN-1997; 97WO-US000895.  
XX  
PR 18-JAN-1996; 96US-00588355.  
PR 16-JAN-1997; 97US-00784757.  
XX  
XX  
PA (AVIG-) AVIGEN INC.  
PA (UYCO ) UNITV JOHNS HOPKINS.  
PI Podsakoff GM, Kessler PD, Byrne BV, Kurtzman CJ;  
XX  
DR WPI; 1997-385340/35.  
XX  
PT Delivering gene to muscle cell or tissue - using recombinant adeno-  
PT associated virus encoding therapeutic gene, e.g for acid alpha-  
PT glucosidase for treating glycogen storage disease type II.  
XX

PS Disclosure; Page 35; 76pp; English.  
XX  
XX The invention relates to production of a composition for delivering a  
CC gene (I) to muscle cell or tissue and involves mixing (a) recombinant  
CC adeno-associated virus (AAV) virion consisting of an AAV vector including  
CC (i) linked to suitable control elements and (b) a vehicle. (I) is  
CC delivered to skeletal muscle (myoblasts or myocytes), smooth muscle or  
CC cardiac muscle (cardiomyocytes). It is under control of a muscle-specific  
CC or inducible promoter, e.g. the promoter of the myod gene or steroid-  
CC responsive elements. The virions are used to express therapeutic proteins  
CC in muscle, specifically acid alpha-glucosidase in cardiomyocytes (for  
CC treating type II glycogen storage disease (Pompe's disease), an inherited  
CC cardiomyopathy caused by deficiency of acid alpha-glucosidase), but also  
CC erythropoietin and more generally any protein capable of treating  
CC endocrine, metabolic, haematological and cardiovascular diseases,  
CC including e.g. AIDS, cancer and diabetes, including delivery of antigens  
CC for immunisation. The virions are injected directly into muscle or they  
CC are used to transduce cells in vitro for subsequent return to the  
CC patient. The present sequence represents an oligonucleotide used in the  
CC construction of a vector p1909adhla2  
XX  
SQ Sequence 14 BP; 2 A; 5 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 315 GGCAGCTGCCTTACA 328  
DB 1 GGCAGCTGCCTTACA 14  
|||||  
|  
RESULT 549  
AAT79147/C  
ID AAT79147 standard; DNA; 14 BP.  
XX  
AC AAT79147;  
XX  
DT 08-OCT-1997 (first entry)  
XX  
DE Human VEGF cDNA antisense oligonucleotide A217N.  
XX  
KM Human; vascular endothelial growth factor; VEGF; antisense; preparation;  
KM oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
PN JP09154579-A.  
XX  
PD 17-JUN-1997.  
XX  
PF 05-JUL-1996; 96JP-00195419.  
XX  
PR 03-OCT-1995; 95JP-00279752.  
XX  
XX  
PA (TOAG ) TOA GOSSEI CHEM IND LTD.  
XX  
DR WPI; 1997-375653/35.  
XX  
PT Method for preparing an anti-sense nucleic acid - useful for preventing  
PT expression of a target gene.  
XX  
XX Example; Page 18; 25pp; Japanese.  
XX  
XX The present sequence is an oligonucleotide antisense to human vascular  
CC endothelial growth factor (hVEGF) cDNA. It was prepared by hybridising  
CC several random nucleotide sequences to DNA or RNA encoding a target  
CC protein, i.e. hVEGF cDNA, to obtain hybridising antisense  
CC oligonucleotides, which preferably prevent the expression of the target  
CC protein, and optionally lysing the hybridisation site with a nucleic acid  
CC degrading substance  
XX  
SQ Sequence 14 BP; 4 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match	Score 12.4	DB 1	Length 14
Best Local Similarity 92.9%	Prod. No. 2.8e+02		
Matches 13	Conservative 0	Mismatches 1	Indels 0
			Gaps 0
QY	468 AGTGTGTAAGTCTCA	481	
Db	14 AGTGTGTAAGTCTCA	1	
RESULT 550			
AAK54378			
AC	AAK54378 standard; DNA; 14 BP.		
XX	AAK54378;		
XX	05-JUL-1999 (first entry)		
DE	NK-KB antisense oligonucleotide fragment.		
XX	Antisense oligonucleotide; multiple target; antisense treatment;		
KM	impaired respiration; inflammation; lung disease;		
KM	pulmonary vasoconstriction; inflammation; allergic rhinitis;		
KM	acute asthma; allergy; asthma; impaired respiration;		
KM	respiratory distress syndrome; pain; cystic fibrosis;		
KM	pulmonary hypertension; pulmonary vasoconstriction; emphysema;		
KM	chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;		
KM	colon cancer; breast cancer; lung cancer; pancreatic cancer;		
KM	hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;		
XX	prostate cancer; ss.		
OS	Synthetic.		
PN	WO9913886-A1.		
XX	25-MAR-1999.		
PD	17-SEP-1998; 98WC-US019419.		
XX			
PF	17-SEP-1997; 97US-0059160P.		
PR	09-JUN-1998; 98US-00093972.		
PA	(UYEC-) UNIV EAST CAROLINA.		
PI	Nyce JW;		
XX	WPI; 1999-229400/19.		
DR	New antisense oligonucleotides used in treatment of, e.g. pulmonary		
PT	vasoconstriction.		
PS	Disclosure; Page 63; 120pp; English.		
XX	The specification describes antisense oligonucleotides (AAK52869-X55271)		
CC	directed against at least 2 mRNAs selected from target genes, coding and		
CC	non-coding regions of RNAs corresponding to target genes, gene initiation		
CC	codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'		
CC	-end and the juxta-section between coding and non-coding regions and all		
CC	segments of RNAs encoding proteins associated with one or more diseases,		
CC	conditions or mixtures. The antisense oligonucleotides may be derived		
CC	from sequences AAK55272-74. These multiple target oligonucleotides		
CC	(specifically AAK55180-271) can be used for the antisense treatment of		
CC	diseases and conditions. Typical diseases and inflammation, including lung		
CC	associated with impaired respiration and inflammation, allergic rhinitis,		
CC	diseases, pulmonary vasoconstriction, inflammation, respiratory		
CC	acute asthma, allergies, asthma, impaired respiration, emphysema;		
CC	chronic obstructive pulmonary disease, leukemia, lymphoma, carcinoma;		
CC	pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary		
CC	disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g		
CC	colon cancer, breast cancer, lung cancer, pancreatic cancer,		
CC	hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, at		
CC	well as all types of cancers which may metastasize or have metastasized		
CC	to the lungs, including breast and prostate cancer		

XX Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 344 CCTCTGTGTGGTGGC 357  
|||||  
Db 1 CCTCTGTGTGGTGGC 14  
RESULT 551  
AAA33822  
ID AAA33822 standard; DNA; 14 BP.  
XX  
AC AAA33822;  
XX  
DT 28-JUL-2000 (first entry)  
DE  
XX Low adenosine antisense oligonucleotide SEQ ID NO:1511.  
XX  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
XX phosphorothioate; impaired respiration; inflammation; allergy;  
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
XX antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; SS.  
XX  
OS Homo sapiens.  
PN MO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX PF  
XX 03-AUG-1998; 98US-0095212P.  
XX PR  
XX (UYEC-) UNIV EAST CAROLINA.  
PA  
PI Nyce JW;  
XX  
XX WPI; 2000-205971/18.  
DR  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX  
PS Claim 18; Page 453; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cyostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinoma, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA33213 to AAA3312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 1859

CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2323 to AAA33992) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

CC XX Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 2.8e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 344 CCTCTGCTGGCGC 357  
Db 1 CCTCTGCTGGCGC 14

RESULT 552

AAZ64750 standard; RNA; 14 BP.

AC AAZ64750;

DT 28-MAR-2000 (first entry)

DE Substrate for hairpin ribozyme which cleaves HCV at nt. 2740.

KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;

KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;

KW autoimmune disease; se.

OS Hepatitis C virus.

PN WO955847-A2.

PD 04-NOV-1999.

PF 26-APR-1999; 99WO-US009027.

PR 27-APR-1998; 98US-0083217P.

PR 18-SEP-1998; 98US-0100842P.

PR 25-FEB-1999; 99US-00257608.

PR 23-MAR-1999; 99US-00274553.

PA (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.

PT Novel ribozymes for the treatment of diseases and conditions related to

XX hepatitis C infection.

PS Claim 2; Page 96; 123pp; English.

CC The present sequence represents the preferred target sequence of an

CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the

CC Hepatitis C virus (HCV) RNA sequence at the base position given in the

CC descriptor line. The HCV sequence was screened for optimal ribozyme

CC target sites using a computer folding algorithm and regions of the mRNA

CC which did not form secondary folding structures and contained potential

CC ribozyme cleavage sites were identified. Ribozymes were synthesized to

CC target these sites and their activities optimised by either varying the

CC length of the binding arms or by modification to prevent degradation by

CC nucleases. The ribozymes of the invention inhibit gene expression and/or

CC viral replication, and are used to treat diseases associated with

CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and

CC hepatocellular carcinoma. The ribozymes may be used in combination with

CC interferon to treat HCV infection, other infectious diseases, autoimmune

CC diseases, and cancer

CC Sequence 14 BP; 0 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 57.1%; Pred. No. 2.8e+02;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 685 CTCCTGCTGGCGCT 698  
Db 1 CTCCTGCTGGCGCT 14

RESULT 553

AAZ65593 standard; DNA; 14 BP.

AC AAZ65593;

DT 30-MAR-2000 (first entry)

DE Immunosuppressant inhibitor oligonucleotide VEGF-638.

KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;

KW glomerulonephritis; acute respiratory distress syndrome; se;

KW atherosclerosis.

OS Unidentified.

PN WO9963975-A2.

PD 16-DEC-1999.

PF 10-JUN-1999; 99WO-EP004013.

PR 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

PA (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.

PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX WPI; 2000-097470/08.

PT Composition containing immune stimulant and inhibitor of agent that

XX adversely affects the immune response, for treating cancers and

XX infections.

PS Claim 10; Fig 1; 30pp; English.

CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is

CC used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.

CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10, IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This

CC oligonucleotide is an example of an inhibitor that is used in the

CC composition. The composition is used as an immunostimulant for the

CC treatment of neoplasms and infections, particularly hyperproliferation;

CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

CC most of which are directed against TGFbeta or VEGF, are inhibitors of

CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatory factors for treating e.g. asthma, Crohn's disease, ulcerative

CC colitis, diabetes glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque

CC Sequence 14 BP; 0 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 12.4; DB 1; Length 14;











CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasocostriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX Sequence 14 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 2.8e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

344 CCTCTGTGTGGGC 357

1 CCTCTGTGTGGGC 14

RESULT 560

AD285160 AD285160 standard; DNA; 14 BP.

AC AD285160;

DT 28-JUL-2005 (first entry)

XX MODY 3 diabetes-associated probe, SEQ ID 36.

KM Analyte detection; microarray; probe; ss; diabetes.

OS Unidentified.

PN US2005112677-A1.

PD 26-MAY-2005.

PF 22-NOV-2004; 2004US-00994626.

PR 22-NOV-2003; 2003KR-00083356.

PA (SHIM/) SHIM J.

PI Shim J;

DR WPI; 2005-403357/41.

PT Substrate for use in optically detecting target materials, comprises an  
PT oxide layer having thickness that may vary to wavelength of excitation  
PT light used.

PS Example 1; SEQ ID NO 36; 20pp; English.

XX The present invention relates to a novel substrate having an oxide layer.

CC which is useful in optically detecting a target material. The thickness  
CC of the oxide layer may vary to the wavelength of excitation light used.  
CC Also claimed is a method for detecting a target material, comprising  
CC immobilizing a probe material on a substrate, reacting the immobilized  
CC probe material and the target material, illuminating a reaction product  
CC with excitation light, and measuring light emitted from the reaction  
CC product by the excitation light. In an example from the invention,  
CC microarrays were fabricated by forming fused silica (SiO2) layers on  
CC silicon wafers, followed by linkage with a coupling agent and  
CC immobilization of oligonucleotide probes. The microarrays were then  
CC incubated with labeled oligonucleotides and exposed to excitation light,  
CC and light emitted from the target oligonucleotides was measured, to  
CC evaluate the intensity of detected signals with respect to the thickness  
CC of the SiO2 layers. AD285128-AD285203, MODY 3 diabetes-associated probes  
CC used with the target sequence of human glyceraldehyde-3-phosphate  
CC dehydrogenase (GAPDH), were used to show that when a target  
CC oligonucleotide is detected using a microarray including a substrate with  
CC an oxide layer a good signal is obtained compared to that with no oxide  
CC layers.

XX Sequence 14 BP; 5 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

QY Query Match 0.7%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 2.8e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1307 AGGAGAGCCGAG 1320

1 AGGAGAGCCGAG 14

RESULT 561

AE801280 AE801280 standard; DNA; 14 BP.

AC AE801280;

DT 08-SEP-2005 (first entry)

XX VEGF inhibition oligonucleotide SEQ ID NO 124.

KM pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;

KW Immunostimulant; Antiarthritic; Antirheumatic; Antiproliferative;

XX TGF-beta antagonist; Vaccine.

OS Synthetic.

PN WO2005059133-A2.

PD 30-JUN-2005.

PF 20-DEC-2004; 2004WO-EP053604.

PR 19-DEC-2003; 2003EP-00029367.

PR 05-FEB-2004; 2004US-0541771P.

PA (ANT1-) ANTISENSE PHARMA GMBH.

PI Schlingensiepen K, Schlingensiepen R;

DR WPI; 2005-479334/48.

PT Pharmaceutical composition useful for treating neoplasm, comprises  
PT stimulators stimulating function of immune system and/or immune cells and  
PT substances inhibiting cell proliferation and/or inducing cell death.

PS Claim 4; SEQ ID NO 124; 46pp; English.

XX The invention relates to a pharmaceutical composition (PC) comprising one  
CC or more stimulators that stimulate the function of immune system and/or  
CC immune cells and one or more substances inhibiting cell proliferation  
CC and/or inducing cell death. A pharmaceutical composition is useful for  
CC treating neoplasms chosen from solid tumors; blood born tumors such as

CC leukemias, acute or chronic myeloid or lymphoblastic leukemia; tumor  
 CC metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder  
 CC carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma,  
 CC carcinoma of kidney, choriocarcinoma, cystadenocarcinoma, embryonal  
 CC carcinoma, epithelial carcinoma, esophageal carcinoma, cervical  
 CC carcinoma, colon carcinoma, colorectal carcinoma, endometrial carcinoma, liver  
 CC gallbladder carcinoma, gastric carcinoma, head and neck carcinoma, liver  
 CC carcinoma, lung carcinoma, medullary carcinoma, non-small cell  
 CC bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma, small  
 CC papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, skin  
 CC intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin  
 CC carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell  
 CC carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine  
 CC carcinoma, rheumatoid arthritis and psoriasis. The present sequence  
 CC represents a VEGF inhibition oligonucleotide.

XX  
 SQ Sequence 14 BP; 0 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1008 CTTCTCTCTCTGC 1021  
 |||||  
 1 CTCCTCTCTCTGC 14

Db

RESULT 562  
 AEC63812  
 ID AEC63812 standard; DNA; 14 BP.

AC AEC63812;  
 XX 17-NOV-2005 (first entry)  
 XX  
 DE Novel microarray-related oligonucleotide probe SeqID49.  
 XX  
 KM DNA detection; DNA chip; DNA microarray; probe; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2005202492-A1.  
 XX  
 PD 15-SEP-2005.  
 XX  
 PF 11-MAR-2005; 2005US-00078601.  
 XX  
 PR 12-MAR-2004; 2004KR-00017026.

XX  
 PA (NAMT/) NAM Y.  
 PA (HUHN/) HUH N.  
 PA (SHIM/) SHIM H.  
 PA (OHUJ/) OH J.  
 XX  
 PI Nam Y, Huh N, Shim H, Oh J;  
 PT WPI; 2005-618101/63.  
 DR

XX Polynucleotide microarray for photolithographic or spotting method,  
 PT comprises probe polynucleotides spots capable of binding to same target  
 PT polynucleotide immobilized on microarray.

XX  
 XX Example; SEQ ID NO 49; 25bp; English.

XX  
 CC This invention relates to a novel polynucleotide microarray comprising at  
 CC least two probe polynucleotides capable of binding to the same target  
 CC polynucleotide immobilized on the microarray. A spot region on a  
 CC substrate of the polynucleotide microarray is segmented into blocks  
 CC arranged in rows and columns adjacent to each other. The blocks are  
 CC separated and a space is formed between the blocks. The microarray may be  
 CC used for photolithographic or spotting methods and provides good  
 CC analytical results of a target nucleic acid. The present sequence is that  
 CC of an oligonucleotide probe which was used during the exemplification of

CC the novel microarrays of the invention.

XX  
 SQ Sequence 14 BP; 5 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1307 AGGAGGAGCCAGAG 1320  
 |||||  
 1 AGGAGGAGGAGAG 14

Db

RESULT 563  
 AAQ70347/c  
 ID AAQ70347 standard; DNA; 15 BP.

AC AAQ70347;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 15-FEB-1995 (first entry)  
 XX  
 DE Antisense oligonucleotide for mouse FGF.

XX  
 KM Fibroblast growth factor; hybridisation; laser procedures;  
 KM vascular smooth muscle cell; proliferation; SMC; vascular stenosis;  
 KM post angioplasty restenosis; atherosclerosis; cardiac hypertrophy;  
 KM organ transplant; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9415945-A1.  
 XX  
 PD 21-JUL-1994.  
 XX  
 PF 28-DEC-1993; 93WO-US012600.  
 XX  
 PR 31-DEC-1992; 92US-00999706.  
 XX  
 PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
 XX  
 PI Denner LA, Rege AA, Dixon RA;  
 XX  
 DR WPI; 1994-249123/30.  
 XX  
 PD New anti-sense polynucleotide(s) to fibroblast growth factor receptor -  
 PT used for inhibiting vascular smooth muscle cell proliferation, partic.  
 PT for treating restenosis.  
 XX  
 PS Claim 3; Page 9; 53pp; English.

XX  
 CC The sequence is an antisense molecule directed against position +1 to  
 CC +15, relative to the start codon of the gene for mouse fibroblast growth  
 CC factor 1. The polynucleotide can be used for inhibiting vascular smooth  
 CC muscle cell proliferation and for treating a disease e.g. vascular  
 CC stenosis, post angioplasty restenosis, atherectomy, atherosclerosis,  
 CC atrial venous shunt failure, cardiac hypertrophy, vascular surgery and  
 CC organ transplant. See also AAQ70333-60. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1202 ATGAGGAGGCTGGA 1215  
 |||||  
 15 ATGAGGAGGCTGGA 2

Db

RESULT 564  
 AA666605

XX AAX66605 standard; RNA, 15 BP.  
XX AAX66605;  
XX 20-JUL-1999 (first entry)  
XX  
DE Human CD40 hammerhead ribozyme target SEQ ID NO:3237.  
XX  
XX Arthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX streptomycin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX Homo sapiens.  
XX  
XX MO9618736-A2.  
XX  
XX 20-JUN-1996.  
XX  
XX 22-NOV-1995; 95WO-US015516.  
XX  
XX 13-DEC-1994; 94US-00354920.  
XX 23-DEC-1994; 94US-00363253.  
XX 17-FEB-1995; 95US-00363254.  
XX 20-APR-1995; 95US-00390850.  
XX 02-MAY-1995; 95US-00426124.  
XX 04-MAY-1995; 95US-00432874.  
XX 07-JUL-1995; 95US-000434509.  
XX 07-JUL-1995; 95US-0000951P.  
XX 07-AUG-1995; 95US-0000974P.  
XX 07-AUG-1995; 95US-00512861.  
XX 05-OCT-1995; 95US-00541365.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P,  
XX Mewissen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J,  
XX Karpetsky A, Thompson JD, Modak A, Burgin A;  
XX  
XX WPI; 1996-300653/30.  
XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for  
XX the treatment of arthritis, induction of graft tolerance or treatment of  
XX auto-immune diseases.  
XX  
XX Claim 10; Page 204; 307pp; English.  
XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
XX; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
XX can inhibit collagenase and streptomycin production in the synovial  
XX membrane of joints for the treatment or prevention of arthritis,  
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
XX be used to treat antigen presenting cells of a donor to induce tolerance  
XX in a recipient to an alloantigen of a donor. They can also be used for  
XX enhancing graft tolerance or for treating autoimmune disease, and for  
XX treating allergies and other inflammatory conditions. The ENA's can also  
XX be used in diagnosis. Ribozyme therapy impacts on the expression of  
XX streptomycin without introducing the non-specific effects upon gene  
XX expression which accompany treatment with retinoids and dexamethasone.  
XX The concentration of ribozyme required to affect a therapeutic treatment  
XX is lower than that required of antisense molecules, and is highly  
XX specific. The present sequence is used in the exemplification of the  
XX present invention  
XX  
XX Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;  
XX  
XX Query Match 0.74; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 57.1%; Pred. No. 3.3e+02;  
XX Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCCTCTCTCCCAT 1422  
DB 2 GCUCUCUCUCAU 15  
XX  
XX RESULT 565  
XX AAX66802  
XX ID AAX66802 standard; RNA, 15 BP.  
XX  
XX AAX66802;  
XX  
XX 20-JUL-1999 (first entry)  
XX  
XX Mouse CD40 hammerhead ribozyme target SEQ ID NO:3434.  
XX  
XX Arthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX streptomycin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX  
XX Mus sp.  
XX  
XX MO9618736-A2.  
XX  
XX 20-JUN-1996.  
XX  
XX 22-NOV-1995; 95WO-US015516.  
XX  
XX 13-DEC-1994; 94US-00354920.  
XX 23-DEC-1994; 94US-00363253.  
XX 17-FEB-1995; 95US-00363254.  
XX 20-APR-1995; 95US-00390850.  
XX 02-MAY-1995; 95US-00426124.  
XX 04-MAY-1995; 95US-00432874.  
XX 07-JUL-1995; 95US-000434509.  
XX 07-JUL-1995; 95US-0000951P.  
XX 07-JUL-1995; 95US-0000974P.  
XX 07-AUG-1995; 95US-00512861.  
XX 05-OCT-1995; 95US-00541365.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P,  
XX Mewissen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J,  
XX Karpetsky A, Thompson JD, Modak A, Burgin A;  
XX  
XX WPI; 1996-300653/30.  
XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used for  
XX the treatment of arthritis, induction of graft tolerance or treatment of  
XX auto-immune diseases.  
XX  
XX Claim 10; Page 209; 307pp; English.  
XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
XX; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
XX can inhibit collagenase and streptomycin production in the synovial  
XX membrane of joints for the treatment or prevention of arthritis,  
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
XX be used to treat antigen presenting cells of a donor to induce tolerance  
XX in a recipient to an alloantigen of a donor. They can also be used for  
XX enhancing graft tolerance or for treating autoimmune disease, and for  
XX treating allergies and other inflammatory conditions. The ENA's can also  
XX be used in diagnosis. Ribozyme therapy impacts on the expression of  
XX streptomycin without introducing the non-specific effects upon gene  
XX expression which accompany treatment with retinoids and dexamethasone.  
XX The concentration of ribozyme required to affect a therapeutic treatment  
XX is lower than that required of antisense molecules, and is highly  
XX specific. The present sequence is used in the exemplification of the  
XX present invention

XX SQ Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 57.1%; Pred. No. 3.3e+02;  
XX Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1409 GCTTCTCTCCAT 1422  
DB 1 GCUUCUUCUCAAU 14  
RESULT 566  
AAK65304/C  
ID AAK65304 standard; RNA; 15 BP.  
XX AAK65304;  
XX AC  
XX 20-JUL-1999 (first entry)  
XX DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1936.  
XX ARthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX Mus sp.  
XX WO9618736-A2.  
XX PD 20-JUN-1996.  
XX PF 22-NOV-1995; 95MO-US015516.  
XX PR 13-DEC-1994; 94US-00354920.  
XX PR 23-DEC-1994; 94US-00363253.  
XX PR 23-DEC-1994; 94US-00363254.  
XX PR 17-FEB-1995; 95US-00390850.  
XX PR 20-APR-1995; 95US-00426124.  
XX PR 02-MAY-1995; 95US-00434509.  
XX PR 04-MAY-1995; 95US-0000951P.  
XX PR 07-JUL-1995; 95US-0000974P.  
XX PR 07-JUL-1995; 95US-00512861.  
XX PR 07-AUG-1995; 95US-00512861.  
XX PR 05-OCT-1995; 95US-00541365.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Payco P;  
XX Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
XX Karpelsky A, Thompson JD, Modak A, Burgin A;  
XX DR WPI; 1996-300653/30.  
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
XX the treatment of arthritis, induction of graft tolerance or treatment of  
XX auto-immune diseases.  
XX PS Claim 10; Page 179; 307pp; English.  
XX CC The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
XX ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
XX can inhibit collagenase and stromelysin production in the synovial  
XX membrane of joints for the treatment or prevention of arthritis,  
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
XX be used to treat antigen presenting cells of a donor to induce tolerance  
XX in a recipient to an alloantigen of a donor. They can also be used for  
XX enhancing graft tolerance or for treating autoimmune disease, and for  
XX treating allergies and other inflammatory conditions. The ENA's can also

CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC stromelysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention  
XX SQ Sequence 15 BP; 5 A; 4 C; 3 G; 0 T; 3 U; 0 Other;  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 296 CCTGGCAATTGTC 309  
DB 14 CCTGGCAATTGTC 1  
RESULT 567  
AAK66801  
ID AAK66801 standard; RNA; 15 BP.  
XX AAK66801;  
XX AC  
XX 20-JUL-1999 (first entry)  
XX DE Mouse CD40 hammerhead ribozyme target SEQ ID NO:3433.  
XX ARthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX Mus sp.  
XX WO9618736-A2.  
XX PD 20-JUN-1996.  
XX PF 22-NOV-1995; 95MO-US015516.  
XX PR 13-DEC-1994; 94US-00354920.  
XX PR 23-DEC-1994; 94US-00363253.  
XX PR 23-DEC-1994; 94US-00363254.  
XX PR 17-FEB-1995; 95US-00390850.  
XX PR 20-APR-1995; 95US-00426124.  
XX PR 02-MAY-1995; 95US-00432874.  
XX PR 04-MAY-1995; 95US-00434509.  
XX PR 07-JUL-1995; 95US-0000951P.  
XX PR 07-JUL-1995; 95US-0000974P.  
XX PR 07-AUG-1995; 95US-00512861.  
XX PR 05-OCT-1995; 95US-00541365.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Payco P;  
XX Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
XX Karpelsky A, Thompson JD, Modak A, Burgin A;  
XX DR WPI; 1996-300653/30.  
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
XX the treatment of arthritis, induction of graft tolerance or treatment of  
XX auto-immune diseases.  
XX PS Claim 10; Page 209; 307pp; English.  
XX CC The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
XX ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
XX ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's

XX Claim 10; Page 179; 307bp; English.

PS The present invention describes a novel enzymatic nucleic acid (ENA)

CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues

CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least

CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's

CC can inhibit collagenase and stromelysin production in the synovial

CC membrane of joints for the treatment or prevention of arthritis,

CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also

CC be used to treat antigen presenting cells of a donor to induce tolerance

CC in a recipient to an alloantigen of a donor. They can also be used for

CC enhancing graft tolerance or for treating autoimmune disease, and for

CC treating allergies and other inflammatory conditions. The ENA's can also

CC be used in diagnosis. Ribozyme therapy impacts on the expression of

CC stromelysin without introducing the non-specific effects upon gene

CC expression which accompany treatment with retinoids and dexamethasone.

CC The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the

CC present invention

XX SQ Sequence 15 BP; 4 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

OY Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 296 CCTGGCAATTGTC 309  
15 CCTGGCAATTGTC 2  
|||||  
|||

RESULT 569

ID AAT15256/c  
XX AAT15256 standard; cDNA; 15 BP.  
XX AC  
XX AAT15256;  
DT 18-DEC-1996 (first entry)  
DE Antisense sequence #5 for cell growth factor cDNA.  
XX  
XX Glial cell; growth factor; antisense oligonucleotide; cell surface;  
KW cell shape; promoting factor; functional identification; probe; ss.  
XX OS Synthetic.  
XX EP110721-A2.  
PM 08-MAY-1996.  
PD 31-OCT-1995; 95EP-00117121.  
PF 02-NOV-1994; 94JP-00269417.  
RR (TAKE ) TAKEDA CHEM IND LTD.  
PA Tanimura H, Hosoya M;  
PI WPI; 1996-231854/24.  
DR  
XX Determining protein function from only partial cDNA sequence - by  
PT assessing change in biological activity on addition of anti-sense  
PT molecule.  
XX Example 2; Page 17; 25pp; English.

CC AAT15252-n15257 represent antisense sequences used in the method of the

CC invention. These sequences are antisense to a partial cDNA sequence (see

CC AAT15251) for a protein with unknown function. The method of the

CC invention is for probing the function of a protein encoded by a cDNA of

CC partially known sequence. The method comprises assessing the change of





CC ratio of intensity of the donor and acceptor fluorescence peaks is  
CC measured to indicate the amount of interaction of the donor and acceptor  
CC labels, which is a measure of the quantity of probes which are hybridised  
CC to the completed RNA molecules. The process provides a highly sensitive  
CC and simple method for monitoring the progress of RNA transcription in  
CC vitro  
XX  
SQ Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Dy 1155 CTTGACGATGCT 1168  
Db 14 CTTGACGATGCT 1  
RESULT 572  
AAV48607/c  
ID AAV48607 standard; DNA; 15 BP.  
XX  
AC AAV48607;  
XX  
DT 15-OCT-1998 (first entry)  
XX  
DE jund gene antisense oligonucleotide Jund-24.  
XX  
jund; jund; antisense oligonucleotide; modulate; gene expression; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
EN EP856579-A1.  
PD  
PD 05-AUG-1998.  
XX  
PF 31-JAN-1997; 97EP-00101531.  
XX  
PR 31-JAN-1997; 97EP-00101531.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
PI Schlingensiepen K, Brysch W;  
XX  
DR WPI; 1998-400910/35.  
XX  
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of  
PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.  
XX  
PS Claim 10; Fig 5a; 286pp; English.  
XX  
AAV48564-708 represent antisense oligonucleotides directed against the  
CC jund and jund genes. Of these, only oligonucleotides AAV48565-614  
CC resulted in effective downregulation of negative growth control by jund  
CC or jund, while AAV48615-708 had little effect. The oligonucleotides  
CC exemplify the invention. The specification describes oligonucleotides  
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that  
CC can each form three hydrogen bonds to cytosine; do not contain four  
CC consecutive nucleotides able to form three H-bonds each to four  
CC consecutive cytosines; do not contain two sequences of three consecutive  
CC nucleotides each able to form three H-bonds to three consecutive  
CC cytosines, and the ratio between residues able to form two H-bonds each  
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The  
CC oligonucleotides are used to modulate expression of genes, particularly  
CC the genes for p53, ErbB-2, jund, jund, TGF-beta 1 or beta 2 to control  
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or  
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The  
CC oligonucleotides can also be used to analyse function of proteins (by  
CC altering their expression or activity) and therapeutically, e.g. in cases

CC of cancer or (targeting TGF) for stimulating the immune system  
XX  
SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Dy 936 CAAGCGCAAGCTGG 949  
Db 14 CAAGCGCAAGCTGG 1  
RESULT 573  
AAAX31113/c  
ID AAAX31113 standard; DNA; 15 BP.  
XX  
AC AAAX31113;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Tag sequence of a transcript increased in colorectal cancer.  
XX  
KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;  
KW diagnosis; prognosis; treatment; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO9853319-A2.  
XX  
PD 26-NOV-1998.  
XX  
PD 20-MAY-1998; 98WO-US010277.  
XX  
PR 21-MAY-1997; 97US-0047352P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1999-070161/06.  
XX  
PT Use of isolated gene transcripts - useful for developing products for the  
PT diagnosis, prognosis and treatment of cancers, particularly colon and  
PT pancreatic cancer.  
XX  
PS Claim 2; Page 31; 120pp; English.  
XX  
AAAX30947-31815 represent tag sequences of transcripts that are  
CC differentially expressed in colorectal cancer, in pancreatic cancer, or  
CC in both. The tag sequences can be used to identify genes by matching the  
CC tag to a gen data base member, or by using the tag sequences as probes to  
CC isolate unidentified genes from cDNA libraries. The tag sequences can  
CC also be used in a method for diagnosing colon or pancreatic cancer in a  
CC sample suspected of being neoplastic. The method comprises comparing the  
CC level of at least one transcript in a first sample of a tissue to a  
CC second sample, where the first sample is a colonic tissue suspected of  
CC being neoplastic and the second sample is a normal human colonic tissue.  
CC The transcript is identified by a tag selected from AAAX30947-31815. The  
CC methods of the invention can be used in the diagnosis, prognosis and  
CC treatment of cancer  
XX  
SQ Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Dy 367 GTGATGTCATCAT 380  
Db 15 GCGATGTCATCAT 2

```

RESULT 574
AAA07158/c
ID AAA07158 standard; DNA; 15 BP.
XX
AC AAA07158;
XX
DT 16-JUN-2000 (first entry)
XX
DE Probe for XELFI-1 alpha mRNA.
XX
XX Probe; Xenopus laevis; elongation factor-1 alpha chain; XELFI-1 alpha;
XX biological activity screening; real-time monitoring; RNA transcription;
XX RNA synthesis; detection; ss.
XX
OS Xenopus laevis.
XX
PN JP2000041700-A.
XX
PD 15-FEB-2000.
XX
PF 31-JUL-1998; 98JP-00218025.
XX
PR 31-JUL-1998; 98JP-00218025.
XX
PA (BUNS-) BUNSHI BIOHOTOONICS KENKYUSHO KK.
XX
DR WPI; 2000-295786/26.
XX
PT Determination and screening of biological activity of a drug, uses real-
XX time monitoring of RNA transcription without electrophoresis.
XX
PS Example 1; Page 13; 25pp; Japanese.
XX
CC This sequence represents a probe for the mRNA encoding the Xenopus laevis
CC elongation factor-1 (XELFI-1 alpha) alpha chain. The invention relates to a
CC method for the determination and screening of the biological activity of
CC a drug, with real-time monitoring of RNA transcription and synthesis
CC without using electrophoresis. The method for the determination and
CC screening of the biological activity of a drug in an RNA transcription
CC and synthesis system, comprises: addition of the test drug to the system
CC to alter the transcription and synthesis of the RNA; and determining the
CC fluorescence of 2 probe sequences capable of hybridising with the base
CC sequence of the transcribed and synthesized RNA, where one probe is a
CC donor probe labelled with an energy donor fluorescent molecule and the
CC other probe is an acceptor probe labelled with an energy acceptor
CC fluorescent molecule. The method is used for the determination and
CC screening of the biological activity of a drug. The method allows for the
CC automatic determination of the biological activity of a drug
XX
SQ Sequence 15 BP; 5 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1155 CTTCAAGCAGTCCT 1168
DB 14 CTTCAAGTATGCTT 1
XX
RESULT 575
AAA66946
ID AAA66946 standard; DNA; 15 BP.
XX
AC AAA66946;
XX
DT 19-OCT-2000 (first entry)
XX
DE Human leukocyte antigen A allele DNA probe A239A SEQ ID NO:4.
XX
XX Human leukocyte antigen; HLA; class I allele type; probe; PCR primer;
XX amplification; hybridisation; organ transplant; gene typing; diagnosis;
XX ss.

```

```

XX
OS Homo sapiens.
XX
PN WO200031295-A1.
XX
PD 02-JUN-2000.
XX
PF 07-OCT-1999; 99WO-JP005527.
XX
PR 26-NOV-1998; 98JP-00335151.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PT Moribe T, Kaneshige T;
XX
DR WPI; 2000-400097/34.
XX
PT Simple, rapid and accurate method for distinguishing HLA class I allele
XX type with possibility of mechanization and automation, applicable in
XX judging donor-recipient compatibility during organ transplant and disease
XX diagnosis.
XX
PS Claim 8; Page 50; 83pp; Japanese.
XX
CC The present invention describes a method for distinguishing a human
XX leukocyte antigen (HLA) class I antigen or allele by a combination of
XX polymerase chain reaction (PCR) using a primer pair whereby all HLA-A, -B
XX or -C alleles can be amplified or using reverse hybridisation analysis
XX comprising a DNA probe covalently bonded to microtitre plate wells which
XX are hybridisable specifically with the base sequence of at least one
XX specific HLA-A, -B or -C allele. The method is applicable in gene typing,
XX judging donor-recipient compatibility during organ transplant and
XX correlation analysis for diagnosis of various diseases. The method is
XX simple, rapid and accurate, with possibility of mechanisation and
XX automation, without the problems encountered by using the prior-art
XX techniques. AAA66943 to AAA67072 represent oligonucleotide probes and PCR
XX primers for use in the method of the present invention
XX
SQ Sequence 15 BP; 4 A; 3 C; 8 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1307 AGGAGAGCCGAG 1320
DB 2 AGGAGAGCCGAG 15
XX
RESULT 576
AAF45174/c
ID AAF45174 standard; DNA; 15 BP.
XX
AC AAF45174;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #13.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhea; rubea;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.

```

```
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 6; Page 34; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 6 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
XX XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
QY 1008 CTTCTCTCTCTCTGC 1021
Db 14 CTTCTCTCTCTCTCC 1
XX XX
XX RESULT 577
XX AAF49868/c
XX ID AAF49868 standard; DNA; 15 BP.
XX XX
XX AC AAF49868;
XX XX
XX DT 30-MAR-2001 (first entry)
XX XX
XX DE IGF-I oligonucleotide #828.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PR 21-JUN-2000; 2000WO-AU000693.
XX PF 21-JUN-1999; 99US-0140345P.
XX PR 21-JUN-1999; 99US-0140345P.
```

```
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX
XX DR WPI; 2001-041421/05.
XX XX
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 8; Page 66; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 0 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
QY 15 GCGGCGAGCGCGC 28
Db 14 GCGGCGAGCGAGC 1
XX XX
XX RESULT 578
XX AAF52635/c
XX ID AAF52635 standard; DNA; 15 BP.
XX XX
XX AC AAF52635;
XX XX
XX DT 30-MAR-2001 (first entry)
XX XX
XX DE IGF-I oligonucleotide #3595.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PR 21-JUN-2000; 2000WO-AU000693.
XX PF 21-JUN-1999; 99US-0140345P.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
```

XX WPI; 2001-041421/05.  
 DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PS Example 8; Page 84; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1576 ATTCCATCCTTGAG 1589  
 ID | |||||  
 DB 14 ACTCCATCCTTGAG 1  
 RESULT 579  
 AAF54012/C  
 ID AAF54012 standard; DNA; 15 BP.  
 XX AAF54012;  
 AC 30-MAR-2001 (first entry)  
 DT XX  
 DE IGF-I oligonucleotide #4972.  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cyostatic; dermatological; cardiant; vincide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 FN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 PI WPI; 2001-041421/05.  
 DR  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PS Example 8; Page 93; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 SQ Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1403 GCTTCAGCTTCTCC 1416  
 ID | |||||  
 DB 15 GCTTCAGCTTCTCC 2  
 RESULT 580  
 AAF49641/C  
 ID AAF49641 standard; DNA; 15 BP.  
 XX AAF49641;  
 AC 30-MAR-2001 (first entry)  
 DT XX  
 DE IGF-I oligonucleotide #601.  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cyostatic; dermatological; cardiant; vincide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 FN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 PI WPI; 2001-041421/05.  
 DR  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.

PS Example 8; Page 64; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1407 CAGCTTCCTCCCA 1420

DB 15 CGGCTTCCTCCA 2

RESULT 581

AAF49643/C

ID AAF49643 standard; DNA; 15 BP.

XX AAF49643;

AC

XX 30-MAR-2001 (first entry)

DT

XX IGF-I oligonucleotide #603.

DE

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS

XX Homo sapiens.

OS

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 64; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1406 TCAGCTTCCTCC 1419

DB 14 TCGGCTTCCTCC 1

RESULT 582

AAF54013/C

ID AAF54013 standard; DNA; 15 BP.

XX AAF54013;

AC

XX 30-MAR-2001 (first entry)

DT

XX IGF-I oligonucleotide #4973.

DE

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS

XX Homo sapiens.

OS

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 93; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

CC

SQ Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1406 TCAGCTTCCTCC 1419

DB 14 TCGGCTTCCTCC 1

RESULT 582

AAF54013/C

ID AAF54013 standard; DNA; 15 BP.

XX AAF54013;

AC

XX 30-MAR-2001 (first entry)

DT

XX IGF-I oligonucleotide #4973.

DE

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; seborrheoa; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

OS

XX Homo sapiens.

OS

XX WO200078341-A1.

PN

XX 28-DEC-2000.

PD

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA

XX Wraight CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 93; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotide of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 CC  
 XX Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1403 GCTTCAGCTTCTCC 1416  
 Db 14 GGTTCAGCTTCTCC 1  
 RESULT 583  
 AAF45225/c  
 ID AAF45225 standard; DNA; 15 BP.  
 XX AAF45225;  
 AC  
 XX 30-MAR-2001 (first entry)  
 DT  
 XX  
 DE IGFBP2 oligonucleotide #64.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.  
 XX  
 XX Example 6; Page 34; 201pp; English.  
 XX  
 XX The present invention relates to a method for ameliorating the effects of  
 XX skin disorders. The method comprises contacting the skin with an  
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX inhibiting or reducing growth factor mediated cell proliferation,  
 XX inflammation and/or other disorders. The present sequence is an  
 XX oligonucleotide which can be used to design the antisense  
 XX oligonucleotide of the present invention (see AAF45151 and AAF45153-  
 XX F45161). The method is useful for ameliorating the effects of psoriasis,  
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 XX hyperneovascular condition such as a neovascular condition of the retina,  
 XX brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX disease, kidney disease, hyperproliferation of the inside of blood  
 XX vessels or any other hyperplasia

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 CC  
 XX Sequence 15 BP; 0 A; 10 C; 4 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 15 GCGGCGGCGGCGC 28  
 Db 14 GCGGCGGCGGCGC 1  
 RESULT 584  
 AAF52480  
 ID AAF52480 standard; DNA; 15 BP.  
 XX AAF52480;  
 AC  
 XX 30-MAR-2001 (first entry)  
 DT  
 XX  
 DE IGF-1 oligonucleotide #3440.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.  
 XX  
 XX Example 8; Page 83; 201pp; English.  
 XX  
 XX The present invention relates to a method for ameliorating the effects of  
 XX skin disorders. The method comprises contacting the skin with an  
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX inhibiting or reducing growth factor mediated cell proliferation,  
 XX inflammation and/or other disorders. The present sequence is an  
 XX oligonucleotide which can be used to design the antisense  
 XX oligonucleotide of the present invention (see AAF45151 and AAF45153-  
 XX F45161). The method is useful for ameliorating the effects of psoriasis,  
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 XX hyperneovascular condition such as a neovascular condition of the retina,  
 XX brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX disease, kidney disease, hyperproliferation of the inside of blood  
 XX vessels or any other hyperplasia

Query Match		0.7%;	Score 12.4;	DB 1;	Length 15;
Best Local Similarity		92.9%;	Pred. NO. 3.3e+02;		
Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	1315 CCAGAGGACGGCCC 1328				
Dd					
	14 CCAAGAGGACGACC 1				
RESULT 586					
AAFS4011/c					
ID	AAFS4011 standard; DNA; 15 BP.				
XX AC	AAFS4011;				
XX DT	30-MAR-2001 (first entry)				
XX DE	IGF-I oligonucleotide #4971.				
XX KW	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;				
KW KW	Cytostatic; dermatological; cardian; virucide; ophthalmological; keloid;				
KW KW	skin disorder; insulin-like Growth Factor I receptor; IGF-1; pityriasis;				
KW KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;				
KW KW	growth factor mediated cell proliferation; ichthyosis; serborrhoea; rubra;				
KW KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;				
KW KW	hypervascular condition; hyperplasia; kidney disease;				
KM KM	neovascular condition of the retina; ss.				
XX OS	Homo sapiens.				
XX PN	MO200078341-A1.				
XX PD	28-DEC-2000.				
XX PF	21-JUN-2000; 2000WO-AU000693.				
XX PR	21-JUN-1999; 99US-0140345P.				
XX PA	(MURD-) MURDOCH CHILDRENS RES INST.				
PI PI	wright CJ, Werther GA, Edmondson SR,				
DR DR	WPI; 2001-041421/05.				
PT PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.				
PS PS	Example 8; Page 93; 201pp; English.				
XX XX	The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, scleroderma, rubra, pilaris, serborrhoea, keloids, keratosis, neoplasmia, sclerodermis, wart, benign growths, cancers of the skin, a hypervascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia				
SO SO	Sequence 15 BP; 5 A; 2 C; 7 G; 1 T; 0 U; 0 Other;				
Query Match		0.7%;	Score 12.4;	DB 1;	Length 15;
Best Local Similarity		92.9%;	Pred. No. 3.3e+02;		
Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1405 TTCAGCTTCTCCTC 1418  
 |||||  
 Db 14 TTCAGCTTCTCCTC 1

RESULT 587  
 AAF49866/c  
 ID AAF49866 standard; DNA; 15 BP.  
 XX AAF49866;  
 AC  
 XX  
 XX 30-MAR-2001 (first entry)  
 DE IGF-1 oligonucleotide #826.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURDOCH CHILDRENS RES INST.  
 PA Wraight CJ, Werther GA, Edmondson SR;  
 PI WPI; 2001-041421/05.  
 DR  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 8; Page 66; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC P45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SO Sequence 15 BP; 0 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CGGGCAGCGCGGCA 29  
 |||||  
 Db 15 CGGGCAGCGAGGCA 2

RESULT 588  
 AAF52634/c  
 ID AAF52634 standard; DNA; 15 BP.  
 XX AAF52634;  
 AC  
 XX  
 XX 30-MAR-2001 (first entry)  
 DE IGF-1 oligonucleotide #3594.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cyostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200078341-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 PF  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURDOCH CHILDRENS RES INST.  
 PA Wraight CJ, Werther GA, Edmondson SR;  
 PI WPI; 2001-041421/05.  
 DR  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 8; Page 84; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC P45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SO Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ATTCCATCCTTGAG 1589  
 |||||  
 Db 15 ACTCCATCCTTGAG 2

RESULT 589  
 AAF54010/c  
 ID AAF54010 standard; DNA; 15 BP.



```

XX AC AAF54010;
XX DT 30-MAR-2001 (first entry)
XX DE IGF-I oligonucleotide #4970.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX OS
XX PN MO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000MO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX PT
XX Example 8; Page 93; 201pp; English.
XX PS
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX P45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX CC
XX Sequence 15 BP; 5 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1405 TTGAGCTTCTCTC 1418
DB 15 TTGAGCTTCTCTCC 2

```

```

XX DE IGFBP2 oligonucleotide #61.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX OS
XX PN MO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000MO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX DR
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX PT
XX Example 6; Page 34; 201pp; English.
XX PS
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX P45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX CC
XX Sequence 15 BP; 0 A; 11 C; 3 G; 1 T; 0 U; 0 Other;
XX SQ
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 GGGCAGCGCGGCGAG 30
DB 15 GGGCAGCGCGGCGAG 2

```

```

RESULT 590
AAF45222/C
ID AAF45222 standard; DNA; 15 BP.
AC AAF45222;
XX
XX 30-MAR-2001 (first entry)
DT

```

```

RESULT 591
AAF52679/C
ID AAF52679 standard; DNA; 15 BP.
AC AAF52679;
XX
XX 30-MAR-2001 (first entry)
DT
XX IGF-I oligonucleotide #3639.
DE
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX

```

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-AU000693.  
XX  
PR 21-JUN-1999; 99US-0140345P.  
XX  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
PI Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
PS Example 8; Page 84; 201pp; English.  
XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 0 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1316 CAGAGGACGGCCCC 1329  
DB 15 CAGAGGACGACCCCC 2  
RESULT 592  
AAF45172/C  
ID AAF45172 standard; DNA; 15 BP.  
XX  
AC AAF45172;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGFBP2 oligonucleotide #11.  
XX  
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-AU000693.  
XX  
PR 21-JUN-1999; 99US-0140345P.  
XX  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
PI Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX  
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
PS Example 6; Page 34; 201pp; English.  
XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 7 A; 0 C; 8 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1009 TTCTTCTCTCTGCC 1022  
DB 15 TTCTTCTCTCTGCC 2  
RESULT 593  
AAF52482  
ID AAF52482 standard; DNA; 15 BP.  
XX  
AC AAF52482;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGF-I oligonucleotide #3442.  
XX  
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX

OS Homo sapiens.  
 XX WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 PI Wright CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 DR  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 83; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, rubea, pilaris, seborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 QY  
 DB 720 CACAGAGACCATGC 733  
 1 CACAGAGACCTGC 14  
 XX  
 RESULT 594  
 AAF70390/C  
 ID AAF70390 standard; DNA; 15 BP.  
 XX  
 AC AAF70390;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Human DRD2 allele specific oligonucleotide primer SEQ ID NO:133.  
 XX  
 KW Human; dopamine receptor D2; DRD2; polymorphism; allele specific;  
 KW drug target isogene; detection; single nucleotide polymorphism; SNP;  
 KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;  
 KW probe; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200105832-A1.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 19-JUL-2000; 2000WO-US019644.  
 XX

PR 19-JUL-1999; 99US-0144493P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
 XX WPI; 2001-091967/10.  
 DR  
 XX  
 PT polynucleotides comprising single nucleotide polymorphisms in the human  
 PT dopamine receptor D2, useful for detecting mutations associated with,  
 PT e.g. schizophrenia, Parkinson's and myoclonus dystonia.  
 XX  
 PS Claim 15; Page 24; 135pp; English.  
 XX  
 CC The present invention describes polynucleotides comprising single  
 CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).  
 CC The polynucleotides may be used in assays to detect and characterise  
 CC polymorphisms in DRD2 that affect its expression and activity and are  
 CC involved in disorders such as schizophrenia, Parkinson's and myoclonus  
 CC dystonia (MD). This information would be useful for studying the  
 CC biological function of DRD2 as well as in identifying drug targeting  
 CC this protein for the treatment of disorders related to its abnormal  
 CC expression or function. Polymorphisms in the DRD2 gene affect the  
 CC expression of active and functional polypeptides. Therefore it is  
 CC advantageous to detect polymorphisms in the DRD2 gene and how those  
 CC polymorphisms are combined in different copies of the gene. AAF70261 to  
 CC AAF70308 represent human DRD2 allele specific oligonucleotide probes, and  
 CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide  
 CC primers which are used in the detection of DRD2 polymorphisms. AAF70405  
 CC to AAF70452 represent oligonucleotide primers for the detection of human  
 CC DRD2 polymorphisms which are given in the exemplification of the present  
 CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2  
 CC gene which are used in examples from the present invention  
 XX  
 SQ Sequence 15 BP; 1 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
 XX  
 QY  
 DB 879 ATGGGCCAGTGAG 892  
 14 AGGGGCCAGTGAGA 1  
 XX  
 RESULT 595  
 AAF69430  
 ID AAF69430 standard; DNA; 15 BP.  
 XX  
 AC AAF69430;  
 XX  
 DT 18-APR-2001 (first entry)  
 XX  
 DE Human IL4Ralpha gene probe #70.  
 XX  
 KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
 KW allergic disease; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200104270-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 13-JUL-2000; 2000WO-US019094.  
 XX  
 PR 13-JUL-1999; 99US-0143435P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
 PI Windemuth AK;  
 XX

DR WPI, 2001-103078/11.  
XX New isolated polynucleotide useful for the identification of therapeutics  
PT in allergic diseases is new.  
XX  
PS Claim 15; Page 43; 188pp; English.  
XX  
CC The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha  
CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a probe for human IL4R-alpha  
CC  
SQ Sequence 15 BP; 2 A; 5 C; 7 G; 1 T; 0 U; 0 Other;  
XX  
XX  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1299 GGGCCACGAGGAGG 1312  
Db 1 GGCCACGCTGAGG 14  
XX  
RESULT 596  
AAF69387/c  
ID AAF69387 standard; DNA; 15 BP.  
XX  
XX AAF69387;  
AC  
XX 18-APR-2001 (first entry)  
DT  
XX  
XX Human IL4Ralpha gene probe #27.  
DE  
XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
XX allergic disease; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200104270-A1.  
PN  
XX 18-JAN-2001.  
PD  
XX  
XX 13-JUL-2000; 2000WO-US019094.  
PF  
XX  
XX 13-JUL-1999; 99US-0143435P.  
PR  
XX  
XX (GENA-) GENA1SSANCE PHARM INC.  
PA  
XX  
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;  
P1  
XX WPI; 2001-103078/11.  
DR  
XX  
XX New isolated polynucleotide useful for the identification of therapeutics  
PT in allergic diseases is new.  
XX  
XX  
XX Claim 15; Page 42; 188pp; English.  
PS  
XX  
CC The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha

CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a probe for human IL4R-alpha  
CC  
SQ Sequence 15 BP; 1 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1235 TCCAGCCCGAGGCG 1248  
Db 14 TCCAGCCCGAGGCG 1  
XX  
RESULT 597  
AAF69537  
ID AAF69537 standard; DNA; 15 BP.  
XX  
XX AAF69537;  
AC  
XX 18-APR-2001 (first entry)  
DT  
XX  
XX Human IL4Ralpha gene probe #177.  
DE  
XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
XX allergic disease; probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200104270-A1.  
PN  
XX 18-JAN-2001.  
PD  
XX  
XX 13-JUL-2000; 2000WO-US019094.  
PF  
XX  
XX 13-JUL-1999; 99US-0143435P.  
PR  
XX  
XX (GENA-) GENA1SSANCE PHARM INC.  
PA  
XX  
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;  
P1  
XX WPI; 2001-103078/11.  
DR  
XX  
XX New isolated polynucleotide useful for the identification of therapeutics  
PT in allergic diseases is new.  
XX  
XX  
XX Claim 15; Page 45; 188pp; English.  
PS  
XX  
CC The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha  
CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a probe for human IL4R-alpha  
CC  
SQ Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 U; 0 Other;  
XX  
XX  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1451 CAGGTGACGCCCC 1464  
III +|||||

Db 1 CAGCTGACGCCCC 14

RESULT 598  
AAF73926  
ID AAF73926 standard; DNA; 15 BP.  
XX  
XX AAF73926;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Human SLC6A4 allele-specific oligonucleotide primer #46.  
XX  
XX Solute carrier family 6 neurotransmitter transporter, serotonin 4; SLC6A4;  
XX genotyping; allele specific oligonucleotide; ss.  
XX  
XX Homo sapiens.  
XX  
XX W0200109161-A1.  
XX  
XX 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000WO-US020638.  
XX  
XX 29-JUL-1999; 99US-0146290P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Denton RR, Duda A, Mandabalan K, Sanchis A, Stephens JC;  
XX  
XX WPI; 2001-123317/13.  
XX  
XX New isolated polynucleotide comprising a polymorphic variant for the  
XX PT solute carrier family 6 neurotransmitter transporter, serotonin member 4  
XX PT gene for identifying drugs for treating disorders related to expression  
XX PT of the protein.  
XX  
XX  
XX Claim 12; Page 21; 152pp; English.  
XX  
XX The present invention relates to a polymorphic variant of a reference  
XX CC sequence for the solute carrier family 6 neurotransmitter transporter,  
XX CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence  
XX CC complementary to the first sequence. The invention is used in producing a  
XX CC recombinant organism that can be used to express SLC6A4 for protein  
XX CC structure analysis and binding studies. A composition comprising a  
XX CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4  
XX CC gene.  
XX  
XX Sequence 15 BP; 1 A; 5 C; 4 G; 5 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1471 TTGACCTGCCTCC 1484  
Db 1 TTGAGCTGCCTCC 14

RESULT 599  
AAF73930  
ID AAF73930 standard; DNA; 15 BP.  
XX  
XX AAF73930;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Human SLC6A4 allele-specific oligonucleotide primer #50.  
XX  
XX Solute carrier family 6 neurotransmitter transporter, serotonin 4; SLC6A4;  
XX KM genotyping; allele specific oligonucleotide; ss.  
XX  
XX Homo sapiens.

XX  
XX W0200109161-A1.  
XX  
XX 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000WO-US020638.  
XX  
XX 29-JUL-1999; 99US-0146290P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Denton RR, Duda A, Mandabalan K, Sanchis A, Stephens JC;  
XX  
XX WPI; 2001-123317/13.  
XX  
XX New isolated polynucleotide comprising a polymorphic variant for the  
XX PT solute carrier family 6 neurotransmitter transporter, serotonin member 4  
XX PT gene for identifying drugs for treating disorders related to expression  
XX PT of the protein.  
XX  
XX  
XX Claim 12; Page 21; 152pp; English.  
XX  
XX The present invention relates to a polymorphic variant of a reference  
XX CC sequence for the solute carrier family 6 neurotransmitter transporter,  
XX CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence  
XX CC complementary to the first sequence. The invention is used in producing a  
XX CC recombinant organism that can be used to express SLC6A4 for protein  
XX CC structure analysis and binding studies. A composition comprising a  
XX CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4  
XX CC gene.  
XX  
XX Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1471 TTGACCTGCCTCC 1484  
Db 2 TTGAGCTGCCTCC 15

RESULT 600  
ADV36833/C  
ID ADV36833 standard; RNA; 15 BP.  
XX  
XX ADV36833;  
XX  
XX 10-FEB-2005 (first entry)  
XX  
XX Human anti-HER2 NCH ribozyme substrate sequence #806.  
XX  
XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
XX KM protein-tyrosine-phosphatase-1b; PTP-1B; methionine aminopeptidase;  
XX KM MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
XX KM beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
XX KM c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
XX KM hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
XX KM amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
XX KM diabetes; obesity; cardiac disease; heart disease; age-related disease;  
XX KM hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
XX KM ss.  
XX  
XX Homo sapiens.  
XX  
XX W0200116312-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 30-AUG-2000; 2000WO-US023998.  
XX  
XX 31-AUG-1999; 99US-0151713P.  
XX  
XX 27-SEP-1999; 99US-00406643.

PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.  
 PR 29-DEC-1999; 99US-0173612P.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 PI Kapelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 PR WPI; 2001-244406/25.  
 DR Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 PT  
 PR  
 PS Example 7; Page 488; 717pp; English.  
 XX  
 XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention of  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTN-1B), methionine  
 CC aminopeptidase (MeAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zincyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH  
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID  
 CC Nos are repeated more than once in the specification, but these have  
 CC different sequences associated with them.  
 XX  
 SO Sequence 15 BP; 5 A; 3 C; 5 G; 0 T; 2 U; 0 Other;  
 Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
 QY 1055 TTATCCAGCAGGTC 1068  
 DB 14 TTTTCCAGCAGGTC 1  
 RESULT 601  
 ABL46309  
 ID ABL46309 standard; DNA; 15 BP.  
 XX  
 AC ABL46309;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 DE Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:276.  
 KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KM PCR primer; probe; ss.

OS	Mus sp.
XX	Synthetic.
XX	
PN	WO200198537-A2.
XX	
PD	27-DEC-2001.
XX	
PF	15-JUN-2001; 2001WO-US019401.
XX	
PR	17-JUN-2000; 2000US-0212308P.
PR	15-JUN-2001; 2001US-00212308.
XX	
PA	(THIR-) THIRD WAVE TECHNOLOGIES INC.
PI	Lymichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX	
XX	WPI; 2002-049698/06.
DR	
PT	Identifying oligonucleotides hybridizing to nucleic acids containing
PT	secondary structure, useful in clinical diagnosis, comprises identifying
PT	primers that interact with the target to form an extension product under
PT	amplification conditions.
XX	
PS	Claim 48; Fig 79A; 40pp; English.
XX	
CC	The present invention describes a method for identifying oligonucleotides
CC	with desired hybridisation properties to nucleic acid targets containing
CC	secondary structure. The method comprises amplifying a target nucleic
CC	acid having at least one accessible and one inaccessible site. Primers
CC	that form an extension product are identified as the oligonucleotides
CC	which can interact with the folded target nucleic acid. Oligonucleotides
CC	from the present invention can be used in novel detection methods for
CC	clinical diagnostic purposes, including the detection and identification
CC	of pathogenic organisms (e.g., HIV). The method allows the ability to
CC	rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC	sequences used in the exemplification of the present invention
XX	
SQ	Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match	0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity	92.9%; Pred. No. 3.3e+02;
Matches 13; Conservative	0; Mismatches 1; Indels 0; Gaps 0
DG	669 CATCTGGGTCTCG 682       2 CATCTTGGTCTCG 15
RESULT 602	
AAD43755	
ID	AAD43755 standard; DNA; 15 BP.
XX	
AC	AAD43755;
XX	
DT	14-NOV-2002 (first entry)
XX	
DE	Human AGR2 gene polymorphism detecting ASO probe #3.
XX	
KM	Human; angiotensin receptor 2; forensic application; drug response;
KM	AGR2; congenital abnormality of kidney and urinary tract; CAKUT;
KM	cardiovascular disorder; premature ovarian failure; gene therapy; POF;
KM	polymorphism; ASO; allele-specific oligonucleotide; probe; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200263045-A1.
XX	
PD	15-AUG-2002.
XX	
PF	02-FEB-2001; 2001MO-US003620.
XX	
PR	02-FEB-2001; 2001MO-US003620.

XX (GENA-) GENAISANCE PHARM INC.  
XX PA Chew A, Choi JY, Koshy B, Stephens JC;  
XX PI WPI; 2002-636599/68.  
XX DR  
XX PT Novel genetic variants of angiotensin receptor 2 isogenes, useful in  
XX PT therapeutic purposes and in screening for drugs targeting the angiotensin  
XX PT receptor protein.  
XX PS Claim 16; Page 20; 69pp; English.  
XX CC The invention relates to genetic variants of human angiotensin receptor 2  
XX CC (AGTR2) isogenes and methods for detecting variants of AGTR2 gene.  
XX CC Polynucleotides of the invention are useful in studying the expression  
XX CC and biological function of AGTR2 and in developing drugs targeting AGTR2  
XX CC protein. Methods of the invention are useful for studying population  
XX CC diversity, anthropological lineage, the significance of diversity and  
XX CC lineage at the phenotypic level, paternity testing, forensic applications  
XX CC and for identifying associations between AGTR2 genetic variations and a  
XX CC trait such as levels of drug response or susceptibility to disease. It is  
XX CC useful in developing diagnostic tests and therapeutic treatments for  
XX CC cardiovascular disorders, congenital abnormalities of kidney and urinary  
XX CC tract (CAKUT) and premature ovarian failure (POF). The invention is  
XX CC useful in gene therapy. The present sequence is an allele-specific  
XX CC oligonucleotide (ASO) probe used to detect human AGTR2 gene polymorphisms  
XX SQ Sequence 15 BP; 1 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 991 TGCGTGCCTTCCA 1004  
XX Db 1 TGGCTTCCCTTCCA 14  
XX  
XX RESULT 603  
XX ABK32066/c  
XX ID ABK32066 standard; DNA; 15 BP.  
XX AC ABK32066;  
XX XX  
XX DT 23-APR-2002 (first entry)  
XX DE Human colon cancer SAGE tag #167.  
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
XX KW serial analysis of gene expression; diagnostic; prognostic; probe;  
XX KW cancer marker; ss.  
XX OS Homo sapiens.  
XX XX  
XX PN U56333152-B1.  
XX PD 25-DEC-2001.  
XX PF 20-MAY-1998; 98US-00081646.  
XX PR 20-MAY-1998; 98US-00081646.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;  
XX XX WPI; 2002-153821/20.  
XX DR  
XX PT New human nucleic acid containing specific SAGE tags, useful as  
XX PT diagnostic markers for cancer, also derived probes.  
XX PS Disclosure; Col 24; 161pp; English.

XX The invention relates to an isolated, purified human nucleic acid (I)  
XX CC that has the same sequence as a mRNA found in humans and is a SAGE  
XX CC (serial analysis of gene expression) tag comprising a single stranded  
XX CC probe containing at least 10 consecutive nucleotides. SAGE tags, are  
XX CC diagnostic and prognostic markers of cancer, especially of the colon and  
XX CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer  
XX CC SAGE tags of the invention  
XX XX  
XX SQ Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 367 GTGATGTGATCAT 360  
XX Db 15 GCGATGTGATCAT 2  
XX  
XX RESULT 604  
XX ACA09887  
XX ID ACA09887 standard; RNA; 15 BP.  
XX AC ACA09887;  
XX XX  
XX DT 03-JUN-2003 (first entry)  
XX DE Necrosis factor kappa B sub-unit modulating enzyme target #80.  
XX KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; linozyme; zinozyme;  
XX KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
XX KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
XX KW osteopagel cancer; stomach cancer; bladder cancer; pancreatic cancer;  
XX KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
XX KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
XX KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
XX KW cyclophosphamide; doxorubin; fluorouracil carboxiplatin; edatrexate;  
XX KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
XX KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
XX KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
XX KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
XX KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX PN US202177568-A1.  
XX PD 28-NOV-2002.  
XX PF 23-MAY-2001; 2001US-00864785.  
XX PR 07-DEC-1992; 92US-00987132.  
XX PR 18-MAY-1994; 94US-00245466.  
XX PR 15-AUG-1994; 94US-00291932.  
XX PR 23-DEC-1996; 96US-00777916.  
XX PA (STIN/) STINGHCOMB D T.  
XX PA (MCSW/) MCSWIGEN J.  
XX PA (DRAP/) DRAPER K G.  
XX PI Stinchcomb DT, Mcswiggen J, Draper KG;  
XX XX WPI; 2003-340953/32.  
XX DR  
XX PT Novel enzymatic nucleic acid molecules which down regulates expression of  
XX PT a sequence encoding a subunit of nuclear factor kappa B useful for  
XX PT treating cancer, inflammatory disorders and autoimmune diseases.  
XX PS Claim 3; Page 61; 72pp; English.  
XX CC The invention describes an enzymatic nucleic acid molecule (I) which down  
XX CC regulates expression of a sequence encoding a subunit of nuclear factor

CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating RBL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of RBL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule

CC Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.3e+02;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Gy 1410 CTCTCTCCCAATG 1423

Db 2 CUUCUCCUCCAUUG 15

RESULT 605

ACA09888

ID ACA09888 standard; RNA; 15 BP.

AC ACA09888;

DT 03-JUN-2003 (first entry)

DE Necrosis factor kappa B sub-unit modulating enzyme target #81.

KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberyze; cancer; RBL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; RBL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; ss.

OS Homo sapiens.

PN US200217568-A1.

PD 28-NOV-2002.

PF 23-MAY-2001; 2001US-00864785.

PR 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

PA (STIN/) STINGCOMB D T.

PA (MCSM/) MCSMIGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswigen J, Draper KG;

PI WPI; 2003-340953/32.

DR Novel enzymatic nucleic acid molecules which down regulates expression of

PT a sequence encoding a subunit of nuclear factor kappa B useful for

PT treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 61; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating RBL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of RBL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule

CC Sequence 15 BP; 1 A; 7 C; 1 G; 0 T; 6 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.3e+02;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Gy 1410 CTCTCTCCCAATG 1423

Db 1 CUUCUCCUCCAUUG 14

RESULT 606

ABX94796/C

ID ABX94796 standard; DNA; 15 BP.

AC ABX94796;

DT 08-JUL-2003 (first entry)

DE Beta-actin PCR primer #2.

KW Androgen receptor; human; acne; acneform skin disorder; acne rosacea;  
 KW antisense; steroid hormone receptor; steroid hormone metabolising enzyme;  
 KW 5alpha-reductase; dermatological; antiseborrheic; sebaceous gland;  
 KW phosphorocholate; RT-PCR; primer; beta-actin; ss.

OS Unidentified.

PN WO2003017917-A2.

PD 06-MAR-2003.

PR 23-AUG-2002; 2002WO-EP009452.

PR 23-AUG-2001; 2001DE-01041443.



PA (RINA-) RINA TECHNOLOGIEN GMBH.  
PA (ZOUR/) ZOURBOLIS C C.  
XX Zouboulis CC;  
XX WPI; 2003-278606/27.  
XX  
PT Use of non-viral agents for treating acne or acneform skin conditions,  
PT particularly antisense oligonucleotides directed against androgen  
PT receptor or 5alpha reductase.  
XX  
PS Example 1; Page 18; 36pp; German.  
XX  
CC This invention describes a novel method for treatment of acne and  
CC acneform skin disorders, including rosacea, using a non-viral active  
CC agent, prepared by molecular biological methods. The method comprises an  
CC antisense oligonucleotide; (stabilised) ribozyme; (mirror) aptamer;  
CC chimeric RNA/DNA oligonucleotide; naked plasmid DNA or DNA encapsulated  
CC in a liposome, especially an antisense oligonucleotide specific for a  
CC gene that encodes a steroid hormone receptor or steroid hormone  
CC metabolising enzyme, particularly the androgen receptor and/or 5alpha-  
CC reductase. The products of the invention have dermatological and  
CC antiseborrheic activity and can inhibit the androgen-induced stimulation  
CC of sebaceous gland activity. The method of the invention provides  
CC effective treatment with reduced side effects and without the  
CC difficulties associated with systemic administration. This sequence  
CC represents a RT-PCR primer used to amplify the beta-actin gene, which is  
CC used as a control during the amplification of the human androgen receptor  
CC described in the disclosure of the invention  
XX  
SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 134 GCCCCAGGCGCCAG 147  
DB 14 GCCCCAGGCGCCAG 1  
XX  
RESULT 607  
ADL50873  
ID ADL50873 standard; RNA; 15 BP.  
XX  
AC ADL50873;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human PKR substrate sequence #1987.  
XX  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
KW substrate; ds.  
XX  
OS Undifferentiated.  
XX  
PN WO200281628-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002WO-US010512.  
XX  
XX 05-APR-2001; 2001US-00827395.  
PR 29-MAY-2001; 2001US-0294412P.  
PR 28-AUG-2001; 2001US-0315315P.  
XX

XX (RIBO-) RIBOZYME PHARM INC.  
PA Blatt L, Chowrira B, Haeblerl P, Mcawiggen J, Fosnaugh K;  
XX WPI; 2003-058513/05.  
XX  
XX WPI; 2003-058513/05.  
XX  
PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX  
PS Claim 59; SEQ ID NO 4406; 317pp; English.  
XX  
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
CC that down regulate the expression or inhibit the function of a receptor  
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
CC invention are useful for treating: cerebrovascular accident, central  
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
CC nucleic acids of the invention are also useful for down-regulating the  
CC expression of a target gene and as a diagnostic tool to examine genetic  
CC drifts and mutations within diseased cells or to detect the presence of a  
CC target RNA in a cell. The present RNA sequence represents a human PKR  
CC substrate sequence.  
XX  
SQ Sequence 15 BP; 0 A; 7 C; 2 G; 0 T; 6 U; 0 Other;  
XX  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 57.1%; Pred. No. 3.3e+02;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 105 CCCTCCCTGCTGCT 118  
DB 1 CCCUCUCGUCGCU 14  
XX  
RESULT 608  
ADP64570  
ID ADP64570 standard; DNA; 15 BP.  
XX  
AC ADP64570;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE VIC probe for typing SNP260 in a disease sensitivity gene.  
XX  
XX disease-sensitive gene; single nucleotide polymorphism; SNP;  
KW linkage disequilibrium analysis; type II diabetes sensitive gene; probe;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004049234-A1.  
XX  
PD 10-JUN-2004.  
XX  
XX 21-NOV-2003; 2003WO-JP014888.  
XX  
XX 22-NOV-2002; 2002JP-00339901.  
XX  
PA (BIOS-) APPLIED BIOSYSTEMS JAPAN LTD.  
PA (FUIT) FUJITSU LTD.  
PA (ITAK/) ITAKURA M.  
XX  
XX Itakura M, Kato H, Katashima R, Shinohara S, Nomura K;  
XX WPI; 2004-460856/43.  
XX



CC The present invention relates to novel binding agents comprising at least  
CC one peptide capable of binding myostatin and inhibiting its activity. In  
CC one embodiment, the binding agent comprises at least one myostatin-  
CC binding peptide attached directly or indirectly to at least one vehicle  
CC such as a polymer or an Fc domain. Myostatin (also known as  
CC growth/differentiation factor 8, GDF-8) is a transforming growth factor-  
CC beta (TGF-beta) family member known to be involved in regulation of  
CC skeletal muscle mass. The binding agents increase lean muscle mass when  
CC administered to animals and decrease fat to muscle ratios. The binding  
CC agents are useful for treating muscle-wasting disease, e.g. muscular  
CC dystrophy, amyotrophic lateral sclerosis, congestive obstructive  
CC pulmonary disease, chronic heart failure, cancer, AIDS, renal failure,  
CC uremia, rheumatoid arthritis, age-related sarcopenia, muscle-wasting due  
CC to prolonged bedrest, spinal cord injury, stroke, bone fracture, or  
CC aging, and myosin-related metabolic disorder, e.g. diabetes, obesity,  
CC hyperlipaemia, bone loss, or osteoporosis. The present sequence is a  
CC linker peptide coding sequence used to illustrate the invention.

XX  
SQ Sequence 15 BP; 1 A; 0 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1276 ACCGACATCTCCAC 1289

Db 15 ACCGACATCTCCAC 2

RESULT 611  
ADS12596/C  
ID ADS12596 standard; DNA; 15 BP.

XX ADS12596;

AC 16-DEC-2004 (first entry)

XX  
DE Reverse RT-PCR primer used to amplify human beta-actin DNA SegID.

XX PCR; primer; 89; microarray; inflammatory bowel disease; Crohn's disease;

XX ulcerative colitis; screening method; antiinflammatory; antitumor;

XX RT-PCR; real-time PCR; beta-actin.

XX Homo sapiens.

XX EPI462527-A1.

XX 29-SEP-2004.

XX 26-MAR-2003; 2003EP-00006943.

XX 26-MAR-2003; 2003EP-00006943.

XX (CONA-) CONARIS RES INST AG.

XX Costello C, Ma N, Schreiber SD, Seegert D;

XX WPI; 2004-663617/65.

XX New diagnostic composition comprising specific nucleic acid molecules,

XX PT useful for diagnosing or developing a compound for treating inflammatory

XX PT bowel diseases or related disease e.g., Crohn's disease and ulcerative

XX PT colitis.

XX Example 1; SEQ ID NO 6; 63pp; English.

XX This invention relates to a novel diagnostic composition that comprises  
CC nucleic acid molecules bound to a solid support (or microarray), wherein  
CC each nucleic acid can hybridise to an mRNA of a gene that shows abnormal  
CC expression in an gastrointestinal condition. Specifically, it refers to  
CC DNA oligos useful for preparing a microarray chip for the diagnosis of  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis or a  
CC disposition thereof. The present invention describes nucleic acid

CC molecules useful for screening methods to identify compounds that can be  
CC used for therapy or to prevent progression of the aforementioned  
CC conditions. As such, the pharmaceutical compositions developed  
CC according exhibit antiinflammatory and antitumor activities. This  
CC oligonucleotide sequence is an RT-PCR primer used to amplify human beta-  
CC actin, an endogenous control gene used in an exemplification of the  
CC invention.

XX  
SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 GCCCCAGGCCGAC 147

Db 14 GCCCCAGGCCGAC 1

RESULT 612

ADV95329/C  
ID ADV95329 standard; DNA; 15 BP.

XX ADV95329;

AC 24-FEB-2005 (first entry)

XX Sequence #1 from human BMP-4 DNA.

XX Methanol Yeast; gene expression; cloning; bone morphogenetic protein-4;

XX BMP-4; de.

XX Homo sapiens.

XX CN1513979-A.

XX 21-JUL-2004.

XX 20-MAY-2003; 2003CN-00136581.

XX 20-MAY-2003; 2003CN-00136581.

XX (UVFU-) UNIV FUJIAN.

XX Zhang Y, Chen Y, Huang Y;

XX WPI; 2004-710695/70.

XX High efficiency expression of recombinant human bone forming protein 4

XX and 7 using methanol yeast.

XX Disclosure; Fig 1; 14pp; Chinese.

XX The invention relates to a technique for using methanol yeast to

XX efficiently express human bone morphogenetic proteins (BMPs). The method

XX includes using the plasmids pBluescript KS-BMP4 and pBluescript KS-BMP7

XX containing human BMP-4 and BMP-7 cDNA sequences as template. PCR

XX amplification, fixed-point mutation to the arginine codon in the

XX sequence, and cloning it to methanol yeast expression plasmid pPIC9K. The

XX method further comprises transforming this plasmid into methanol yeast

XX GS115. The method is useful for using methanol yeast to efficiently

XX express human bone morphogenetic protein. This sequence represents a

XX sequence from BMP-4 DNA.

XX  
SQ Sequence 15 BP; 5 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1402 AGCTTCAGCTTCTC 1415

Db 15 AGCTTCAGCTTCTC 2



XX 68; aptamer.  
XX Synthetic.  
XX WO2005019430-A2.  
XX 03-MAR-2005.  
XX 23-AUG-2004; 2004WO-US027284.  
XX 22-AUG-2003; 2003US-0497104P.  
XX (RERE-) RES DEV FOUND.  
XX Ellington A, Manjula R;  
XX WPI; 2005-202637/21.  
XX Selecting aptamer beacons in vitro comprises generating a pool of single-  
XX stranded nucleic acid species comprising a fluorophore F1, and a random  
XX insert of N nucleotides.  
XX Example 1; SEQ ID NO 7, 124pp; English.  
XX The invention relates to a method of selecting aptamer beacons in vitro  
XX which comprises generating a pool of single-stranded nucleic acid species  
XX having a fluorophore F1, and a random insert of N nucleotides. The method  
XX is useful for selecting aptamer beacons in vitro. The present sequence  
XX represents a randomized DNA pool capture oligonucleotide.  
XX Sequence 15 BP; 6 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 397 ATGAGCAGCTGAC 410  
XX 2 ATGAGCAGCTGAC 15  
XX  
XX RESULT 616  
XX ID ADY52800 standard; DNA; 15 BP.  
XX AC ADY52800;  
XX 19-MAY-2005 (first entry)  
XX Human CHRNA2 gene P52 detecting reverse ASO primer, SEQ ID NO: 13.  
XX Selectable marker; pharmaceutical; gene therapy; diagnosis;  
XX SNP detection; cognitive disorder; nootropic; neurological disease;  
XX dementia; Alzheimer's disease; neuroprotective; degeneration;  
XX Parkinson's disease; antiparkinsonian;  
XX cholinergic receptor; nicotinic, alpha polypeptide 2; CHRNA2; primer; ss.  
XX Homo sapiens.  
XX US2005048543-A1.  
XX 03-MAR-2005.  
XX 09-JUL-2004; 2004US-00887650.  
XX 11-JUL-2003; 2003US-0486331P.  
XX  
XX (AERS/) AERSENG J.  
XX (ATHA/) ATHANASIOU M.  
XX (BRAI/) BRAIN C.  
XX (COHE/) COHEN N.  
XX (DAIN/) DAIN B.

PA (DENT/) DENTON R R.  
PA (JUDS/) JUDSON R S.  
PA (OZDE/) OZDEMIR V.  
PA (REED/) REED C R.  
XX Aerssens J, Athanasio M, Brain C, Cohen N, Dain B, Denton RR;  
XX Judson RS, Ozdemir V, Reed CR;  
XX WPI; 2005-202086/21.  
XX Determining whether an individual has a response marker I or II comprises  
XX determining whether the individual has zero copies or at least one copy  
XX of any of the CHRNA2 haplotypes.  
XX Claim 42; SEQ ID NO 13; 52pp; English.  
XX The present invention relates to a method for determining whether an  
XX individual has a response marker I or II. The method involves determining  
XX whether the individual has zero copies or at least one copy of any of the  
XX cholinergic receptor, nicotinic, alpha polypeptide 2 (CHRNA2) haplotypes.  
XX The composition and methods are useful for diagnosing and creating a  
XX cognitive disorder, e.g. mild or moderate dementia of the Alzheimer's  
XX type, or dementia associated with Parkinson's disease. The method of the  
XX invention is also useful for predicting the expected therapeutic response  
XX of an individual to treatment with galantamine and for gene therapy. The  
XX present sequence is the human CHRNA2 gene polymorphic site 2 (P52)  
XX detecting allele-specific oligonucleotide (ASO) primer.  
XX Sequence 15 BP; 0 A; 3 C; 5 G; 6 T; 0 U; 1 Other;  
XX  
XX Query Match 0.7%; Score 12.4; DB 1; Length 15;  
XX Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 671 TCTGGCTCTGCT 684  
XX 2 TCTGGCTCTGCT 15  
XX  
XX RESULT 617  
XX ID AD245541/c  
XX AD245541 standard; DNA; 15 BP.  
XX AC AD245541;  
XX 30-JUN-2005 (first entry)  
XX Murine factor IX directed antibody CDR1 DNA SEQ ID NO 245.  
XX bispecific antibody; blood coagulation factor VIII; bleeding;  
XX fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;  
XX factor VIII deficiency; von Willebrand's disease; hemostatic;  
XX immunostimulator; antibody engineering; ds; gene.  
XX Mus musculus.  
XX WO2005035756-A1.  
XX 21-APR-2005.  
XX 08-OCT-2004; 2004WO-JP014911.  
XX 10-OCT-2003; 2003WO-JP013062.  
XX 14-OCT-2003; 2003WO-JP013123.  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX Hattori K, Kojima T, Miyazaki T, Soeda T;  
XX WPI; 2005-315563/32.  
XX P-PSDB; AD245542.  
XX Novel bispecific antibody substituting for function of cofactor that

PT enhances enzyme reaction, and recognizing both enzyme and substrates of  
PT enzyme, useful for treating hemophilia A.  
PS Disclosure; SEQ ID NO 245; 69bp; Japanese.  
XX  
CC This invention describes a novel bispecific antibody which can act as a  
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and  
CC the enzyme substrate. The antibody specifically binds to blood  
CC coagulation factor VIII. The invention also describes a composition  
CC comprising the antibody and a carrier, a kit useful in preventing and/or  
CC treating bleeding associated with a disorder or from a disease caused by  
CC bleeding. The composition includes blood coagulation factor VIII. The  
CC antibody of the invention can be a blood-coagulation fibrinolytic related  
CC factor including blood-coagulation factor VIII, blood coagulation factor  
CC X, or blood-coagulation factor IX. The antibody comprises a complementary  
CC determining region (CDR) of anti-blood-coagulation factor IX/Xa factor  
CC antibody. The novel antibody or composition is useful for preventing  
CC and/or treating a disease accompanying bleeding, or the disease resulting  
CC from bleeding, where the disease accompanying bleeding or the disease  
CC resulting from bleeding develops and/or progresses by an active reduction  
CC or deletion of the blood coagulation factor VIII. The disease the  
CC develops and/or progresses by an active reduction or deletion of the  
CC blood coagulation factor VIII and/or activation blood coagulation factor  
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is  
CC an acquired hemophilia A. This sequence encodes a fragment of the  
CC antibody described in the method of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
QY  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 30 GTGCATCCAGAGC 43  
15 GTGCATCCAGAGC 2

RESULT 618  
AEA40005/c  
ID AEA40005 standard; DNA; 15 BP.  
XX  
AC AEA40005;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE DNA encoding TNF resistant monoclonal antibody VH region, D2VH CDR1.  
XX  
KW tumor necrosis factor; TNF; monoclonal antibody; D2 mAb;  
KW light chain variable region; heavy chain variable region; D2VH; ds.  
XX  
OS Unidentified.  
XX  
FT Key Location/Qualifiers  
FT CDS 1..15  
FT /\*tag= a  
FT /product= "CDR1 of D2VH"

CN1544467-A.  
XX  
PD 10-NOV-2004.  
XX  
PF 13-NOV-2003; 2003CN-01105920.  
XX  
PR 13-NOV-2003; 2003CN-01105920.  
XX  
PA (UWFO-) UNIV FOURTH MILITARY MEDICAL.  
XX  
PI Jin B, Liu X, Yang K;  
XX

DR WPI; 2005-153079/17.  
DR P-PsDB; AEA40006.  
XX  
XX Variable region gene of high neutralization activity monoclonal antibody  
PT of tumor necrosis factor and its preparation.  
PS Claim 1; Page 3; 20pp; Chinese.  
XX  
XX The invention relates to a method for preparing variable region genes of  
CC high neutralization activity tumor necrosis factor (TNF) resistant  
CC monoclonal antibody (D2 mAb). The method comprises using recombinant  
CC human TNF immune BALB/c mouse to prepare a plurality of mouse anti-TNF  
CC monoclonal antibody, carrying out an extracorporeal blocking-up  
CC experiment to screen anti-TNF monoclonal antibody with high  
CC neutralization activity. By cloning the monoclonal antibody light chain  
CC and heavy chain variable region (VL and VH respectively) genes, the  
CC monoclonal antibody light chain and heavy chain variable region gene  
CC sequence and amino acid sequence can be obtained, and the utility of the  
CC gene sequence and protein sequence can be confirmed. This sequence  
CC represents DNA encoding the complementarity determining region, CDR1 of  
CC D2VH.  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
QY  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 30 GTGCATCCAGAGC 43  
15 GTGCATCCAGAGC 2

RESULT 619  
AEB21700/c  
ID AEB21700 standard; DNA; 15 BP.  
XX  
AC AEB21700;  
XX  
DT 08-SEP-2005 (first entry)  
XX  
DE Anti-Nogo-antibody A2A10/3 CDR 1 DNA SEQ ID NO 22.  
XX  
KW neuroprotective; nootropic; cerebroprotective; vasotropic;  
KW antiparkinsonian; anticonvulsant; protein production; therapeutic;  
KW pharmaceutical; amyloidosis; metabolic disorder;  
KW cerebrovascular ischemia; cardiovascular disease; neurological disease;  
KW brain injury; injury; spinal cord injury; vulnertary; dementia;  
KW peripheral neuropathy; parkinsons disease; Huntingtons chorea;  
KW genetic disorder; Creutzfeldt Jakob disease; infection;  
KW motor neurone disease; cns-gen.; muscular-gen.; myositis;  
KW antiinflammatory; inflammation; musculoskeletal disease;  
KW Alzheimers disease; degeneration; antibody; heavy chain variable region;  
KW ds.  
XX  
OS Unidentified.  
XX  
FT WO2005061545-A2.  
FT 07-JUL-2005.  
XX  
PF 20-DEC-2004; 2004WO-GB005343.  
XX  
PR 22-DEC-2003; 2003GB-00029684.  
XX  
PR 22-DEC-2003; 2003GB-00029711.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Hussain I, Prinjha RK;  
XX  
DR WPI; 2005-522181/53.  
DR P-PsDB; AEB21682.  
XX

PT Modulating production of amyloidogenic peptide in, e.g. Alzheimer's  
PT disease, by contacting cell and Nogo polypeptide with Nogo antagonist.  
XX  
XX  
PS Disclosure; SEQ ID NO 22; 53pp; English.  
XX  
CC The invention describes a method of modulating production of an  
CC amyloidogenic peptide comprising contacting a cell which is expressing  
CC the precursor from which the amyloidogenic peptide is derived and a Nogo  
CC polypeptide, with a Nogo antagonist. Also described are: use of a Nogo  
CC antagonist in the manufacture of a medicament for the treatment or  
CC prophylaxis of a disease involving amyloidosis; and a method of treatment  
CC or prophylaxis of Alzheimer's disease comprising administering to the  
CC human in need an anti-Nogo antibody. The invention is used for modulating  
CC production of amyloidogenic peptide in, e.g. Alzheimer's disease, stroke,  
CC traumatic brain injury and spinal cord injury, fronto-temporal dementias,  
CC peripheral neuropathy, Parkinson's disease, Huntington's disease,  
CC Creutzfeldt-Jakob disease, amyotrophic lateral sclerosis, multiple  
CC sclerosis, or inclusion body myositis. The invention provides an  
CC unexpected route for therapeutic intervention in particularly Alzheimer's  
CC disease. This sequence encodes anti-Nogo-antibody 2A10/3 heavy chain  
CC complementarily determining region (CDR) 1.  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 30 GTGCATCCAGAGC 43  
|||  
15 GTGCATCCAGAGC 2  
DB  
RESULT 620  
AEB08734/C  
ID AEB08734 standard; DNA; 15 BP.  
XX  
AC AEB08734;  
XX  
DT 08-SEP-2005 (first entry)  
DE antibody 2A10 heavy chain CDR DNA SEQ ID NO 22.  
XX  
XX cerebroprotective; vasotropic; neuroprotective; vlnary; nootropic;  
XX antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;  
XX pharmaceutical; cerebrovascular ischemia; cardiovascular disease;  
XX neurological disease; brain injury; injury; spinal cord injury;  
XX Alzheimer's disease; degeneration; dementia; neuropathy;  
XX parkinsons disease; Huntingtons chorea; genetic disorder;  
XX multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;  
XX infection; schizophrenia; psychiatric disorder; motor neurone disease;  
XX cns-gen.; muscular-gen.; ds.  
XX  
OS Unidentified.  
XX  
XX W02005061544-A2.  
PN 07-JUL-2005.  
XX  
PD 20-DEC-2004; 2004WO-GB005325.  
XX  
PF 22-DEC-2003; 2003GB-00029684.  
PR 22-DEC-2003; 2003GB-00029711.  
XX  
XX (GLAX) GLAXO GROUP LTD.  
PA  
XX  
XX Ella JH, Bon-Duval A, Grundy RI, Hussain F, Mcadam R;  
PI Plumpson C, Pirinjah RK, Wilson PA;  
XX  
XX WPI; 2005-479448/48.  
DR P-PSDB; AEB08717.  
XX  
XX New antibody or its functional fragment that binds with and neutralizes

PT human neurite outgrowth useful for treating or prophylaxis of stroke and  
PT other neurological disease e.g. traumatic brain injury, spinal cord  
PT injury, Alzheimer's disease.  
XX  
XX  
PS Disclosure; SEQ ID NO 22; 143pp; English.  
XX  
XX  
CC The invention describes an antibody (A1) or its functional fragment, that  
CC binds with and neutralizes human neurite outgrowth (NOCO). Also described  
CC are: providing a first vector encoding a heavy chain of the antibody;  
CC providing a second vector encoding a light chain of the antibody; co-  
CC transfecting a mammalian host cell with the first and second vectors;  
CC culturing the host cell in culture media (preferably serum free) under  
CC conditions permissive to the secretion of the antibody from the host cell  
CC into the culture media; recovering (and optionally purifying) the  
CC secreted antibody; and promoting axonal sprouting involving contacting a  
CC human axon with an anti-NOCO antibody. The antibody is useful in the  
CC preparation of a medicament for treating or prophylaxis of stroke and  
CC other neurological diseases/disorders (e.g. traumatic brain injury, spinal  
CC cord injury, Alzheimer's disease, frontotemporal dementias (taupathies),  
CC peripheral neuropathy, Parkinson's disease, Huntington's disease and  
CC multiple sclerosis); Creutzfeldt-Jakob disease (CJD), Schizophrenia,  
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The  
CC antibody inhibits neurodegeneration and/or promotes functional recovery  
CC in a human patient suffering, or at risk of developing, stroke or other  
CC neurological diseases/disorder. This sequence encodes an antibody 2A10  
CC heavy chain complementarily region (CDR) that can be used in the creation  
CC of anti-NOCO-antibody of the invention.  
XX  
SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 30 GTGCATCCAGAGC 43  
|||  
15 GTGCATCCAGAGC 2  
DB  
RESULT 621  
AEB99140  
ID AEB99140 standard; DNA; 15 BP.  
XX  
AC AEB99140;  
XX  
DT 23-FEB-2006 (first entry)  
DE Human c-fos FRET quencher oligonucleotide #4.  
XX  
XX analyte detection; drug screening; c-fos; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 15 /\*tag= a  
FT misc\_feature 15 /note= "Red oxazine dye labeled"  
XX  
XX W02005121359-A1.  
PN 22-DEC-2005.  
XX  
PD 11-JUN-2004; 2004WO-EP006344.  
XX  
PF 11-JUN-2004; 2004WO-EP006344.  
PR 11-JUN-2004; 2004WO-EP006344.  
XX  
XX (EVOT-) EVOTEC AG.  
PA  
XX  
XX Hinnaah SC, Lambroe D, Droegge S, Jaeger S, Gall K, Stuermer W;  
PI Schaefer M;  
XX  
XX WPI; 2006-056856/06.





GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2006, 06:09:50 ; Search time 10 Seconds  
(without alignments)

3.457 Million cell updates/sec

Title: US-09-930-503A-6

Perfect score: 1766  
Sequence: 1 aatcagagccaccgcgcggc.....cgagtgctcattcagatg 1766

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 508 seqs, 9787 residues

Total number of hits satisfying chosen parameters: 1016

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 488 summaries

Database : us-09-930-503a-6.sl.rge4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	1.7	AR109709	ACCESSION:AR109709
2	30	1.7	CO800306	ACCESSION:CO800306
3	28	1.6	CS174800	ACCESSION:CS174800
4	27	1.5	CO800305	ACCESSION:CO800305
5	27	1.5	CO800321	ACCESSION:CO800321
6	27	1.5	CS174801	ACCESSION:CS174801
7	25.8	1.5	CO800314	ACCESSION:CO800314
8	25.2	1.4	AR109708	ACCESSION:AR109708
9	24.8	1.4	134577	ACCESSION:134577
10	24.8	1.4	136528	ACCESSION:136528
11	24.8	1.4	176284	ACCESSION:176284
12	24.2	1.4	AR109715	ACCESSION:AR109715
13	24	1.4	AR109808	ACCESSION:AR109808
14	24	1.4	CS186499	ACCESSION:CS186499
15	24	1.4	AR109637	ACCESSION:AR109637
16	24	1.4	AR150645	ACCESSION:AR150645
17	24	1.4	AR151515	ACCESSION:AR151515
18	24	1.4	E16194	ACCESSION:E16194
19	24	1.4	E27220	ACCESSION:E27220
20	24	1.4	E28278	ACCESSION:E28278
21	24	1.4	AR300947	ACCESSION:AR300947
22	24	1.4	AR583779	ACCESSION:AR583779
23	24	1.4	AR651208	ACCESSION:AR651208
24	23.8	1.3	AR109661	ACCESSION:AR109661
25	23	1.3	117149	ACCESSION:117149
26	23	1.3	AX468718	ACCESSION:AX468718
27	22.4	1.3	117150	ACCESSION:117150
28	22.2	1.3	AR109658	ACCESSION:AR109658
29	22.2	1.3	AR109660	ACCESSION:AR109660
30	21.8	1.2	AR109595	ACCESSION:AR109595
31	21.8	1.2	AR109652	ACCESSION:AR109652
32	21.8	1.2	AR150643	ACCESSION:AR150643
33	21.8	1.2	E11748	ACCESSION:E11748

34	21.8	1.2	27	1	E12466	ACCESSION:E12466
35	21.8	1.2	27	1	E12660	ACCESSION:E12660
36	21.8	1.2	27	1	E14221	ACCESSION:E14221
37	21.8	1.2	27	1	E16192	ACCESSION:E16192
38	21.8	1.2	27	1	E27218	ACCESSION:E27218
39	21.8	1.2	27	1	E28276	ACCESSION:E28276
40	21.8	1.2	27	1	E37242	ACCESSION:E37242
41	21.8	1.2	27	1	AR211515	ACCESSION:AR211515
42	21.8	1.2	27	1	AR266284	ACCESSION:AR266284
43	21.8	1.2	27	1	AR300905	ACCESSION:AR300905
44	21.8	1.2	27	1	AR583777	ACCESSION:AR583777
45	21.8	1.2	27	1	AR651206	ACCESSION:AR651206
46	21.8	1.2	27	1	AR109839	ACCESSION:AR109839
47	21	1.2	21	1	AR109840	ACCESSION:AR109840
48	21	1.2	21	1	CS207678	ACCESSION:CS207678
49	21	1.2	21	1	CS207679	ACCESSION:CS207679
50	21	1.2	21	1	CS207680	ACCESSION:CS207680
51	21	1.2	21	1	CS207681	ACCESSION:CS207681
52	21	1.2	21	1	CS207682	ACCESSION:CS207682
53	21	1.2	21	1	CS207683	ACCESSION:CS207683
54	21	1.2	21	1	CS207684	ACCESSION:CS207684
55	21	1.2	21	1	CS207685	ACCESSION:CS207685
56	21	1.2	21	1	CS207686	ACCESSION:CS207686
57	21	1.2	21	1	CS207687	ACCESSION:CS207687
58	21	1.2	21	1	CS207688	ACCESSION:CS207688
59	21	1.2	21	1	CS207689	ACCESSION:CS207689
60	21	1.2	21	1	CS207690	ACCESSION:CS207690
61	21	1.2	21	1	CS207691	ACCESSION:CS207691
62	21	1.2	21	1	CS207692	ACCESSION:CS207692
63	21	1.2	21	1	CS207693	ACCESSION:CS207693
64	21	1.2	21	1	CS207694	ACCESSION:CS207694
65	21	1.2	21	1	CS207695	ACCESSION:CS207695
66	21	1.2	21	1	CS207696	ACCESSION:CS207696
67	21	1.2	21	1	CS207697	ACCESSION:CS207697
68	21	1.2	21	1	CS207698	ACCESSION:CS207698
69	21	1.2	21	1	CS207699	ACCESSION:CS207699
70	21	1.2	21	1	CS207700	ACCESSION:CS207700
71	21	1.2	21	1	CS207701	ACCESSION:CS207701
72	21	1.2	21	1	CS207702	ACCESSION:CS207702
73	21	1.2	21	1	CS207703	ACCESSION:CS207703
74	21	1.2	21	1	CS207704	ACCESSION:CS207704
75	21	1.2	21	1	CS207705	ACCESSION:CS207705
76	21	1.2	21	1	CS207706	ACCESSION:CS207706
77	21	1.2	21	1	CS207707	ACCESSION:CS207707
78	21	1.2	21	1	CS207708	ACCESSION:CS207708
79	21	1.2	21	1	CS207709	ACCESSION:CS207709
80	21	1.2	21	1	CS207710	ACCESSION:CS207710
81	21	1.2	21	1	CS207711	ACCESSION:CS207711
82	21	1.2	21	1	CS207712	ACCESSION:CS207712
83	21	1.2	21	1	CS207713	ACCESSION:CS207713
84	21	1.2	21	1	CS207714	ACCESSION:CS207714
85	21	1.2	21	1	CS207715	ACCESSION:CS207715
86	21	1.2	21	1	CS207716	ACCESSION:CS207716
87	21	1.2	21	1	CS207717	ACCESSION:CS207717
88	21	1.2	21	1	CS207718	ACCESSION:CS207718
89	21	1.2	21	1	CS207719	ACCESSION:CS207719
90	21	1.2	21	1	CS207720	ACCESSION:CS207720
91	21	1.2	21	1	CS207721	ACCESSION:CS207721
92	21	1.2	21	1	CS207722	ACCESSION:CS207722
93	21	1.2	21	1	CS207723	ACCESSION:CS207723
94	21	1.2	21	1	CS207724	ACCESSION:CS207724
95	21	1.2	21	1	CS207725	ACCESSION:CS207725
96	21	1.2	21	1	CS207726	ACCESSION:CS207726
97	21	1.2	21	1	CS207727	ACCESSION:CS207727
98	21	1.2	21	1	CS207728	ACCESSION:CS207728
99	21	1.2	21	1	CS207729	ACCESSION:CS207729
100	21	1.2	21	1	CS207730	ACCESSION:CS207730
101	21	1.2	21	1	CS207731	ACCESSION:CS207731
102	21	1.2	21	1	CS207732	ACCESSION:CS207732
103	21	1.2	21	1	CS207733	ACCESSION:CS207733
104	21	1.2	21	1	CS207734	ACCESSION:CS207734
105	21	1.2	21	1	CS207735	ACCESSION:CS207735
106	21	1.2	21	1	CS207736	ACCESSION:CS207736
					CS207737	ACCESSION:CS207737
					CS207738	ACCESSION:CS207738
					CS207739	ACCESSION:CS207739

107	21	1.2	21	1	CS207740	ACCESSION:CS207740	C 180	20.6	1.2	24	1	E12479	ACCESSION:E12479
108	21	1.2	21	1	CS207741	ACCESSION:CS207741	C 181	20.6	1.2	24	1	AR300918	ACCESSION:AR300918
109	21	1.2	21	1	CS207742	ACCESSION:CS207742	C 182	20.4	1.2	23	1	AR109811	ACCESSION:AR109811
110	21	1.2	21	1	CS207743	ACCESSION:CS207743	C 183	20	1.1	20	1	BD223567	ACCESSION:BD223567
111	21	1.2	21	1	CS207744	ACCESSION:CS207744	C 184	20	1.1	20	1	CS186497	ACCESSION:CS186497
112	21	1.2	21	1	CS207745	ACCESSION:CS207745	C 185	20	1.1	20	1	117156	ACCESSION:117156
113	21	1.2	21	1	CS207746	ACCESSION:CS207746	C 186	20	1.1	20	1	117157	ACCESSION:117157
114	21	1.2	21	1	CS207747	ACCESSION:CS207747	C 187	20	1.1	20	1	117159	ACCESSION:117159
115	21	1.2	21	1	CS207748	ACCESSION:CS207748	C 188	20	1.1	20	1	117161	ACCESSION:117161
116	21	1.2	21	1	CS207749	ACCESSION:CS207749	C 189	20	1.1	20	1	117164	ACCESSION:117164
117	21	1.2	21	1	CS207750	ACCESSION:CS207750	C 190	20	1.1	20	1	117165	ACCESSION:117165
118	21	1.2	21	1	CS207751	ACCESSION:CS207751	C 191	20	1.1	20	1	AX468706	ACCESSION:AX468706
119	21	1.2	21	1	CS207752	ACCESSION:CS207752	C 192	20	1.1	20	1	AX468709	ACCESSION:AX468709
120	21	1.2	21	1	CS207753	ACCESSION:CS207753	C 193	20	1.1	20	1	AX468711	ACCESSION:AX468711
121	21	1.2	21	1	CS207754	ACCESSION:CS207754	C 194	20	1.1	20	1	AX468713	ACCESSION:AX468713
122	21	1.2	21	1	CS207755	ACCESSION:CS207755	C 195	20	1.1	20	1	AX468714	ACCESSION:AX468714
123	21	1.2	21	1	CS207756	ACCESSION:CS207756	C 196	20	1.1	20	1	AX468725	ACCESSION:AX468725
124	21	1.2	21	1	CS207757	ACCESSION:CS207757	C 197	20	1.1	20	1	AX468728	ACCESSION:AX468728
125	21	1.2	21	1	CS207758	ACCESSION:CS207758	C 198	20	1.1	20	1	AX468730	ACCESSION:AX468730
126	21	1.2	21	1	CS207759	ACCESSION:CS207759	C 199	20	1.1	20	1	AX468732	ACCESSION:AX468732
127	21	1.2	21	1	CS207760	ACCESSION:CS207760	C 200	20	1.1	20	1	AX468733	ACCESSION:AX468733
128	21	1.2	21	1	CS207761	ACCESSION:CS207761	C 201	20	1.1	20	1	AX616473	ACCESSION:AX616473
129	21	1.2	21	1	CS207762	ACCESSION:CS207762	C 202	20	1.1	20	1	AX616485	ACCESSION:AX616485
130	21	1.2	21	1	CS207763	ACCESSION:CS207763	C 203	20	1.1	20	1	AX616486	ACCESSION:AX616486
131	21	1.2	21	1	CS207764	ACCESSION:CS207764	C 204	20	1.1	20	1	AX616487	ACCESSION:AX616487
132	21	1.2	21	1	CS207765	ACCESSION:CS207765	C 205	20	1.1	21	1	117154	ACCESSION:117154
133	21	1.2	21	1	CS207766	ACCESSION:CS207766	C 206	20	1.1	21	1	AX468716	ACCESSION:AX468716
134	21	1.2	21	1	CS207767	ACCESSION:CS207767	C 207	20	1.1	21	1	AX468735	ACCESSION:AX468735
135	21	1.2	21	1	CS207768	ACCESSION:CS207768	C 208	19.8	1.1	23	1	AR109816	ACCESSION:AR109816
136	21	1.2	21	1	CS207769	ACCESSION:CS207769	C 209	19.8	1.1	23	1	AX463104	ACCESSION:AX463104
137	21	1.2	21	1	CS207770	ACCESSION:CS207770	C 210	19.4	1.1	21	1	AR109833	ACCESSION:AR109833
138	21	1.2	21	1	CS207771	ACCESSION:CS207771	C 211	19.2	1.1	24	1	AR001364	ACCESSION:AR001364
139	21	1.2	21	1	CS207772	ACCESSION:CS207772	C 212	19.2	1.1	24	1	AR044849	ACCESSION:AR044849
140	21	1.2	21	1	CS207773	ACCESSION:CS207773	C 213	19.2	1.1	24	1	AR052235	ACCESSION:AR052235
141	21	1.2	21	1	CS207774	ACCESSION:CS207774	C 214	19.2	1.1	24	1	AR078344	ACCESSION:AR078344
142	21	1.2	21	1	CS207775	ACCESSION:CS207775	C 215	19.2	1.1	24	1	AR085195	ACCESSION:AR085195
143	21	1.2	21	1	CS207776	ACCESSION:CS207776	C 216	19.2	1.1	24	1	AR138115	ACCESSION:AR138115
144	21	1.2	21	1	CS207777	ACCESSION:CS207777	C 217	19.2	1.1	24	1	AR178989	ACCESSION:AR178989
145	21	1.2	21	1	CS207778	ACCESSION:CS207778	C 218	19.2	1.1	24	1	CO898470	ACCESSION:CO898470
146	21	1.2	21	1	CS207779	ACCESSION:CS207779	C 219	19.2	1.1	24	1	CS252672	ACCESSION:CS252672
147	21	1.2	21	1	CS207780	ACCESSION:CS207780	C 220	19.2	1.1	24	1	133899	ACCESSION:133899
148	21	1.2	21	1	CS207781	ACCESSION:CS207781	C 221	19.2	1.1	24	1	AR241150	ACCESSION:AR241150
149	21	1.2	21	1	CS207782	ACCESSION:CS207782	C 222	19	1.1	19	1	CS128871	ACCESSION:CS128871
150	21	1.2	21	1	CS207783	ACCESSION:CS207783	C 223	19	1.1	19	1	CS132144	ACCESSION:CS132144
C 151	21	1.2	21	1	117155	ACCESSION:117155	C 224	19	1.1	19	1	CS186498	ACCESSION:CS186498
C 152	21	1.2	21	1	117158	ACCESSION:117158	C 225	19	1.1	19	1	CS207431	ACCESSION:CS207431
C 153	21	1.2	21	1	117160	ACCESSION:117160	C 226	19	1.1	19	1	CS207432	ACCESSION:CS207432
C 154	21	1.2	21	1	117162	ACCESSION:117162	C 227	19	1.1	19	1	CS207433	ACCESSION:CS207433
C 155	21	1.2	21	1	117163	ACCESSION:117163	C 228	19	1.1	19	1	CS207434	ACCESSION:CS207434
C 156	21	1.2	21	1	117167	ACCESSION:117167	C 229	19	1.1	19	1	CS207722	ACCESSION:CS207722
C 157	21	1.2	21	1	AX468707	ACCESSION:AX468707	C 230	19	1.1	19	1	117168	ACCESSION:117168
C 158	21	1.2	21	1	AX468708	ACCESSION:AX468708	C 231	19	1.1	19	1	117170	ACCESSION:117170
C 159	21	1.2	21	1	AX468710	ACCESSION:AX468710	C 232	19	1.1	19	1	AX468719	ACCESSION:AX468719
C 160	21	1.2	21	1	AX468712	ACCESSION:AX468712	C 233	19	1.1	19	1	AX468721	ACCESSION:AX468721
C 161	21	1.2	21	1	AX468715	ACCESSION:AX468715	C 234	19	1.1	19	1	AX468738	ACCESSION:AX468738
C 162	21	1.2	21	1	AX468717	ACCESSION:AX468717	C 235	19	1.1	19	1	AX468740	ACCESSION:AX468740
C 163	21	1.2	21	1	AX468722	ACCESSION:AX468722	C 236	18.8	1.1	22	1	AR109799	ACCESSION:AR109799
C 164	21	1.2	21	1	AX468724	ACCESSION:AX468724	C 237	18.4	1.0	20	1	160476	ACCESSION:160476
C 165	21	1.2	21	1	AX468726	ACCESSION:AX468726	C 238	18.2	1.0	20	1	AR098634	ACCESSION:AR098634
C 166	21	1.2	21	1	AX468727	ACCESSION:AX468727	C 239	18.2	1.0	20	1	165553	ACCESSION:165553
C 167	21	1.2	21	1	AX468729	ACCESSION:AX468729	C 240	18	1.0	18	1	117166	ACCESSION:117166
C 168	21	1.2	21	1	AX468731	ACCESSION:AX468731	C 241	18	1.0	18	1	AX468723	ACCESSION:AX468723
C 169	21	1.2	21	1	AX468734	ACCESSION:AX468734	C 242	18	1.0	18	1	AX468742	ACCESSION:AX468742
C 170	21	1.2	21	1	AX468736	ACCESSION:AX468736	C 243	18	1.0	18	1	AX616471	ACCESSION:AX616471
C 171	21	1.2	21	1	AX468737	ACCESSION:AX468737	C 244	17.8	1.0	21	1	AR109832	ACCESSION:AR109832
C 172	21	1.2	21	1	AX468741	ACCESSION:AX468741	C 245	17.8	1.0	21	1	AR109843	ACCESSION:AR109843
C 173	21	1.2	21	1	AR109845	ACCESSION:AR109845	C 246	17.8	1.0	21	1	AR109846	ACCESSION:AR109846
C 174	20.8	1.2	24	1	AR109807	ACCESSION:AR109807	C 247	17.8	1.0	21	1	CO976990	ACCESSION:CO976990
C 175	20.8	1.2	24	1	AR109809	ACCESSION:AR109809	C 248	17.8	1.0	21	1	AX720862	ACCESSION:AX720862
C 176	20.8	1.2	24	1	AR109813	ACCESSION:AR109813	C 249	17.8	1.0	21	1	AR014600	ACCESSION:AR014600
C 177	20.6	1.2	24	1	117151	ACCESSION:117151	C 250	17	1.0	21	1	AR014608	ACCESSION:AR014608
C 178	20.6	1.2	24	1	AR109608	ACCESSION:AR109608	C 251	17	1.0	21	1	AR014610	ACCESSION:AR014610
C 179	20.6	1.2	24	1	AR109806	ACCESSION:AR109806	C 252	17	1.0	21	1	AR014610	ACCESSION:AR014610

C 253	17	1.0	21	1	BD010392	ACCESSION:BD010392	326	14	0.8	14	1	AR407912	ACCESSION:AR407912
C 254	17	1.0	21	1	BD010400	ACCESSION:BD010400	327	14	0.8	15	1	BD09069	ACCESSION:BD09069
C 255	17	1.0	21	1	BD010402	ACCESSION:BD010402	328	14	0.8	15	1	AX468699	ACCESSION:AX468699
C 256	17	1.0	21	1	126729	ACCESSION:126729	329	14	0.8	16	1	AR043296	ACCESSION:AR043296
C 257	17	1.0	21	1	126731	ACCESSION:126731	330	14	0.8	16	1	AR074951	ACCESSION:AR074951
C 258	17	1.0	21	1	126733	ACCESSION:126733	331	14	0.8	16	1	182147	ACCESSION:182147
C 259	17	1.0	21	1	AR235402	ACCESSION:AR235402	332	14	0.8	17	1	AR075054	ACCESSION:AR075054
C 260	17	1.0	21	1	AR235410	ACCESSION:AR235410	333	14	0.8	17	1	AR141872	ACCESSION:AR141872
C 261	17	1.0	21	1	AR235412	ACCESSION:AR235412	334	14	0.8	17	1	CO622225	ACCESSION:CO622225
C 262	16.8	1.0	21	1	BD240830	ACCESSION:BD240830	335	14	0.8	17	1	CO622229	ACCESSION:CO622229
C 263	16.8	1.0	21	1	AR209863	ACCESSION:AR209863	336	14	0.8	17	1	AR404183	ACCESSION:AR404183
C 264	16.8	1.0	21	1	185799	ACCESSION:185799	337	14	0.8	17	1	AR463288	ACCESSION:AR463288
C 265	16.4	0.9	18	1	117147	ACCESSION:117147	338	14	0.8	17	1	AR463292	ACCESSION:AR463292
C 266	16.4	0.9	18	1	AR190721	ACCESSION:AR190721	339	14	0.8	17	1	AX218126	ACCESSION:AX218126
C 267	16.4	0.9	18	1	AR325569	ACCESSION:AR325569	340	14	0.8	17	1	AR046956	ACCESSION:AR046956
C 268	16.4	0.9	18	1	AR599029	ACCESSION:AR599029	341	13.8	0.8	17	1	BD067403	ACCESSION:BD067403
C 269	16.4	0.9	19	1	CO778932	ACCESSION:CO778932	342	13.8	0.8	17	1	BD104935	ACCESSION:BD104935
C 270	16.4	0.9	20	1	AX958828	ACCESSION:AX958828	343	13.8	0.8	17	1	BD200869	ACCESSION:BD200869
C 271	16.4	0.9	20	1	CO755471	ACCESSION:CO755471	344	13.8	0.8	17	1	CO618016	ACCESSION:CO618016
C 272	16.4	0.9	20	1	AR475720	ACCESSION:AR475720	345	13.8	0.8	17	1	CO622934	ACCESSION:CO622934
C 273	16	0.9	17	1	AX218029	ACCESSION:AX218029	346	13.8	0.8	17	1	DD184601	ACCESSION:DD184601
C 274	15.8	0.9	19	1	CO815064	ACCESSION:CO815064	347	13.8	0.8	17	1	DD185435	ACCESSION:DD185435
C 275	15.8	0.9	19	1	CO815066	ACCESSION:CO815066	348	13.8	0.8	17	1	DD188223	ACCESSION:DD188223
C 276	15.8	0.9	19	1	DOGADRB28	ACCESSION:177385	349	13.8	0.8	17	1	DD189391	ACCESSION:DD189391
C 277	15.4	0.9	17	1	AR190056	ACCESSION:AR190056	350	13.8	0.8	17	1	117148	ACCESSION:117148
C 278	15.4	0.9	17	1	AR325033	ACCESSION:AR325033	351	13.8	0.8	17	1	AR188459	ACCESSION:AR188459
C 279	15.4	0.9	17	1	AR598493	ACCESSION:AR598493	352	13.8	0.8	17	1	AR188631	ACCESSION:AR188631
C 280	15.4	0.9	17	1	AX216399	ACCESSION:AX216399	353	13.8	0.8	17	1	AR190057	ACCESSION:AR190057
C 281	15.4	0.9	18	1	AR109819	ACCESSION:AR109819	354	13.8	0.8	17	1	AR190206	ACCESSION:AR190206
C 282	15.4	0.9	18	1	AR698481	ACCESSION:AR698481	355	13.8	0.8	17	1	AR196300	ACCESSION:AR196300
C 283	15.4	0.9	19	1	CO876950	ACCESSION:CO876950	356	13.8	0.8	17	1	AR324312	ACCESSION:AR324312
C 284	15.4	0.9	19	1	CS096561	ACCESSION:CS096561	357	13.8	0.8	17	1	AR324484	ACCESSION:AR324484
C 285	15.4	0.9	19	1	CS096648	ACCESSION:CS096648	358	13.8	0.8	17	1	AR328943	ACCESSION:AR328943
C 286	15.4	0.9	19	1	DD203034	ACCESSION:DD203034	359	13.8	0.8	17	1	154008	ACCESSION:154008
C 287	15.4	0.9	19	1	DD203281	ACCESSION:DD203281	360	13.8	0.8	17	1	160477	ACCESSION:160477
C 288	15	0.8	17	1	CO622226	ACCESSION:CO622226	361	13.8	0.8	17	1	AR401903	ACCESSION:AR401903
C 289	15	0.8	17	1	CO622327	ACCESSION:CO622327	362	13.8	0.8	17	1	AR459079	ACCESSION:AR459079
C 290	15	0.8	17	1	CO622228	ACCESSION:CO622228	363	13.8	0.8	17	1	AR463997	ACCESSION:AR463997
C 291	15	0.8	17	1	AR463289	ACCESSION:AR463289	364	13.8	0.8	17	1	AR597772	ACCESSION:AR597772
C 292	15	0.8	17	1	AR463290	ACCESSION:AR463290	365	13.8	0.8	17	1	AR597944	ACCESSION:AR597944
C 293	15	0.8	17	1	AR463291	ACCESSION:AR463291	366	13.8	0.8	17	1	AX216138	ACCESSION:AX216138
C 294	15	0.8	17	1	AX047386	ACCESSION:AX047386	367	13.8	0.8	17	1	AX216915	ACCESSION:AX216915
C 295	15	0.8	17	1	AX217961	ACCESSION:AX217961	368	13.8	0.8	17	1	AX216921	ACCESSION:AX216921
C 296	15	0.8	18	1	CO931585	ACCESSION:CO931585	369	13.8	0.8	17	1	AX226878	ACCESSION:AX226878
C 297	15	0.8	18	1	AR257450	ACCESSION:AR257450	370	13.8	0.8	17	1	AX75125	ACCESSION:AX75125
C 298	14.8	0.8	18	1	AR0829	ACCESSION:AR0829	371	13.8	0.8	17	1	AX502961	ACCESSION:AX502961
C 299	14.8	0.8	18	1	AR054536	ACCESSION:AR054536	372	13.8	0.8	17	1	AX531944	ACCESSION:AX531944
C 300	14.8	0.8	18	1	AR138040	ACCESSION:AR138040	373	13.8	0.8	17	1	AX673572	ACCESSION:AX673572
C 301	14.8	0.8	18	1	BD064969	ACCESSION:BD064969	374	13.8	0.8	17	1	AX674304	ACCESSION:AX674304
C 302	14.8	0.8	18	1	BD170368	ACCESSION:BD170368	375	13.8	0.8	17	1	AX688110	ACCESSION:AX688110
C 303	14.8	0.8	18	1	BD226591	ACCESSION:BD226591	376	13.8	0.8	17	1	AX692036	ACCESSION:AX692036
C 304	14.8	0.8	18	1	BD250496	ACCESSION:BD250496	377	13.8	0.8	17	1	AX722337	ACCESSION:AX722337
C 305	14.8	0.8	18	1	AR193175	ACCESSION:AR193175	378	13.8	0.8	17	1	AX729053	ACCESSION:AX729053
C 306	14.8	0.8	18	1	AX146659	ACCESSION:AX146659	379	13.8	0.8	17	1	AX730414	ACCESSION:AX730414
C 307	14.8	0.8	18	1	AX686022	ACCESSION:AX686022	380	13.8	0.8	17	1	AX738266	ACCESSION:AX738266
C 308	14.8	0.8	16	1	AX468698	ACCESSION:AX468698	381	13.8	0.8	17	1	AX744431	ACCESSION:AX744431
C 309	14.4	0.8	17	1	DD184677	ACCESSION:DD184677	382	13.8	0.8	17	1	AX744432	ACCESSION:AX744432
C 310	14.4	0.8	17	1	DD188299	ACCESSION:DD188299	383	13.8	0.8	17	1	AX745037	ACCESSION:AX745037
C 311	14.4	0.8	17	1	AX215478	ACCESSION:AX215478	384	13.8	0.8	17	1	AX760000	ACCESSION:AX760000
C 312	14.4	0.8	17	1	AX218028	ACCESSION:AX218028	385	13.8	0.8	17	1	AX782045	ACCESSION:AX782045
C 313	14.4	0.8	17	1	AX468697	ACCESSION:AX468697	386	13.8	0.8	17	1	AX783524	ACCESSION:AX783524
C 314	14.4	0.8	18	1	AR096338	ACCESSION:AR096338	387	13.8	0.8	17	1	AX783713	ACCESSION:AX783713
C 315	14.4	0.8	18	1	AX923497	ACCESSION:AX923497	388	13.8	0.8	17	1	AR109816	ACCESSION:AR109816
C 316	14.4	0.8	18	1	BD217386	ACCESSION:BD217386	389	13.6	0.8	23	1	AX109816	ACCESSION:AX109816
C 317	14.4	0.8	18	1	CO799859	ACCESSION:CO799859	390	13.4	0.8	15	1	A10650	ACCESSION:A10650
C 318	14.4	0.8	18	1	AR190767	ACCESSION:AR190767	391	13.4	0.8	15	1	A11598	ACCESSION:A11598
C 319	14.4	0.8	18	1	AR299235	ACCESSION:AR299235	392	13.4	0.8	15	1	A35118	ACCESSION:A35118
C 320	14.4	0.8	18	1	AR325611	ACCESSION:AR325611	393	13.4	0.8	15	1	AR133675	ACCESSION:AR133675
C 321	14.4	0.8	18	1	181946	ACCESSION:181946	394	13.4	0.8	15	1	AR133676	ACCESSION:AR133676
C 322	14.4	0.8	18	1	AR442143	ACCESSION:AR442143	395	13.4	0.8	15	1	DD184741	ACCESSION:DD184741
C 323	14.4	0.8	18	1	AR599071	ACCESSION:AR599071	396	13.4	0.8	15	1	DD188363	ACCESSION:DD188363
C 324	14.4	0.8	18	1	AX115374	ACCESSION:AX115374	397	13.4	0.8	15	1	BD184657	ACCESSION:BD184657
C 325	14.4	0.8	18	1	AX468696	ACCESSION:AX468696	398	13.4	0.8	16	1		

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	Best Local Similarity	100.0%	Pred. No. 4.6:			
	Matches	30;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
Qy	678	CCTGAGCTCTCCTGCTGAGCCTTCCCCACAGG	707			
Db	30	CCTGAGCTCTCCTGAGCCTTCCCCACAGG	1			

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
CS174800	CS174800	Sequence 3 from Patent WO2005090401.	CS174800	CS174800.1	GI:77625635
		28 bp DNA			
					linear
					PAT 12-OCT-2005

ORGANISM	synthetic construct other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Drmoča T.
TITLE	Gerbil neurokinin 1 receptor
JOURNAL	Patent: WO 2005050401-A 3 29-SEP-2005; Astrazeneca AB (SE)
FEATURES	Location/Qualifiers
source	1..28

`/db xref="taxon:32630"`  
`/note="Polynucleotide for use in polymerase chain reaction."`

	Query Match	Score 28;	DB 1;	Length 28;
	Best Local Similarity	100.0%;	Pred. No. 7.6;	
Matches	Conservative	28;	Mismatches	0; Indels 0; Gaps 0;
Oy	993 GCTGCCCTTCACATCTTCTCCCTCG 1020			
Db	1 GCTGCCCTTCACATCTTCTCCCTCG 28			

RESULT 4	27 bp	DNA	1 linear	PAT 28-APR-2004
CQ800305	CQ800305	Sequence 4 from Patent WO2004030695.		
LOCUS				
DEFINITION				
ACCESSION	CQ800305			
VERSION	CQ800305.1	GI:46849171		

ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Gibbins, J.M., Lowry, P.J., Graham, G.J. and Page, N.M.
JOURNAL	Treatment of vascular diseases
	Patent: WO 2004030695-A 4 15-APR-2004,
	University of Reading (GB)

```

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:33630"
/notes="Primer"

Query Match      1.5%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY 213 GGATAACGTCCTCCGGTGACTCAGA 239  
|||  
Db 1 GGATAACGTCCTCCGGTGACTCAGA 27

RESULT 5  
CQ800321/c

LOCUS	CQ800321	27 bp	DNA	linear	PAT 28-APR-2004
DEFINITION	Sequence 20 from Patent WO2004030695.				
ACCESSION	CQ800321				
VERSION	CQ800321.1				
KEYWORDS	GI:46849187				
SOURCE	.				
ORGANISM	synthetic construct				
	synthetic construct				

FEATURES	REFERENCE
AUTHORS	1 Gibbins, J. M., Lowry, P. J., Graham, G. J. and Page, N. M.
TITLE	Treatment of vascular diseases
JOURNAL	Patent: WO 2004/030695-A 20 15-APR-2004;
FEATURES	University of Reading (GB)
SOURCE	Location/Qualifiers
	1. .27

```

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

```

Query Match	27	1.5%	Score	27	DB	1	Length	27	
Best Local Similarity			Pred. No.	9	7				
Matches	27	Conservative	0	Mismatches	0	Indels	0	Gaps	0

Qy	711	CTACTCACCACAGAGACCATGCCAG	737
Db	27	CTACTCACCACAGAGACCATGCCAG	1

	RESULT 6				
CS174801/c					
LOCUS	CS174801	27 bp	DNA	linear	PAT 12-OCT-2005
DEFINITION	Sequence	4 from Patent WO2005090401.			
ACCESSION	CS174801				
VERSION	CS174801.1	GI:77625636			

ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Drmoa, T.
JOURNAL	Gerbil neurokinin 1 receptor
FEATURES	Patent: WO 2005090401-A 4 29-SEP-2005; Astrazeneca AB (SE)
	Location/Qualifiers

```

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Polynucleotide for use in polymerase chain
reaction."

```

Query Match	1.5%	Score 27	DB 1	Length 27
Best Local Similarity	100.0%	Pred. No. 9.7		
Matches 27; Conservative	0	Mismatches	0	Gaps 0

QY	669	CATCTGGGTCCTGGCTTCCTCTGCTGGC	695
Db	27	CATCTGGGTCCTGGCTTCCTCTGCTGGC	1

RESULT 7				
CQ800314/C	CQ800314	30 bp	DNA	PAT 28-APR-2004
LOCUS	Sequence 13	from Patent WO2004030695.		
DEFINITION	CQ800314			
ACCESSION	CQ800314.1	GI:46849180		
VERSION				

ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
1  
Gibbins, J.M., Lowry, P.J., Graham, G.J. and Page, N.M.

TITLE Treatment of vascular diseases  
JOURNAL Patent: WO 2004030695-A 13 15-APR-2004,  
University of Reading (GB)  
FEATURES Location/Qualifiers  
source 1..30  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.5%; Score 25.8; DB 1; Length 30;  
Best Local Similarity 93.1%; Pred. No. 19;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 556 GTCTTCGCCAGTACTACTCCATGACGGC 584  
Db 30 GTCTTCGCCAGCATCTACTCCATGACGGC 2

RESULT 8  
ARI09708 30 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 132 from patent US 6114139.  
DEFINITION ARI09708  
ACCESSION ARI09708.1 GI:12825984  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 132 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 25.2; DB 1; Length 30;  
Best Local Similarity 90.0%; Pred. No. 23;  
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008  
Db 1 TTGGCCATCTGCTGCTGCCCTTCACATC 30

RESULT 9  
I34577/c 30 bp DNA linear PAT 06-FEB-1997  
LOCUS Sequence 6 from patent US 5596088.  
DEFINITION I34577  
ACCESSION I34577.1 GI:1825368  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,  
Sullivan,D.M., Erb,L.J. and Lustig,K.D.  
TITLE DNA Encoding the human P.sub.2U receptor and null cells expressing  
JOURNAL Patent: US 5596088-A 6 21-JAN-1997;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
Best Local Similarity 76.7%; Pred. No. 26;  
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008  
Db 1 TTGGCCATCTGCTGCTGCCCTTCACATC 30

Db 30 TTGGCCCTCGCTGCTGCTGCCCTTCACATC 1

RESULT 10  
I36528/c 30 bp DNA linear PAT 13-MAY-1997  
LOCUS Sequence 6 from patent US 5607836.  
DEFINITION I36528  
ACCESSION I36528.1 GI:2086353  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,  
Sullivan,D.M., Erb,L.J. and Lustig,K.D.  
TITLE Methods of detecting compounds which bind to the P.sub.2U receptor  
JOURNAL Patent: US 5607836-A 6 04-MAR-1997;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
Best Local Similarity 76.7%; Pred. No. 26;  
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008  
Db 30 TTGGCCCTCGCTGCTGCTGCCCTTCACATC 1

RESULT 11  
I76284/c 30 bp DNA linear PAT 03-APR-1998  
LOCUS Sequence 6 from patent US 5691156.  
DEFINITION I76284  
ACCESSION I76284.1 GI:3012438  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Boucher,R.C., Weisman,G.A., Turner,J.T., Harden,T.K., Parr,C.E.,  
Sullivan,D.M., Erb,L.J. and Lustig,K.D.  
TITLE Method of inhibiting cell growth with the P.sub.2U receptor  
JOURNAL Patent: US 5691156-A 6 25-NOV-1997;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24.8; DB 1; Length 30;  
Best Local Similarity 76.7%; Pred. No. 26;  
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCCCTTCACATC 1008  
Db 30 TTGGCCCTCGCTGCTGCTGCCCTTCACATC 1

RESULT 12  
ARI09715 30 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 139 from patent US 6114139.  
DEFINITION ARI09715  
ACCESSION ARI09715.1 GI:12825991  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)

AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 139 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24.2; DB 1; Length 30;  
Best Local Similarity 89.7%; Pred. No. 32;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCTTCCACAT 1007  
Db 1 TTGGCATCTGCTGCTGCCCTTCCACGT 29

RESULT 13  
LOCUS ARI09808 24 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 232 from patent US 6114139.  
ACCESSION ARI09808  
VERSION ARI09808.1 GI:12826084  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 232 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCTTC 1002  
Db 1 TTGGCATCTGCTGCTGCCCTTC 24

RESULT 14  
LOCUS CS186499 24 bp DNA linear PAT 04-NOV-2005  
DEFINITION Sequence 5 from Patent WO2005100986.  
ACCESSION CS186499  
VERSION CS186499.1 GI:80748371  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Golz,S.  
TITLE Diagnostic and therapeutics for diseases associated with  
JOURNAL lachykinin receptor 1(tacr1)  
Patent: WO 2005100986-A 5 27-OCT-2005;  
Bayer Healthcare AG (DE)  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="probe"

Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 CCTGCAAAATTGCTTTGGGAG 319

Db 1 CCTGCAAAATTGCTTTGGGAG 24

RESULT 15  
LOCUS ARI09637/c 29 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 61 from patent US 6114139.  
ACCESSION ARI09637  
VERSION ARI09637.1 GI:12825913  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 61 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCTTCCACAT 1007  
Db 29 TTCTRYNTCTGCTGCTGCCCTTCTCMT 1

RESULT 16  
LOCUS ARI50645/c 29 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 32 from patent US 6228984.  
ACCESSION ARI50645  
VERSION ARI50645.1 GI:15115236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.  
TITLE Polypeptides their production and use  
JOURNAL Patent: US 6228984-A 32 08-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCTTCCACAT 1007  
Db 29 TTCTRYNTCTGCTGCTGCCCTTCTCMT 1

RESULT 17  
LOCUS E11515/c 29 bp DNA linear PAT 29-SEP-1997  
DEFINITION primer for screening novel G protein(guanine nucleotide-binding  
protein) coupling type receptor protein from rabbit stomach pylorus  
smooth muscle.  
ACCESSION E11515  
VERSION E11515.1 GI:22025151  
KEYWORDS JP 196154682-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;





SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified sequences.  
AUTHORS 1 (bases 1 to 29)  
TITLE Shuji,H., Ryo,F., Yuji,K. and Hirokazu,M.  
JOURNAL Utilization of peptide  
Patent: JP 199071300-A 18 16-MAR-1999;  
TAKEDA CHEM IND LTD  
COMMENT OS Unidentified  
PN JP 199071300-A/18  
PD 16-MAR-1999  
PF 22-JUN-1998 JP 1998175007  
PR SHUJI HINUMA, RYO FUJII, YUJI KAWAMATA, HIROKAZU MATSUMOTO PC  
A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K38/00, PC  
A61K38/00,  
PC A61K38/00,A61K38/00,C07K7/08,C07K14/705//C12N15/09,C12P21/02,  
PC (C12P21/02,C12R1:91),A61K37/02,A61K37/02,A61K37/02,A61K37/02,  
PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,C12N15/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..29  
Location/Qualifiers  
source 1..29 /organism="unidentified".  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCTGCTTCACAT 1007  
Db 29 TTCRYSNCTCTGCTGCTGCTGCTCTWCTCMT 1

RESULT 21  
AR300947/c 29 bp DNA linear PAT 12-JUN-2003  
LOCUS AR300947  
DEFINITION Sequence 61 from patent US 6538107.  
ACCESSION AR300947  
VERSION AR300947.1 GI:31688620  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 29)  
TITLE Hinuma,S., Ito,Y. and Fujii,R.  
JOURNAL G-protein coupled receptor protein production, and use thereof  
Patent: US 6538107-A 61 25-MAR-2003;  
Takeda Chemical Industries, Ltd.; Osaka;  
JPX;  
FEATURES  
source Location/Qualifiers  
1..29 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCTGCTTCACAT 1007  
Db 29 TTCRYSNCTCTGCTGCTGCTGCTCTWCTCMT 1

RESULT 22  
AR583779/c 29 bp DNA linear PAT 15-DEC-2004  
LOCUS AR583779/c

DEFINITION Sequence 32 from patent US 6794491.  
ACCESSION AR583779  
VERSION AR583779.1 GI:56621382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 29)  
TITLE Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.  
JOURNAL Polypeptides, their production and use  
Patent: US 6794491-A 32 21-SEP-2004;  
Takeda Chemical Industries, Ltd.; Osaka;  
JPX;  
FEATURES  
source Location/Qualifiers  
1..29 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCTGCTTCACAT 1007  
Db 29 TTCRYSNCTCTGCTGCTGCTGCTCTWCTCMT 1

RESULT 23  
AR651208/c 29 bp DNA linear PAT 20-APR-2005  
LOCUS AR651208  
DEFINITION Sequence 32 from patent US 6881545.  
ACCESSION AR651208  
VERSION AR651208.1 GI:62795419  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 29)  
TITLE Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.  
JOURNAL Polypeptides, their production and use  
Patent: US 6881545-A 32 19-APR-2005;  
Takeda Chemical Industries, Ltd.; Osaka;  
JPX;  
FEATURES  
source Location/Qualifiers  
1..29 /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 29;  
Best Local Similarity 72.4%; Pred. No. 32;  
Matches 21; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCCATCTGCTGCTGCTGCTTCACAT 1007  
Db 29 TTCRYSNCTCTGCTGCTGCTGCTCTWCTCMT 1

RESULT 24  
AR109661 27 bp DNA linear PAT 14-FEB-2001  
LOCUS AR109661  
DEFINITION Sequence 85 from patent US 6114139.  
ACCESSION AR109661  
VERSION AR109661.1 GI:12825937  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 27)  
TITLE Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
JOURNAL G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 85 05-SEP-2000;

FEATURES  
source  
Location/Qualifiers  
1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 1.3%; Score 23.8; DB 1; Length 27;  
Best Local Similarity 92.6%; Pred. No. 29;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGGCATTGCTGCTGCTGCTTCCAC 1005  
Db 1 TTGGCATTGCTGCTGCTGCTTCCAC 27

RESULT 25  
117149/c 117149 24 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 4 from patent US 5484886.  
DEFINITION 117149  
ACCESSION 117149.1 GI:1252057  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
TITLE Fong, T.M. and Strader, C.D.  
JOURNAL Human neurokinin-1 receptor  
Patent: US 5484886-A 4 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 1.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACAACCCCATCATCTACTG 1127  
Db 24 ATGTACAACCCCATCATCTACTG 2

RESULT 26  
AX468718/c AX468718 24 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 34 from Patent W00213799.  
DEFINITION AX468718  
ACCESSION AX468718  
VERSION AX468718.1 GI:21901488  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 synthetic construct  
AUTHORS other sequences; artificial sequences.  
TITLE 1 Henry, J.L., Cahill, C.M. and Yaahpal, K.  
JOURNAL Oligonucleotides and other modulators of the nk-1 receptor pathway  
Patent: WO 0213799-A 34 21-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match  
Best Local Similarity 1.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1105 ATGTACAACCCCATCATCTACTG 1127  
Db 24 ATGTACAACCCCATCATCTACTG 2

RESULT 27  
117150/c 117150 24 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 5 from patent US 5484886.  
DEFINITION 117150  
ACCESSION 117150  
VERSION 117150.1 GI:1252058  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
TITLE Fong, T.M. and Strader, C.D.  
JOURNAL Human neurokinin-1 receptor  
Patent: US 5484886-A 5 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 35;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGCTTACTG 1074  
Db 24 AAGTTATCCAGCAGGCTTACTG 1

RESULT 28  
AR109658 AR109658 27 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 82 from patent US 6114139.  
DEFINITION AR109658  
ACCESSION AR109658  
VERSION AR109658.1 GI:12825934  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 27)  
TITLE Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.  
JOURNAL G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 82 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
Best Local Similarity 1.3%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 49;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATTGCTGCTGCTGCTTCCAC 1005  
Db 1 TTGGCATTGCTGCTGCTGCTTCCAC 27

RESULT 29  
AR109660 AR109660 27 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 84 from patent US 6114139.  
DEFINITION AR109660  
ACCESSION AR109660  
VERSION AR109660.1 GI:12825936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 27)  
TITLE Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.  
JOURNAL G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 84 05-SEP-2000;  
FEATURES Location/Qualifiers  
source 1..27

```

/organism="unknown"
/mol_type="unassigned DNA"

Query Match
1.3%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 49;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTGCTTCCAC 1005
Db 1 TTGGCCATCTGCTGCTGCTGCTTCCAC 27

RESULT 30
LOCUS ARI09595 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6114139.
ACCESSION ARI09595
VERSION ARI09595.1 GI:12825871
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 2 05-SEP-2000;
FEATURES
Location/Qualifiers
1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCCATCTGCTGCTGCTGCTTCCAC 1

RESULT 31
LOCUS ARI09652 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 76 from patent US 6114139.
ACCESSION ARI09652
VERSION ARI09652.1 GI:12825928
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 76 05-SEP-2000;
FEATURES
Location/Qualifiers
1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTTCCAC 1005
Db 1 TTGGCCATCTGCTGCTGCTTCCAC 27

RESULT 32
LOCUS ARI50643 27 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6228984.
ACCESSION ARI50643
```

```

VERSION ARI50643.1 GI:15115234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S.
and Kitada,C.
TITLE Polypeptides their production and use
JOURNAL Patent: US 6228984-A 30 08-MAY-2001;
FEATURES
Location/Qualifiers
1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCCATCTGCTGCTGCTTCCAC 1

RESULT 33
LOCUS E11748 27 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for screening rabbit guanine nucleotide-binding protein
coupling type receptor protein.
ACCESSION E11748
VERSION E11748.1 GI:22025384
KEYWORDS JP 1996193099-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,K., Fujii,A. and Kawamata,Y.
TITLE NEW G PROTEIN COUPLATED RECEPTOR PROTEIN, ITS PRODUCTION AND USE
JOURNAL Patent: JP 1996193099-A 3 30-JUL-1996;
COMMENT TAKEDA CHEM IND LTD
OS None
OC Artificial sequences.
PM JP 1996193099-A/3
PD 30-JUL-1996
PR 24-AUG-1995 JP 1995215798
PR 14-NOV-1994 JP 94P 279545
PI HINUMA KUNIJU, FUJII AKIRA, KAWAMATA YUJI
PC C07K14/705,C07H21/04,C12N1/21,C12N5/10,C12N15/09, PC
C12Q1/00//A61K48/00,
PC C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key
FT source
1..27
Location/Qualifiers
/organism='Artificial sequences'.
1..27
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 56;
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCTTCCAC 1005
Db 27 TTGGCCATCTGCTGCTGCTTCCAC 1
```

RESULT 34  
E12466/c  
LOCUS E12466 27 bp DNA linear PAT 27-APR-1998  
DEFINITION PCR primer for selective amplification and cloning of the family of  
genes encoding G protein-coupled receptors.  
ACCESSION E12466  
VERSION E12466.1 GI:3251299  
KEYWORDS JP 1997000268-A/2.  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Hinuma,K., Hosoya,M., Fujii,A., Otaki,T., Fukuzumi,M. and  
Ooyoshi,K.  
TITLE NEW G PROTEIN COUPLATION TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND  
JOURNAL Patent: JP 1997000268-A 2 07-JAN-1997;  
TAKEDA CHEM IND LTD  
OS None  
OC Artificial sequences.  
PN JP 1997000268-A/2  
PD 07-JAN-1997  
PF 10-AUG-1995 JP 1995224544  
PR 11-AUG-1994 JP 94P 189272, 11-AUG-1994 JP 94P 189273, PR  
11-AUG-1994 JP 94P 189274, 30-SEP-1994 JP 94P 236356, PR  
30-SEP-1994 JP 94P 236357, 02-NOV-1994 JP 94P 270017, PR  
28-DEC-1994 JP 94P 326611, 20-JAN-1995 JP 95P 7177, PR  
16-MAR-1995 JP 95P 57186, 19-APR-1995 JP 95P 93989, PI  
HINUMA KUNITI, HOSoya MASAKI, FUJII AKIRA, OTAKI TETSUYA, PI  
FUKUZUMI MASASHI, OYOSHI KAZUHIRO  
PC C12N15/09, C07H21/04, C12N1/21, G01N33/53, G01N33/566//C07K14/705,  
PC C07K16/28,  
PC C12P21/02, C12P21/08, C12Q1/68, (C12N1/21, C12R1:19), (C12P21/02,  
PC C12R1:19);  
CC strandedness: Single;  
CC topology: linear;  
FH key Location/Qualifiers  
FH source 1..27  
FT misc\_feature 1..27 /organism='Artificial sequences', FT  
FT amino acid  
FT sequences of the sixth transmembrane domain of  
FT known G  
FT protein-coupled receptors'.  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="unclassified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 56;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 979 TTGGCATTCTGCTGCTGCTCCCTTCAC 1005  
Db 27 TTGGCMTCTGCTGNTGCCYWCNAC 1  
RESULT 35  
E12660/c  
LOCUS E12660 27 bp DNA linear PAT 27-APR-1998  
DEFINITION Primer.  
ACCESSION E12660  
VERSION E12660.1 GI:3251492  
KEYWORDS JP 1997048800-A/4.  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Hinuma,K., Fujii,A., Fukuzumi,M., Otaki,T., Hosoya,M., Oogi,K. and  
Onda,H.

TITLE GALANIN RECEPTOR PROTEIN, ITS PRODUCTION AND USE  
JOURNAL Patent: JP 1997048800-A 4 18-FEB-1997;  
TAKEDA CHEM IND LTD  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997048800-A/4  
PD 18-FEB-1997  
PF 12-OCT-1995 JP 1995289215  
PR 13-OCT-1994 JP 94P 247599, 28-DEC-1994 JP 94P 326610, PR  
31-MAY-1995 JP 95P 134412  
PI HINUMA KUNITI, FUJII AKIRA, FUKUZUMI MASASHI, OTAKI TETSUYA,  
PI HOSoya MASAKI, OOGI KAZUHIRO, ONDA HARUO  
PC C07K14/72, C07H21/04, C12N5/10, C12N15/09, C12P21/02, PC  
G01N33/566//A61K38/00  
PC A61K38/00, A61K38/00, (C12P21/02, C12R1:91);  
CC strandedness: Single;  
CC topology: linear;  
CC hypothetical: No;  
FH key Location/Qualifiers  
FH source 1..27  
FT misc\_feature 1..27 /organism='Artificial sequences',  
FT amino acid  
FT sequences of the sixth transmembrane domain of  
FT known G  
FT protein-coupled receptors'.  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="unclassified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 1.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 74.1%; Pred. No. 56;  
Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 979 TTGGCATTCTGCTGCTGCTCCCTTCAC 1005  
Db 27 TTGGCMTCTGCTGNTGCCYWCNAC 1  
RESULT 36  
E14221/c  
LOCUS E14221 27 bp DNA linear PAT 28-JUL-1999  
DEFINITION Primer.  
ACCESSION E14221  
VERSION E14221.1 GI:5708904  
KEYWORDS JP 1997278798-A/5.  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Hinuma,K., Sakamoto,J. and Hosoya,M.  
TITLE NEW G PROTEIN COUPLATED TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND  
JOURNAL Patent: JP 1997278798-A 5 28-OCT-1997;  
TAKEDA CHEM IND LTD  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997278798-A/5  
PD 28-OCT-1997  
PF 07-FEB-1997 JP 1997024190  
PR 07-FEB-1996 JP 96P 21562  
PI HINUMA KUNITI, SAKAMOTO JUNICHI, HOSoya MASAKI PC  
C07K14/705, A61K38/00, C07H21/04, C07K16/28, C12N1/21, C12N15/09, PC  
C12P21/02,  
PC G01N33/566//A61K48/00, C12Q1/68, (C12N1/21, C12R1:19), (C12P21/02,  
PC C12R1:19);  
CC strandedness: Single;  
CC topology: linear;  
FH key Location/Qualifiers  
FH source 1..27  
FT misc\_feature 1..27 /organism='Artificial sequences',  
FT amino acid  
FT sequences of the sixth transmembrane domain of  
FT known G  
FT protein-coupled receptors'.  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="unclassified"

```
/mol_type="genomic DNA"  
/db_xref="taxon:32644"
```

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 56;  
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
QY      979 TTGGCAATCTGCTGGCTGCCCTTTCAC 1005
      |||:||||| |||::|||
Db      27  TTGGCAATCTGCTGGCTGCCCTTTCAC 1
```

RESULT 37  
E16192/c

Query Match	1.2%	Score 21.8	DB 1	Length 27
Best Local Similarity	74.1%	Pred. No. 56		
Matches	20	Conservative 4	Mismatches 3	Indels 0
			Gaps 0	
Qy	979	TTCCGCATCTGCTGAGTCGCCCTTCAC	1005	
		:     :     :		
Db	27	TTTGCMTCTCTCTGAGTCCCTTCAC	1	
RESULT 38				
E27218/c				
LOCUS	E27218			
DEFINITION	E27218	27 bp	DNA	linear
		Novel physiologically active substance, process for producing the same and utilization thereof.		
ACCESSION	E27218			
VERSION	E27218.1	GI:13025235		
KEYWORDS	JP 1999009286-A/9.			

SOURCE ORGANISM	unidentified unidentified unclassified sequences.
-----------------	---

Query Match	1.2%;	Score 21.8;	DB 1;	Length 27;
Best Local Similarity	74.1%;	Pred. No. 56;		
Matches	20;	Conservative	4;	Mismatches
			3;	Indels
				Gaps
				0;
0y	979	TTTGGCATTCTGCTGCTGCTTTCAC	1005	
		:     :    :		
Db	27	TTTGCMTCTCTGCTGATGCCCTTGCAC	1	
RESULT 39				
E28276/c				
LOCUS	E28276	27 bp	DNA	linear
DEFINITION	Utilization of peptide.			PAT 18-JUN-2001
ACCESSION	E28276			
VERSION	E28276.1			
KEYWORDS	JP 1999071300-A/16.			
SOURCE	unidentified			
ORGANISM	unidentified			
REFERENCE	unclassified sequences.			
AUTHORS	1 (bases 1 to 27)			
TITLE	Shuji,H., Ryo,F., Yuji,K. and Hirokazu,M.			
JOURNAL	Utilization of peptide			
	Patent: JP 1999071300-A 16 16-MAR-1999;			
	TAKEIDA CHEM IND LTD			
COMMENT	OS Unidentified			
	PN JP 1999071300-A/16			
	PD 16-MAR-1999			
	PF 22-JUN-1998 JP 1998175007			
	PR			
	PI SHUJI HINUMA, RYO FUJII, YUJI KAWAMATA, HIROKAZU MATSUMOTO PC			
	AE61K38/00, AE61K38/00, AE61K38/00, AE61K38/00, AE61K38/00, AE61K38/00, PC			
	PC AE61K38/00, AE61K38/00, C07K7/08, C07K14/705//C12N15/09, C12P21/02,			
	PC (C12P21/02, C12P1:91), AE61K37/02, AE61K37/02, AE61K37/02, AE61K37/02,			
	PC AE61K37/02,			
	PC AE61K37/02, AE61K37/02, AE61K37/02, AE61K37/02, C12N15/00 CC			
	Strandedness: Single;			
	CC Topology: Linear;			
	FI Key			
	Location/Qualifiers			

FT source 1..27 /organism='Unidentified'.  
 FT Location/Qualifiers  
 source 1..27 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 56;  
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 40  
 E37242 27 bp DNA linear PAT 31-JUN-2002  
 LOCUS Novel physiologically active substance, process for producing the  
 DEFINITION same and use thereof.  
 ACCESSION E37242 GI:18624793  
 VERSION E37242.1  
 KEYWORDS JP 2000159798-A/4.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified sequences.  
 1 (bases 1 to 27)  
 Hinuma,S., Tatemoto,K., Hosoya,M., Habata,Y., Fujii,R. and  
 Kitada,C.  
 TITLE Novel physiologically active substance, process for producing the  
 same and use thereof  
 Patent: JP 2000159798-A 4 13-JUN-2000;  
 JOURNAL TAKEDA CHEM IND LTD  
 OS Unidentified  
 PN JP 2000159798-A/4  
 PD 13-JUN-2000  
 PF 22-DEC-1998 JP 1998364656  
 PR

PI SHUJI HINUMA, KAZUHIKO TATEMOTO, MASAKI HOSoya, YUGO HABATA, PI  
 RYO FUJII,  
 PI CHIEKO KITADA  
 PC C07K14/705, A61K31/00, A61K31/00, A61K31/00, A61K31/00,  
 PC A61K38/00,  
 PC A61K39/395, A61K39/395, C07K16/28, C12N1/21, C12N5/10, C12N5/09,  
 PC C12P21/02,  
 PC G01N33/15, G01N33/577//C12P21/08, (C12N1/21, C12R1:19), (C12N5/10,  
 PC C12R1:91),  
 PC A61K37/02, C12N5/00, C12N15/00, (C12N5/00, C12R1:91) CC  
 Strandedness: Single;  
 CC Topology: linear;  
 FH Key Location/Qualifiers  
 FT source 1..27 /organism='Unidentified'.  
 FEATURES  
 source 1..27 Location/Qualifiers  
 1..27 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 56;  
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 41  
 AR211515/c 27 bp DNA linear PAT 20-JUN-2002  
 LOCUS

DEFINITION Sequence 8 from patent US 6399325.  
 ACCESSION AR211515  
 VERSION AR211515.1 GI:21514857  
 KEYWORDS  
 SOURCE  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 27)  
 Hinuma,S., Fujii,R., Fukusumi,S., Ohtaki,T., Hosoya,M., Ohgi,K. and  
 Onda,H.  
 TITLE DNA encoding a galanin receptor  
 Patent: US 6399325-A 8 04-JUN-2002;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 source 1..27 /organism='unknown'  
 /mol\_type='unassigned DNA'

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 56;  
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 42  
 AR266284/c 27 bp DNA linear PAT 10-APR-2003  
 LOCUS Sequence 6 from patent US 6492324.  
 DEFINITION AR266284  
 ACCESSION AR266284.1 GI:29695138  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 27)  
 Hinuma,S., Tatemoto,K., Hosoya,M., Habata,Y., Fujii,R. and  
 Kitada,C.  
 TITLE Aryl ligand polypeptides  
 Patent: US 6492324-A 6 10-DEC-2002;  
 JOURNAL Takeda Chemical Industries, Ltd.; Osaka;  
 WOX;

FEATURES  
 source 1..27 Location/Qualifiers  
 1..27 /organism='unknown'  
 /mol\_type='genomic DNA'

Query Match 1.2%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 74.1%; Pred. No. 56;  
 Matches 20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 979 TTGGCATTCTGCTGGCTGCCCTTCAC 1005  
 Db 27 TTGGCMTCTGCTGANTGCCYWCNAC 1

RESULT 43  
 AR300905/c 27 bp DNA linear PAT 12-JUN-2003  
 LOCUS Sequence 2 from patent US 6538107.  
 DEFINITION AR300905  
 ACCESSION AR300905.1 GI:31688578  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 27)  
 Hinuma,S., Ito,Y. and Fujii,R.  
 TITLE G protein coupled receptor protein production, and use thereof  
 Patent: US 6538107-A 2 25-MAR-2003;  
 JOURNAL Takeda Chemical Industries, Ltd.; Osaka;  
 JPX;

	FEATURES	Location/Qualifiers 1..27 /organism="unknown" /mol_type="unassigned DNA"
	source	
Qy	Query Match	1.2%; Score 21.8; DB 1; Length 27;
	Best Local Similarity	74.1%; Pred. No. 56;
	Matches	20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db	979 TTGCGCATCTGTGGCTGCCCTTCAC 1005	
	27 TTTGCMTCTGCTGNTGCCYMCNAC 1	
RESULT 44		
AR58377/c		
LOCUS	AR583777	27 bp DNA linear PAT 15-DEC-2004
DEFINITION	Sequence 30 from patent US 6794491.	
ACCESSION	AR583777	
VERSION	AR583777.1 GI:56621378	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unclassified. 1 (bases 1 to 27)	
REFERENCE	Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii,R., Fukusumi,S. and Kitada,C. Polypeptides, their production and use Patent: US 6794491-A 30 21-SEP-2004; Takeda Chemical Industries, Ltd.; Osaka, JFX;	
TITLE	JOURNAL	
FEATURES	Location/Qualifiers 1..27 /organism="unknown" /mol_type="unassigned DNA"	
source		
Qy	Query Match	1.2%; Score 21.8; DB 1; Length 27;
	Best Local Similarity	74.1%; Pred. No. 56;
	Matches	20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db	979 TTGCGCATCTGTGGCTGCCCTTCAC 1005	
	27 TTTGCMTCTGCTGANTGCCYMCNAC 1	
RESULT 45		
AR651206/c		
LOCUS	ARE51206	27 bp DNA linear PAT 20-APR-2005
DEFINITION	Sequence 30 from patent US 6881545.	
ACCESSION	ARE51206	
VERSION	ARE51206.1 GI:62795417	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified. 1 (bases 1 to 27)  Hinuma,S., Habata,Y., Kawamata,Y., Hosoya,M., Fujii.R., Fukusumi.S. and Kitada,C. Polypeptides, their production and use Patent: US 6881545-A 30 19-APR-2005; Takeda Chemical Industries, Ltd.; Osaka, JPX;	
TITLE	JOURNAL	
FEATURES	Location/Qualifiers 1..27 /organism="unknown" /mol_type="unassigned DNA"	
source		
Qy	Query Match	1.2%; Score 21.8; DB 1; Length 27;
	Best Local Similarity	74.1%; Pred. No. 56;
	Matches	20; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db	979 TTGCGCATCTGTGGCTGCCCTTCAC 1005	
	27 TTTGCMTCTGCTGANTGCCYMCNAC 1	
979 TTGCGCATCTGTGGCTGCCCTTCAC 1005		
	27 TTTGCMTCTGCTGANTGCCYMCNAC 1	

Db	27	TTTGGCMTCTGCTGANTGCCYYMCNAC	1
RESULT 46			
LOCUS	AR109839	21 bp	DNA
DEFINITION	Sequence 263 from patent US 6114139.		linear
ACCESSION	AR109839		PAT 14-FEB-2001
VERSION	AR109839.1		
KEYWORDS			
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 21)		
TITLE	Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.		
JOURNAL	G-protein coupled receptor protein and a DNA encoding the receptor		
FEATURES	Patent: US 6114139-A 263 05-SBP-2000;		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.2%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 40;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	979	TTGGCATTCTGCTGGCTGCC	999
Db	1	TTGGCATTCTGCTGGCTGCC	21
RESULT 47			
LOCUS	AR109840	21 bp	DNA
DEFINITION	Sequence 264 from patent US 6114139.		linear
ACCESSION	AR109840		PAT 14-FEB-2001
VERSION	AR109840.1		
KEYWORDS			
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 21)		
TITLE	Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.		
JOURNAL	G-protein coupled receptor protein and a DNA encoding the receptor		
FEATURES	Patent: US 6114139-A 264 05-SBP-2000;		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.2%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 40;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	979	TTGGCATTCTGCTGGCTGCC	999
Db	1	TTGGCATTCTGCTGGCTGCC	21
RESULT 48			
LOCUS	CS207678	21 bp	DNA
DEFINITION	Sequence 386 from Patent WO2005109000.		linear
ACCESSION	CS207678		PAT 08-DEC-2005
VERSION	CS207678.1		
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	other sequences; artificial sequences.		
AUTHORS	1		
JOURNAL	Spittela,K.F.		
	Patent: WO 2005109000-A 386 17-NOV-2005;		
	Galapagos Genomics N.V. (BE); Spittela,K.		
	Koenraad Frederick F. (BE)		

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 290 AACGAGCTGGCAATTGTC 310  
|||||  
1 AACGAGCTGGCAATTGTC 21

Db 1 AACGAGCTGGCAATTGTC 21

RESULT 49  
LOCUS CS207679 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 387 from Patent WO2005109000.  
ACCESSION CS207679  
VERSION CS207679.1 GI:83413956  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 387 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 303 AATTGTCCTTGGGAGCTGC 323  
|||||  
1 AATTGTCCTTGGGAGCTGC 21

Db 1 AATTGTCCTTGGGAGCTGC 21

RESULT 50  
LOCUS CS207680 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 388 from Patent WO2005109000.  
ACCESSION CS207680  
VERSION CS207680.1 GI:83413957  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 388 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 358 AACGTGTAAGTATGATGCATC 378  
|||||  
1 AACGTGTAAGTATGATGCATC 378

Db 1 AACGTGTAAGTATGATGCATC 21

RESULT 51  
LOCUS CS207681 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 389 from Patent WO2005109000.  
ACCESSION CS207681  
VERSION CS207681.1 GI:83413958  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 389 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 AATACAGTGGTGAAGTACACC 483  
|||||  
1 AATACAGTGGTGAAGTACACC 21

Db 1 AATACAGTGGTGAAGTACACC 21

RESULT 52  
LOCUS CS207682 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 390 from Patent WO2005109000.  
ACCESSION CS207682  
VERSION CS207682.1 GI:83413959  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 390 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 475 AACTCAGCTATGCTGTCAC 495  
|||||  
1 AACTCAGCTATGCTGTCAC 21

Db 1 AACTCAGCTATGCTGTCAC 21

RESULT 53  
LOCUS CS207683 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 391 from Patent WO2005109000.  
ACCESSION CS207683  
VERSION CS207683.1 GI:83413960  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.



REFERENCE 1  
AUTHORS Spittaels, K. F.  
JOURNAL Patent: WO 2005109000-A 391 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 494 ACAACGAATGCTACTACGGCC 514  
Db 1 ACAACGAATGCTACTACGGCC 21

RESULT 54  
LOCUS CS207684 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 392 from Patent WO2005109000.  
ACCESSION CS207684  
VERSION CS207684.1 GI:83413961  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K. F.  
JOURNAL Patent: WO 2005109000-A 392 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 AAGTCCACAACCTCTTCCC 546  
Db 1 AAGTCCACAACCTCTTCCC 21

RESULT 55  
LOCUS CS207685 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 393 from Patent WO2005109000.  
ACCESSION CS207685  
VERSION CS207685.1 GI:83413962  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K. F.  
JOURNAL Patent: WO 2005109000-A 393 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 643 ACAGCCACCAAGTGTGATC 663  
Db 1 ACAGCCACCAAGTGTGATC 21

RESULT 56  
LOCUS CS207686 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 394 from Patent WO2005109000.  
ACCESSION CS207686  
VERSION CS207686.1 GI:83413963  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K. F.  
JOURNAL Patent: WO 2005109000-A 394 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 649 ACCAAAGTGTGATCTGTGTC 669  
Db 1 ACCAAAGTGTGATCTGTGTC 21

RESULT 57  
LOCUS CS207687 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 395 from Patent WO2005109000.  
ACCESSION CS207687  
VERSION CS207687.1 GI:83413964  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K. F.  
JOURNAL Patent: WO 2005109000-A 395 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 652 AAAGTGTGATCTGTGTCATC 672  
Db 1 AAAGTGTGATCTGTGTCATC 21

RESULT 58  
LOCUS CS207688 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 396 from Patent WO2005109000.  
ACCESSION CS207688  
VERSION CS207688.1 GI:83413965

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spittaels, K.F.  
Patent: WO 2005109000-A 396 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTGACCCAGAGACCATGC 713  
Db 1 ACTGACCCAGAGACCATGC 21

RESULT 59  
CS207689 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 397 from Patent WO2005109000.  
ACCESSION CS207689  
VERSION CS207689.1 GI:83413966  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spittaels, K.F.  
Patent: WO 2005109000-A 397 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGTGACTGTGC 817  
Db 1 ACCACATCTGTGTGACTGTGC 21

RESULT 60  
CS207690 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 398 from Patent WO2005109000.  
ACCESSION CS207690  
VERSION CS207690.1 GI:83413967  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spittaels, K.F.  
Patent: WO 2005109000-A 398 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 ACTGTGCTGATCTACTTCCTC 831  
Db 1 ACTGTGCTGATCTACTTCCTC 21

RESULT 61  
CS207691 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 399 from Patent WO2005109000.  
ACCESSION CS207691  
VERSION CS207691.1 GI:83413968  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spittaels, K.F.  
Patent: WO 2005109000-A 399 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 ACACCGTAGTGGGATCACAC 877  
Db 1 ACACCGTAGTGGGATCACAC 21

RESULT 62  
CS207692 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 400 from Patent WO2005109000.  
ACCESSION CS207692  
VERSION CS207692.1 GI:83413969  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spittaels, K.F.  
Patent: WO 2005109000-A 400 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 ACACTATGGGCCAGATGATC 894  
Db 1 ACACTATGGGCCAGATGATC 21

RESULT 63  
CS207693

LOCUS CS207693 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 401 from Patent WO2005109000.  
ACCESSION CS207693  
VERSION CS207693.1 GI:83413970  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Spitlaels,K.F.  
AUTHORS Patent: WO 2005109000-A 401 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 876 ACTATGGGCGCATGATCCC 896  
DB 1 ACTATGGGCGCATGATCCC 21

RESULT 64  
LOCUS CS207694 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 402 from Patent WO2005109000.  
ACCESSION CS207694  
VERSION CS207694.1 GI:83413971  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Spitlaels,K.F.  
AUTHORS Patent: WO 2005109000-A 402 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 920 ACGAGCAAGTCTGCCAAGC 940  
DB 1 ACGAGCAAGTCTGCCAAGC 21

RESULT 65  
LOCUS CS207695 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 403 from Patent WO2005109000.  
ACCESSION CS207695  
VERSION CS207695.1 GI:83413972  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Spitlaels,K.F.  
AUTHORS Patent: WO 2005109000-A 403 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
location/Qualifiers

source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1025 ACATCAACCGAGTCTTACC 1045  
DB 1 ACATCAACCGAGTCTTACC 21

RESULT 66  
LOCUS CS207696 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 404 from Patent WO2005109000.  
ACCESSION CS207696  
VERSION CS207696.1 GI:83413973  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Spitlaels,K.F.  
AUTHORS Patent: WO 2005109000-A 404 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1043 ACCTGAAGAATTATCCAGC 1063  
DB 1 ACCTGAAGAATTATCCAGC 21

RESULT 67  
LOCUS CS207697 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 405 from Patent WO2005109000.  
ACCESSION CS207697  
VERSION CS207697.1 GI:83413974  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 Spitlaels,K.F.  
AUTHORS Patent: WO 2005109000-A 405 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1048 AAGAAGTTATCCAGCAGTC 1068  
DB 1 AAGAAGTTATCCAGCAGTC 21

RESULT 68  
CS207698 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207698  
DEFINITION Sequence 406 from Patent WO2005109000.  
ACCESSION CS207698  
VERSION CS207698.1 GI:83413975  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 406 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGTCTAC 1071  
Db 1 AAGTTATCCAGCAGGTCTAC 21  
|||||  
|||||

RESULT 69  
CS207699 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207699  
DEFINITION Sequence 407 from Patent WO2005109000.  
ACCESSION CS207699  
VERSION CS207699.1 GI:83413976  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 407 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 AATGACAGTTCCTGCTGAGC 1155  
Db 1 AATGACAGTTCCTGCTGAGC 21  
|||||  
|||||

RESULT 70  
CS207700 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207700  
DEFINITION Sequence 408 from Patent WO2005109000.  
ACCESSION CS207700  
VERSION CS207700.1 GI:83413977  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 408 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 408 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1214 AATGAATCCACCCGGTATC 1234  
Db 1 AATGAATCCACCCGGTATC 21  
|||||  
|||||

RESULT 71  
CS207701 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207701  
DEFINITION Sequence 409 from Patent WO2005109000.  
ACCESSION CS207701  
VERSION CS207701.1 GI:83413978  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 409 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1363 AACTGCTCTTCACGAAGTGAC 1383  
Db 1 AACTGCTCTTCACGAAGTGAC 21  
|||||  
|||||

RESULT 72  
CS207702 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207702  
DEFINITION Sequence 410 from Patent WO2005109000.  
ACCESSION CS207702  
VERSION CS207702.1 GI:83413979  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 410 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 AAGTACTCCAAGACATGAC 1397  
DB 1 AAGTGACTCCAAGACATGAC 21

RESULT 73  
LOCUS CS207703 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 411 from Patent WO2005109000.  
ACCESSION CS207703  
VERSION CS207703.1 GI:83413980  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 411 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 AAGACCATGACAGAGCTTC 1407  
DB 1 AAGACCATGACAGAGCTTC 21

RESULT 74  
LOCUS CS207704 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 412 from Patent WO2005109000.  
ACCESSION CS207704  
VERSION CS207704.1 GI:83413981  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 412 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1390 ACCATGACAGAGCTTCAGC 1410  
DB 1 ACCATGACAGAGCTTCAGC 21

RESULT 75  
LOCUS CS207705 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 413 from Patent WO2005109000.  
ACCESSION CS207705  
VERSION CS207705.1 GI:83413982  
KEYWORDS

SOURCE  
ORGANISM  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 413 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ACAGAGAGCTTCAGCTTCTCC 1416  
DB 1 ACAGAGAGCTTCAGCTTCTCC 21

RESULT 76  
LOCUS CS207706 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 414 from Patent WO2005109000.  
ACCESSION CS207706  
VERSION CS207706.1 GI:83413983  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 414 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 AAATTCCTTCATCTGGAAC 1517  
DB 1 AAATTCCTTCATCTGGAAC 21

RESULT 77  
LOCUS CS207707 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 415 from Patent WO2005109000.  
ACCESSION CS207707  
VERSION CS207707.1 GI:83413984  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 415 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 AACCATGAGAAACACCTTCAC 1534  
1 AACCATGAGAAACACCTTCAC 21

RESULT 78  
LOCUS CS207708 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 416 from Patent WO2005109000.  
ACCESSION CS207708  
VERSION CS207708.1 GI:83413985  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 416 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1648 AATCACTGAACCTTGTGTGAGC 1668  
1 AATCACTGAACCTTGTGTGAGC 21

RESULT 79  
LOCUS CS207709 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 417 from Patent WO2005109000.  
ACCESSION CS207709  
VERSION CS207709.1 GI:83413986  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 417 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1733 ACTTGGCTGCATGCGAGTGC 1753  
1 ACTTGGCTGCATGCGAGTGC 21

RESULT 80  
LOCUS CS207710 21 bp DNA linear PAT 08-DEC-2005

DEFINITION Sequence 418 from Patent WO2005109000.  
ACCESSION CS207710  
VERSION CS207710.1 GI:83413987  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 418 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 AACGAGCTGGCAATTGTCC 310  
1 AACGAGCTGGCAATTGTCC 21

RESULT 81  
LOCUS CS207711 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 419 from Patent WO2005109000.  
ACCESSION CS207711  
VERSION CS207711.1 GI:83413988  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 419 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 AATTGTCTTTGGCGACGCTGC 323  
1 AATTGTCTTTGGCGACGCTGC 21

RESULT 82  
LOCUS CS207712 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 420 from Patent WO2005109000.  
ACCESSION CS207712  
VERSION CS207712.1 GI:83413989  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 420 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21

```

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      358 AACGTGATGATGATGATC 378
Db      1 AACGTGATGATGATGATC 21

RESULT 83
LOCUS      CS207713      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 421 from Patent WO2005109000.
ACCESSION  CS207713
VERSION     CS207713.1 GI:83413990
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 421 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      463 AATACAGTGTGTAACCTTCACC 483
Db      1 AATACAGTGTGTAACCTTCACC 21

RESULT 84
LOCUS      CS207714      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 422 from Patent WO2005109000.
ACCESSION  CS207714
VERSION     CS207714.1 GI:83413991
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 422 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      475 AACTTCACCTATGCTGTCCAC 495
Db      1 AACTTCACCTATGCTGTCCAC 21
```

```

RESULT 85
LOCUS      CS207715      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 423 from Patent WO2005109000.
ACCESSION  CS207715
VERSION     CS207715.1 GI:83413992
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 423 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      494 ACAACGAATGTTACTACGCGC 514
Db      1 ACAACGAATGTTACTACGCGC 21

RESULT 86
LOCUS      CS207716      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 424 from Patent WO2005109000.
ACCESSION  CS207716
VERSION     CS207716.1 GI:83413993
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS     Patent: WO 2005109000-A 424 17-NOV-2005;
JOURNAL     Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES
SOURCE      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      643 ACAGCCACCAAGTGTGATC 663
Db      1 ACAGCCACCAAGTGTGATC 21

RESULT 87
LOCUS      CS207717      21 bp      DNA      linear      PAT 08-DEC-2005
DEFINITION Sequence 425 from Patent WO2005109000.
ACCESSION  CS207717
VERSION     CS207717.1 GI:83413994
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 Spittaels,K.F.
AUTHORS
```

JOURNAL Patent: WO 2005109000-A 425 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 649 ACCAAGTGTGATCTGTGTC 669  
Db 1 ACCAAGTGTGATCTGTGTC 21

RESULT 88  
LOCUS CS207718 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 426 from Patent WO2005109000.  
ACCESSION CS207718  
VERSION CS207718.1 GI:83413995  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
JOURNAL  
Patent: WO 2005109000-A 426 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 652 AAAGTGTGATCTGTGTCATC 672  
Db 1 AAAGTGTGATCTGTGTCATC 21

RESULT 89  
LOCUS CS207719 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 427 from Patent WO2005109000.  
ACCESSION CS207719  
VERSION CS207719.1 GI:83413996  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
JOURNAL  
Patent: WO 2005109000-A 427 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 ACTGACCAAGAGACATGC 733  
Db 1 ACTGACCAAGAGACATGC 21

RESULT 90  
LOCUS CS207720 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 428 from Patent WO2005109000.  
ACCESSION CS207720  
VERSION CS207720.1 GI:83413997  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
JOURNAL  
Patent: WO 2005109000-A 428 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 797 ACCACATCTGTGACTGTGC 817  
Db 1 ACCACATCTGTGACTGTGC 21

RESULT 91  
LOCUS CS207721 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 429 from Patent WO2005109000.  
ACCESSION CS207721  
VERSION CS207721.1 GI:83413998  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
JOURNAL  
Patent: WO 2005109000-A 429 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spilttaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 ACTGTGCTGATCTACTTCCTC 831  
Db 1 ACTGTGCTGATCTACTTCCTC 21

RESULT 92  
LOCUS CS207723 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 431 from Patent WO2005109000.  
ACCESSION CS207723  
VERSION CS207723.1 GI:83414000  
KEYWORDS  
SOURCE  
synthetic construct



ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 431 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 ACACATGCGCCAGTGCATC 894  
Db 1 ACACATGCGCCAGTGCATC 21

RESULT 93  
LOCUS CS207724 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 432 from Patent WO2005109000.  
ACCESSION CS207724  
VERSION CS207724.1 GI:83414001  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 432 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 876 ACTATGGGCGCATGATCCC 896  
Db 1 ACTATGGGCGCATGATCCC 21

RESULT 94  
LOCUS CS207725 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 433 from Patent WO2005109000.  
ACCESSION CS207725  
VERSION CS207725.1 GI:83414002  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 433 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 920 ACGAGCAAGTCTGCGCAGC 940  
Db 1 ACGAGCAAGTCTGCGCAGC 21

RESULT 95  
LOCUS CS207726 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 434 from Patent WO2005109000.  
ACCESSION CS207726  
VERSION CS207726.1 GI:83414003  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 434 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 ACATCAACCCAGATCTCACC 1045  
Db 1 ACATCAACCCAGATCTCACC 21

RESULT 96  
LOCUS CS207727 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 435 from Patent WO2005109000.  
ACCESSION CS207727  
VERSION CS207727.1 GI:83414004  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 435 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1043 ACCTGAAGAGTTATCCAGC 1063  
Db 1 ACCTGAAGAGTTATCCAGC 21

RESULT 97  
LOCUS CS207728 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 436 from Patent WO2005109000.

ACCESSION CS207728  
VERSION CS207728.1 GI:83414005  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 436 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
Source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1048 AAGAATTATCCAGCAGCTC 1068  
DB 1 AAGAATTATCCAGCAGCTC 21  
RESULT 98  
LOCUS CS207729 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 437 from Patent WO2005109000.  
ACCESSION CS207729  
VERSION CS207729.1 GI:83414006  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 437 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
Source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1051 AAGTTATCCAGCAGCTCTAC 1071  
DB 1 AAGTTATCCAGCAGCTCTAC 21  
RESULT 99  
LOCUS CS207732 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 440 from Patent WO2005109000.  
ACCESSION CS207732  
VERSION CS207732.1 GI:83414009  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 440 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
Source Location/Qualifiers  
1..21  
/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 290 AACGACCTGGCAAAATTGTC 310  
DB 1 AACGACCTGGCAAAATTGTC 21  
RESULT 100  
LOCUS CS207733 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 441 from Patent WO2005109000.  
ACCESSION CS207733  
VERSION CS207733.1 GI:83414010  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 441 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
Source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 303 AATTGCTCTTTGGGACGCTGC 323  
DB 1 AATTGCTCTTTGGGACGCTGC 21  
RESULT 101  
LOCUS CS207734 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 442 from Patent WO2005109000.  
ACCESSION CS207734  
VERSION CS207734.1 GI:83414011  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
REFERENCE 1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 442 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
Source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 358 AACGCTAGTAGATGTGATC 378  
DB 1 AACGCTAGTAGATGTGATC 21

RESULT 102  
CS207735 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207735 Sequence 443 from Patent WO2005109000.  
DEFINITION CS207735  
ACCESSION CS207735  
VERSION CS207735.1 GI:83414012  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 443 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 463 AATACAGTGTGAACCTCACC 483  
Db 1 AATACAGTGTGAACCTCACC 21  
RESULT 103  
CS207736 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207736 Sequence 444 from Patent WO2005109000.  
DEFINITION CS207736  
ACCESSION CS207736  
VERSION CS207736.1 GI:83414013  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 444 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 475 AACTTACCTATGCTGTCAC 495  
Db 1 AACTTACCTATGCTGTCAC 21  
RESULT 104  
CS207737 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207737 Sequence 445 from Patent WO2005109000.  
DEFINITION CS207737  
ACCESSION CS207737  
VERSION CS207737.1 GI:83414014  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 445 17-NOV-2005;  
JOURNAL

Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 494 ACAACGAATGCTACTACGCC 514  
Db 1 ACAACGAATGCTACTACGCC 21  
RESULT 105  
CS207738 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207738 Sequence 446 from Patent WO2005109000.  
DEFINITION CS207738  
ACCESSION CS207738  
VERSION CS207738.1 GI:83414015  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 446 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 526 AAGTTCACCAACTCTTTCCC 546  
Db 1 AAGTTCACCAACTCTTTCCC 21  
RESULT 106  
CS207739 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207739 Sequence 447 from Patent WO2005109000.  
DEFINITION CS207739  
ACCESSION CS207739  
VERSION CS207739.1 GI:83414016  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 447 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 643 ACAGCCACCAAGTGTATC 663

Db 1 ACAGCCACCAAGTGTATC 21  
|||||  
RESULT 107  
CS207740 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 448 from Patent WO2005109000.  
ACCESSION CS207740  
VERSION CS207740.1 GI:83414017  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 448 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 649 ACCAAGTGTATCTGTCTC 669  
Db 1 ACCAAGTGTATCTGTCTC 21  
|||||  
RESULT 108  
CS207741 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 449 from Patent WO2005109000.  
DEFINITION CS207741  
ACCESSION CS207741  
VERSION CS207741.1 GI:83414018  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 449 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 652 AAAGTGTATCTGTGTATC 672  
Db 1 AAAGTGTATCTGTGTATC 21  
|||||  
RESULT 109  
CS207742 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 450 from Patent WO2005109000.  
DEFINITION CS207742  
ACCESSION CS207742  
VERSION CS207742.1 GI:83414019  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 450 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

other sequences; artificial sequences.  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 450 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 713 ACTCACCACAGACCATGC 733  
Db 1 ACTCACCACAGACCATGC 21  
|||||  
RESULT 110  
CS207743 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 451 from Patent WO2005109000.  
DEFINITION CS207743  
ACCESSION CS207743  
VERSION CS207743.1 GI:83406147  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 451 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 797 ACCACATCTGTGTGACTGTC 817  
Db 1 ACCACATCTGTGTGACTGTC 21  
|||||  
RESULT 111  
CS207744 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 452 from Patent WO2005109000.  
DEFINITION CS207744  
ACCESSION CS207744  
VERSION CS207744.1 GI:83406347  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 452 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTTCCTC 831  
|||||  
1 ACTGTGCTGATCTACTTCCTC 21

Db

RESULT 112  
LOCUS CS207745 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 453 from Patent WO2005109000.  
ACCESSION CS207745  
VERSION CS207745.1 GI:83406348  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spitlaels, K.F.  
JOURNAL Patent: WO 2005109000-A 453 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGAGATCAGAC 877  
|||||  
1 ACACCGTAGTGGAGATCAGAC 21

Db

RESULT 113  
LOCUS CS207746 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 454 from Patent WO2005109000.  
ACCESSION CS207746  
VERSION CS207746.1 GI:83406349  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spitlaels, K.F.  
JOURNAL Patent: WO 2005109000-A 454 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 ACACTATGGCCAGTGAGATC 894  
|||||  
1 ACACTATGGCCAGTGAGATC 21

Db

RESULT 114  
LOCUS CS207747 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 455 from Patent WO2005109000.  
ACCESSION CS207747

VERSION CS207747.1 GI:83406350  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spitlaels, K.F.  
JOURNAL Patent: WO 2005109000-A 455 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 ACTATGGCCAGTGAGATCCC 896  
|||||  
1 ACTATGGCCAGTGAGATCCC 21

Db

RESULT 115  
LOCUS CS207748 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 456 from Patent WO2005109000.  
ACCESSION CS207748  
VERSION CS207748.1 GI:83406351  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spitlaels, K.F.  
JOURNAL Patent: WO 2005109000-A 456 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 ACGAGCAAGTCTGCGCAAC 940  
|||||  
1 ACGAGCAAGTCTGCGCAAC 21

Db

RESULT 116  
LOCUS CS207749 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 457 from Patent WO2005109000.  
ACCESSION CS207749  
VERSION CS207749.1 GI:83406352  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spitlaels, K.F.  
JOURNAL Patent: WO 2005109000-A 457 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 ACATCAACCGAGATCTTACC 1045  
Db 1 ACATCAACCGAGATCTTACC 21  
|||||

RESULT 117  
LOCUS CS207750 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 458 from Patent WO2005109000.  
ACCESSION CS207750  
VERSION CS207750.1 GI:83406353  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 458 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
SOURCE 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1048 AAGAAGTTATCCAGCAGGTC 1068  
Db 1 AAGAAGTTATCCAGCAGGTC 21  
|||||

RESULT 119

CS207752 21 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207752  
DEFINITION Sequence 460 from Patent WO2005109000.  
ACCESSION CS207752  
VERSION CS207752.1 GI:83406355  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 460 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
SOURCE 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGCAGGTCCTAC 1071  
Db 1 AAGTTATCCAGCAGGTCCTAC 21  
|||||

RESULT 120  
LOCUS CS207753 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 461 from Patent WO2005109000.  
ACCESSION CS207753  
VERSION CS207753.1 GI:83406356  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 461 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
SOURCE 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 AATGACAGTTCGCTGGGC 1155  
Db 1 AATGACAGTTCGCTGGGC 21  
|||||

RESULT 121  
LOCUS CS207754 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 462 from Patent WO2005109000.  
ACCESSION CS207754  
VERSION CS207754.1 GI:83406357  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 462 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES  
Source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1214 AATGAATCCACCGGTATC 1234  
1 AATGAATCCACCGGTATC 21

RESULT 122  
CS207755 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 463 from Patent WO2005109000.  
ACCESSION CS207755  
VERSION CS207755.1 GI:83406358  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 463 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES  
Source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1363 AACTGCTCTTCACGAGTGAC 1383  
1 AACTGCTCTTCACGAGTGAC 21

RESULT 123  
CS207756 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 464 from Patent WO2005109000.  
ACCESSION CS207756  
VERSION CS207756.1 GI:83406359  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 464 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES  
Source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1377 AAGTACTCCAGACCATGAC 1397  
1 AAGTACTCCAGACCATGAC 21

Db 1 AAGTACTCCAGACCATGAC 21

RESULT 124  
CS207757 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 465 from Patent WO2005109000.  
ACCESSION CS207757  
VERSION CS207757.1 GI:83406360  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 465 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES  
Source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1387 AAGACCATGACAGAGCTTC 1407  
1 AAGACCATGACAGAGCTTC 21

RESULT 125  
CS207758 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 466 from Patent WO2005109000.  
ACCESSION CS207758  
VERSION CS207758.1 GI:83406361  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Spittaels,K.F.  
JOURNAL Patent: WO 2005109000-A 466 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)

FEATURES  
Source  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1390 ACCATGACAGAGCTTCAGC 1410  
1 ACCATGACAGAGCTTCAGC 21

RESULT 126  
CS207759 21 bp DNA linear PAT 08-DEC-2005  
LOCUS  
DEFINITION Sequence 467 from Patent WO2005109000.  
ACCESSION CS207759  
VERSION CS207759.1 GI:83406362  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 467 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ACAGAGAGCTTCAGCTTCTCC 1416  
DB 1 ACAGAGAGCTTCAGCTTCTCC 21  
|||||  
|||||

RESULT 127  
LOCUS CS207760 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 468 from Patent WO2005109000.  
ACCESSION CS207760  
VERSION CS207760.1 GI:83406363  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 468 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 AAATCCCTTCATCTGGAAC 1517  
DB 1 AAATCCCTTCATCTGGAAC 21  
|||||  
|||||

RESULT 128  
LOCUS CS207761 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 469 from Patent WO2005109000.  
ACCESSION CS207761  
VERSION CS207761.1 GI:83406364  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 469 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 AACCATCAGAAACACCTCAC 1534  
DB 1 AACCATCAGAAACACCTCAC 21  
|||||  
|||||

RESULT 129  
LOCUS CS207762 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 470 from Patent WO2005109000.  
ACCESSION CS207762  
VERSION CS207762.1 GI:83406365  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 470 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AATCATGAACTTGTCTGAGC 1668  
DB 1 AATCATGAACTTGTCTGAGC 21  
|||||  
|||||

RESULT 130  
LOCUS CS207763 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 471 from Patent WO2005109000.  
ACCESSION CS207763  
VERSION CS207763.1 GI:83406366  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 471 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 ACTTGGCTGATGCGAGTGC 1753  
DB 1 ACTTGGCTGATGCGAGTGC 21  
|||||  
|||||

RESULT 131  
LOCUS CS207764 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 472 from Patent WO2005109000.  
ACCESSION CS207764  
VERSION CS207764.1 GI:83406367



KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spitlaels, K.F.  
Patent: WO 2005109000-A 472 17-NOV-2005;  
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1. . 21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AACCAAGCTGGCAATTGTCC 310  
DB 1 AACCAAGCTGGCAATTGTCC 21

RESULT 132  
LOCUS CS207765 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 473 from Patent WO2005109000.  
ACCESSION CS207765  
VERSION CS207765.1 GI:83406368  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spitlaels, K.F.  
Patent: WO 2005109000-A 473 17-NOV-2005;  
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1. . 21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AATTGCTCTTGGGACGCTGC 323  
DB 1 AATTGCTCTTGGGACGCTGC 21

RESULT 133  
LOCUS CS207766 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 474 from Patent WO2005109000.  
ACCESSION CS207766  
VERSION CS207766.1 GI:83406369  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spitlaels, K.F.  
Patent: WO 2005109000-A 474 17-NOV-2005;  
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1. . 21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AACGTGTAGTGTGATGC 378  
DB 1 AACGTGTAGTGTGATGC 21

RESULT 134  
LOCUS CS207767 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 475 from Patent WO2005109000.  
ACCESSION CS207767  
VERSION CS207767.1 GI:83406370  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spitlaels, K.F.  
Patent: WO 2005109000-A 475 17-NOV-2005;  
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1. . 21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 AATACAGTGTGAACTTCACC 483  
DB 1 AATACAGTGTGAACTTCACC 21

RESULT 135  
LOCUS CS207768 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 476 from Patent WO2005109000.  
ACCESSION CS207768  
VERSION CS207768.1 GI:83406371  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
JOURNAL  
FEATURES  
source

synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1  
Spitlaels, K.F.  
Patent: WO 2005109000-A 476 17-NOV-2005;  
Genomics N.V. (BE); Spitlaels, Koenraad Frederick F. (BE)  
Location/Qualifiers  
1. . 21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AACTTACCTATGCTGTCAC 495  
DB 1 AACTTACCTATGCTGTCAC 21

RESULT 136  
LOCUS CS207769

LOCUS CS207769 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 477 from Patent WO2005109000.  
ACCESSION CS207769  
VERSION CS207769.1 GI:83406372  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS Spititael's, K.F.  
JOURNAL Patent: WO 2005109000-A 477 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititael's, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 494 ACAACGAATGGTACTACGCGC 514  
Db 1 ACAACGAATGGTACTACGCGC 21  
RESULT 137  
LOCUS CS207770 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 478 from Patent WO2005109000.  
ACCESSION CS207770  
VERSION CS207770.1 GI:83406373  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS Spititael's, K.F.  
JOURNAL Patent: WO 2005109000-A 478 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititael's, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 643 ACAGCCACCAAGTGTGTCATC 663  
Db 1 ACAGCCACCAAGTGTGTCATC 21  
RESULT 138  
LOCUS CS207771 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 479 from Patent WO2005109000.  
ACCESSION CS207771  
VERSION CS207771.1 GI:83406374  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS Spititael's, K.F.  
JOURNAL Patent: WO 2005109000-A 479 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititael's, Koenraad Frederick F. (BE)  
FEATURES  
location/Qualifiers

source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 649 ACCAAGTGTGTCATCTGTGTC 669  
Db 1 ACCAAGTGTGTCATCTGTGTC 21  
RESULT 139  
LOCUS CS207772 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 480 from Patent WO2005109000.  
ACCESSION CS207772  
VERSION CS207772.1 GI:83406375  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS Spititael's, K.F.  
JOURNAL Patent: WO 2005109000-A 480 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititael's, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 652 AAAGTGTGTCATCTGTGTCATC 672  
Db 1 AAAGTGTGTCATCTGTGTCATC 21  
RESULT 140  
LOCUS CS207773 21 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 481 from Patent WO2005109000.  
ACCESSION CS207773  
VERSION CS207773.1 GI:83406376  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS Spititael's, K.F.  
JOURNAL Patent: WO 2005109000-A 481 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititael's, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"  
Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 713 ACTCAACGACGAGACCATGC 733  
Db 1 ACTCAACGACGAGACCATGC 21

RESULT 141  
CS207774 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 482 from Patent WO2005109000.  
DEFINITION CS207774  
ACCESSION CS207774.1 GI:83406377  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 482 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 ACCACATCTGTGACTGTGC 817  
Db 1 ACCACATCTGTGACTGTGC 21

RESULT 142  
CS207775 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 483 from Patent WO2005109000.  
DEFINITION CS207775  
ACCESSION CS207775.1 GI:83406378  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 483 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACTGTGCTGATCTACTCTTC 831  
Db 1 ACTGTGCTGATCTACTCTTC 21

RESULT 143  
CS207776 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 484 from Patent WO2005109000.  
DEFINITION CS207776  
ACCESSION CS207776.1 GI:83406379  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1

AUTHORS Spittaels, K.F.  
JOURNAL Patent: WO 2005109000-A 484 17-NOV-2005;  
FEATURES Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGAAATCACAC 877  
Db 1 ACACCGTAGTGGGAAATCACAC 21

RESULT 144  
CS207777 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 485 from Patent WO2005109000.  
DEFINITION CS207777  
ACCESSION CS207777.1 GI:83406380  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 485 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AACTATGGGCGCAGTGAGATC 894  
Db 1 AACTATGGGCGCAGTGAGATC 21

RESULT 145  
CS207778 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 486 from Patent WO2005109000.  
DEFINITION CS207778  
ACCESSION CS207778.1 GI:83406381  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 Spittaels, K.F.  
AUTHORS Patent: WO 2005109000-A 486 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 876 ACTATGGGCCAGTGATGCC 896  
Db 1 ACTATGGGCCAGTGATGCC 21

RESULT 146  
CS207779 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 487 from Patent WO2005109000.  
DEFINITION CS207779  
ACCESSION CS207779.1 GI:83406382  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Spittaels,K.F.  
AUTHORS Patent: WO 2005109000-A 487 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES Location/Qualifiers  
1..21  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 920 ACGAGCAAGTCTCTGCCAAG 940  
Db 1 ACGAGCAAGTCTCTGCCAAG 21

RESULT 147  
CS207780 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 488 from Patent WO2005109000.  
DEFINITION CS207780  
ACCESSION CS207780.1 GI:83406383  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Spittaels,K.F.  
AUTHORS Patent: WO 2005109000-A 488 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES Location/Qualifiers  
1..21  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1025 ACATCAACCCAGATCTTACC 1045  
Db 1 ACATCAACCCAGATCTTACC 21

RESULT 148  
CS207781 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 489 from Patent WO2005109000.  
DEFINITION CS207781  
ACCESSION CS207781.1 GI:83406384  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Spittaels,K.F.  
AUTHORS Patent: WO 2005109000-A 489 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES Location/Qualifiers  
1..21  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1043 ACCGAGAGAGTTATCCAGC 1063  
Db 1 ACCGAGAGAGTTATCCAGC 21

RESULT 149  
CS207782 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 490 from Patent WO2005109000.  
DEFINITION CS207782  
ACCESSION CS207782.1 GI:83406385  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Spittaels,K.F.  
AUTHORS Patent: WO 2005109000-A 490 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES Location/Qualifiers  
1..21  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1048 AAGAGTTTATCCAGCAGTC 1068  
Db 1 AAGAGTTTATCCAGCAGTC 21

RESULT 150  
CS207783 21 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 491 from Patent WO2005109000.  
DEFINITION CS207783  
ACCESSION CS207783.1 GI:83406386  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Spittaels,K.F.  
AUTHORS Patent: WO 2005109000-A 491 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spittaels, Koenraad Frederick F. (BE)  
FEATURES Location/Qualifiers  
1..21  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1051 AAGTTATCCAGAGCTCTAC 1071  
|||||  
Db 1 AAGTTATCCAGAGCTCTAC 21

RESULT 151  
117155/c 117155 21 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 10 from patent US 5484886.  
ACCESSION 117155 GI:1252063  
VERSION 117155.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 10 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 559 TTGCGCAGTATCTACTCCATG 579  
|||||  
Db 21 TTGCGCAGTATCTACTCCATG 1

RESULT 152  
117158/c 117158 21 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 13 from patent US 5484886.  
ACCESSION 117158  
VERSION 117158.1 GI:1252066  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 13 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 836 TGCCTGATGCTGCTATGCAT 856  
|||||  
Db 21 TGCCTGATGCTGCTATGCAT 1

RESULT 153  
117160/c 117160 21 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 15 from patent US 5484886.  
ACCESSION 117160  
VERSION 117160.1 GI:1252068  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 15 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 956 TGATGATTGCTGCTGTGCA 976  
|||||  
Db 21 TGATGATTGCTGCTGTGCA 1

RESULT 154  
117162 117162 21 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 17 from patent US 5484886.  
ACCESSION 117162  
VERSION 117162.1 GI:1252070  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 17 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 924 GCAAGTCTTGCCAGCGCAA 944  
|||||  
Db 1 GCAAGTCTTGCCAGCGCAA 21

RESULT 155  
117163 117163 21 bp DNA linear PAT 03-APR-1996  
LOCUS Sequence 18 from patent US 5484886.  
ACCESSION 117163  
VERSION 117163.1 GI:1252071  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 18 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 956 TGATGATTGCTGCTGTGCA 976

Db 1 TGATGATGTCGTGTGCA 21

RESULT	156		
LOCUS	117167/c		
DEFINITION	Sequence 22 from patent US 5464886.	21 bp	DNA
ACCESSION	117167		linear
VERSION	117167.1	GI:1252075	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM			

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Best local Similarity	100.0%;	Pred. No. 40;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```

Oy      1567 AGGGAACATTCATCCTTG 1587
        |||||
Db      21  AGGGAACATTCATCCTTG 1

```

RESULT 157			
AX468707			
LOCUS	AX468707	21 bp	DNA
DEFINITION	Sequence 23 from Patent WO0213799.		linear
ACCESSION	AX468707		
VERSION	AX468707.1	GI:21901477	

REFERENCE	1
AUTHORS	Henry, J. L., Cahill, C. M., and Yashpal, K.
TITLE	Oligonucleotides and other modulators of the nk-1 receptor pathway and therapeutic uses thereof
JOURNAL	Patent: WO 0213799-A 23 21-FEB-2002;
	MCGILL UNIVERSITY (Ca)

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Similarity	100.0%	Pred. No. 40;		
Best Local	0;	Mismatches	0;	Gaps 0;
Matches	21;	Conservative		

Oy      956 TGATGATTGTCTGGTGTGA 976  
         |||||  
Db      1 TGATGATTGTCTGGTGTGA 21

RESULT	158		
LOCUS	AX468708	21 bp	DNA
DEFINITION	Sequence 24 from Patent WO0213799.		linear
ACCESSION	AX468708		
VERSION	AX468708.1	GI:21901478	
KEYWORDS			
SOURCE	.		
ORGANISM	synthetic construct		
	synthetic construct		

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SOURCE

1 other sequences; artificial sequences.  
Henry, J. L., Cahill, C. M. and Vashpal, K.  
Oligonucleotide and other modulators of the nk-1 receptor pathway  
and therapeutic uses thereof  
Patent: WO 0213799-A 24 21-FEB-2002;  
MCGILL UNIVERSITY (CA)  
Location/Qualifiers  
1. "21-FEB-2002"="earliest construct"

```

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	924	GCAAGTCTCTGCCAAGCGCAA	944
Db	1	GCAAGTCTCTGCCAAGCGCAA	21

[illegible]

REFERENCE 1  
AUTHORS Henry, J. L., Cahill, C. M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL and therapeutic uses thereof  
Patent: WO 0213799-A 26 21-FEB-2002;  
MCGILL UNIVERSITY (CA)

Query Match	1.2%	Score 21;	DB 1;	Length 21;
Similarity	100.0%	Pred. No. 40;		
Best Local				
Matches	21;	Conservative	0;	Mismatches
				0;
				Indels
				0;
				Gaps
				0;

```

Qy      956 TGATGATTGTCGTGTGCA 976
          |||||
Db      21  TGATGATTGTCGTGTGCA 1

```

RESULT	160				
AX468712/C		21 bp	DNA		PAT 16-JUL-2002
LOCUS	AX468712			linear	
DEFINITION	Sequence 28 from Patent WO0213799.				
ACCESSION	AX468712				
VERSION	AX468712.1	GI:21901482			
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	other sequences; artificial sequences.				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE

1  
Henry, J.D., Cahill, C.M. and Yashpal, K.  
Oligonucleotides and other modulators of the nk-1 receptor pathway  
and therapeutic uses thereof  
Patent: WO 0213799-A 28 21-FEB-2002;  
MCGILL UNIVERSITY (CA)  
Location/Qualifiers  
1. .21

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 836 TCGTGTGATTCGCTATGTCAT 856  
DB 21 TCGTGTGATTCGCTATGTCAT 1

RESULT 161  
AX468715/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468715  
DEFINITION Sequence 31 from Patent WO0213799.  
ACCESSION AX468715  
VERSION AX468715.1 GI:21901485  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 31 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 559 TTGCGCAGTATCTATCTCCATG 579  
DB 21 TTGCGCAGTATCTATCTCCATG 1

RESULT 162  
AX468717/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468717  
DEFINITION Sequence 33 from Patent WO0213799.  
ACCESSION AX468717  
VERSION AX468717.1 GI:21901487  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 33 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTATCCAGCAGGTCTAC 1071  
DB 21 AAGTTATCCAGCAGGTCTAC 1

RESULT 163  
AX468722/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468722  
DEFINITION Sequence 38 from Patent WO0213799.  
ACCESSION AX468722  
VERSION AX468722.1 GI:21901492  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 38 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGGAACATTCATCTCTTG 1587  
DB 21 AGGGAACATTCATCTCTTG 1

RESULT 164  
AX468724 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468724  
DEFINITION Sequence 40 from Patent WO0213799.  
ACCESSION AX468724  
VERSION AX468724.1 GI:21901494  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 40 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 TTGGAATGATTAACGTCTC 225  
DB 1 TTGGAATGATTAACGTCTC 21

RESULT 165  
AX468726/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468726  
DEFINITION Sequence 42 from Patent WO0213799.

ACCESSION AX468726  
VERSION AX468726.1 GI:21901496  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 42 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976  
Db 21 TGATGATTGTCGTGTGCA 1

RESULT 166  
AX468727/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468727  
DEFINITION Sequence 43 from Patent WO0213799.  
ACCESSION AX468727  
VERSION AX468727.1 GI:21901497  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 43 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 924 GCAAGTCTGCGCAGCGCA 944  
Db 21 GCAAGTCTGCGCAGCGCA 1

RESULT 167  
AX468729 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468729  
DEFINITION Sequence 45 from Patent WO0213799.  
ACCESSION AX468729  
VERSION AX468729.1 GI:21901499  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL and therapeutic uses thereof  
Patent: WO 0213799-A 45 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TGATGATTGTCGTGTGCA 976  
Db 1 TGATGATTGTCGTGTGCA 21

RESULT 168  
AX468731 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468731  
DEFINITION Sequence 47 from Patent WO0213799.  
ACCESSION AX468731  
VERSION AX468731.1 GI:21901501  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 47 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TGCTGTGATTGGCTATGCAT 856  
Db 1 TGCTGTGATTGGCTATGCAT 21

RESULT 169  
AX468734 21 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468734  
DEFINITION Sequence 50 from Patent WO0213799.  
ACCESSION AX468734  
VERSION AX468734.1 GI:21901504  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 50 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"



Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 TTGGCAGTATCTACTCATG 579  
1 TTGGCAGTATCTACTCATG 21

RESULT 170  
LOCUS AX468736 21 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 52 from Patent WO0213799.  
ACCESSION AX468736  
VERSION AX468736.1 GI:21901506  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 52 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 AAGTTTATCCAGCAGGTCTAC 1071  
1 AAGTTTATCCAGCAGGTCTAC 21

RESULT 171  
LOCUS AX468737 21 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 53 from Patent WO0213799.  
ACCESSION AX468737  
VERSION AX468737.1 GI:21901507  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 53 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 ATGTACAACCCATCATCTAC 1125  
1 ATGTACAACCCATCATCTAC 21

RESULT 172  
LOCUS AX468741 21 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 57 from Patent WO0213799.  
ACCESSION AX468741  
VERSION AX468741.1 GI:21901511  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 57 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 AGGAAACATTCATCTCTG 1587  
1 AGGAAACATTCATCTCTG 21

RESULT 173  
LOCUS AX468743 21 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 59 from Patent WO0213799.  
ACCESSION AX468743  
VERSION AX468743.1 GI:21901513  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 59 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.2%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 TTGGAATGATTAAGTCTTC 225  
21 TTGGAATGATTAAGTCTTC 1

RESULT 174  
LOCUS AR109807 24 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 231 from patent US 6114139.  
ACCESSION AR109807  
VERSION AR109807.1 GI:12826083  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 231 05-SEP-2000;  
FEATURES  
SOURCE 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGGCTGCCCTTC 1002  
Db 1 TTGCGCATCTGCTGGCTGCCCTAC 24

RESULT 175  
ARI09809 24 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 233 from patent US 6114139.  
DEFINITION ARI09809  
ACCESSION ARI09809.1 GI:12826085  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 233 05-SEP-2000;  
FEATURES  
SOURCE 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGGCTGCCCTTC 1002  
Db 1 TTGCGCATCTGCTGGCTGCCCTAC 24

RESULT 176  
ARI09813 24 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 237 from patent US 6114139.  
DEFINITION ARI09813  
ACCESSION ARI09813.1 GI:12826089  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 237 05-SEP-2000;  
FEATURES  
SOURCE 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGGCTGCCCTTC 1002  
Db 1 TTGCGCATCTGCTGGCTGCCCTTC 1002

Db 1 TTCACCCCTGCTGCTGCCCTTC 24

RESULT 177  
ARI09810 24 bp DNA linear PAT 03-APR-1996  
LOCUS 117151  
DEFINITION Sequence 6 from patent US 548486.  
ACCESSION 117151  
VERSION 117151.1 GI:1252059  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 548486-A 6 16-JUN-1996;  
FEATURES  
SOURCE 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 59;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1051 AAGTTATCCAGAGGCTACTCTG 1074  
Db 24 AAGTTCATCCAGAGGTACTCTG 1

RESULT 178  
ARI09608 24 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 15 from patent US 6114139.  
DEFINITION ARI09608  
ACCESSION ARI09608.1 GI:12825884  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 15 05-SEP-2000;  
FEATURES  
SOURCE 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
Best Local Similarity 70.8%; Pred. No. 63;  
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGGCTGCCCTTC 1002  
Db 24 TTGCGCATCTGCTGGCTGCCCTTC 1

RESULT 179  
ARI09806 24 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 230 from patent US 6114139.  
DEFINITION ARI09806  
ACCESSION ARI09806.1 GI:12826082  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 230 05-SEP-2000;

FEATURES  
source  
1.24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
Best Local Similarity 70.8%; Pred. No. 63;  
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTC 1002  
1 TTGGCCNTSTGCTGCTGCCCMWC 24

RESULT 180  
LOCUS E12479/c 24 bp DNA linear PAT 27-APR-1998  
DEFINITION PCR primer for selective amplification and cloning of the family of  
genes encoding G protein-coupled receptors.  
ACCESSION E12479.1 GI:3251312  
VERSION E12479.1 GI:3251312  
KEYWORDS JP 1997000268-A/15.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,K., Hosoya,M., Fujii,A., Ohtaki,T., Fukuzumi,M. and  
Ooyoshi,K.  
TITLE NEW G PROTEIN CONJUGATION TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND  
JOURNAL Patent: JP 1997000268-A 15 07-JAN-1997;  
TAKEDA CHEM IND LTD  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1997000268-A/15  
PD 07-JAN-1997  
PR 11-AUG-1995 JP 1995224544  
PR 11-AUG-1994 JP 94P 189272, 11-AUG-1994 JP 94P 189273, PR  
11-AUG-1994 JP 94P 189274, 30-SEP-1994 JP 94P 226356, PR  
30-SEP-1994 JP 94P 236357, 02-NOV-1994 JP 94P 270017, PR  
28-DEC-1994 JP 94P 326611, 20-JAN-1995 JP 95P 7177, PR  
16-MAR-1995 JP 95P 57186, 19-APR-1995 JP 95P 93989, PI  
HINUMA KUNII, HOSoya MASAKI, FUJII AKIRA, OTAKI TETSUYA, PI  
FUKUZUMI MASASHI, OYOSHI KAZUHIRO  
PC C12N15/09, C07H21/04, C12N1/21, G01N3/53, G01N3/566//C07K14/705,  
PC C07K16/28,  
PC C12P21/02, C12P21/08, C12Q1/68, C12N1/21, C12R1/19, C12P21/02,  
PC C12R1/19;  
CC strandedness: Single;  
CC topology: Linear;  
FH Key  
FH Location/Qualifiers  
FT source 1.24  
FT misc\_feature 1.24  
FT /organism='Artificial sequences' FT  
FT /note='degenerate primer based on conserved  
amino acid  
sequences of the sixth transmembrane domain of  
known G  
protein-coupled receptors'.  
FT Location/Qualifiers  
FT 1.24  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
Best Local Similarity 70.8%; Pred. No. 63;  
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTC 1002  
1 TTGGCCNTSTGCTGCTGCCCMWC 1

Db 24 TTGGCCNTSTGCTGCTGCCCMWC 1

RESULT 181  
LOCUS AR300918/c 24 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 15 from patent US 6538107.  
ACCESSION AR300918  
VERSION AR300918.1 GI:31688591  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Hinuma,S., Ito,Y. and Fujii,R.  
TITLE G protein coupled receptor protein production, and use thereof  
JOURNAL Patent: US 6538107-A 15 25-MAR-2003;  
Takeda Chemical Industries, Ltd.; Osaka;  
JPX;  
FEATURES  
source  
1.24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.6; DB 1; Length 24;  
Best Local Similarity 70.8%; Pred. No. 63;  
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCTTC 1002  
1 TTGGCCNTSTGCTGCTGCCCMWC 1

Db 24 TTGGCCNTSTGCTGCTGCCCMWC 1

RESULT 182  
LOCUS AR109811 23 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 235 from patent US 6114139.  
ACCESSION AR109811  
VERSION AR109811.1 GI:12826087  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukuzumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 235 05-SEP-2000;  
FEATURES  
source  
1.23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 61;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCCATCTGCTGCTGCCCT 1000  
1 TTGGCCATCTGCTGCTGCCCT 22

Db 1 TTGGCCATCTGCTGCTGCCCT 22

RESULT 183  
LOCUS BD223567 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Gene polymorphism in human neurokinin 1 receptor gene and  
utilization thereof in diagnosing and treating disease.  
ACCESSION BD223567  
VERSION BD223567.1 GI:33033337  
KEYWORDS JP 2002521062-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 20)

AUTHORS Smith,J.C., Anand,R. and Morten,J.E.N.  
TITLE Gene polymorphism in human neurokinin 1 receptor gene and  
utilization thereof in diagnosing and treating disease  
JOURNAL Patent: JP 2002521062-A 2 16-JUL-2002;  
ASTRAZENECA AB  
COMMENT OS Homo sapiens (human)  
PN JP 2002521062-A/2  
PD 16-JUL-2002  
PF 20-JUL-1999 JP 2000562550  
PR 25-JUL-1998 GB 9816192.0,22-AUG-1998 GB 9818280.1 PI  
JOHN CRAIG SMITH, RAKESH ANAND, JOHN EDWARD NORRIS MORTEN PC  
C12N15/09,A61K45/00,A61P11/06,A61P43/00,C12M1/00,C12Q1/68, PC  
G01N33/50,  
PC G01N33/53,G01N33/566,C12N15/00  
CC Gene polymorphism in human neurokinin 1 receptor gene and CC  
utilization  
CC thereof in diagnosing and treating disease  
FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source 1..20  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
QY 524 GCAAGTCCACACTCTTT 543  
Db 1 GCAAGTCCACACTCTTT 20  
RESULT 184  
CS186497  
LOCUS CS186497 20 bp DNA linear PAT 04-NOV-2005  
DEFINITION Sequence 3 from Patent WO2005100986.  
ACCESSION CS186497  
VERSION CS186497.1 GI:80748369  
KEYWORDS  
SOURCE .  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Golz,S.  
TITLE Diagnostics and therapeutics for diseases associated with  
tachykinin receptor 1(tacr1)  
JOURNAL Patent: WO 2005100986-A 3 27-OCT-2005;  
Bayer Healthcare AG (DE)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="forward primer"  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
QY 276 CAATCAGTTCGTGCAACGAG 295  
Db 1 CAATCAGTTCGTGCAACGAG 20  
RESULT 185  
I17156/c  
LOCUS I17156 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 11 from patent US 5484886.  
ACCESSION I17156  
VERSION I17156.1 GI:1252064

KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 11 16-JAN-1996;  
Location/Qualifiers  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
QY 601 TACATGGCATCATATCATCC 620  
Db 20 TACATGGCATCATATCATCC 1  
RESULT 186  
I17157/c  
LOCUS I17157 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 12 from patent US 5484886.  
ACCESSION I17157  
VERSION I17157.1 GI:1252065  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 12 16-JAN-1996;  
Location/Qualifiers  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
QY 637 TCAGCCACAGCCACCAAGT 656  
Db 20 TCAGCCACAGCCACCAAGT 1  
RESULT 187  
I17159/c  
LOCUS I17159 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 14 from patent US 5484886.  
ACCESSION I17159  
VERSION I17159.1 GI:1252067  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 14 16-JAN-1996;  
Location/Qualifiers  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

Qy 862 GTAGTGGGATCAGACTATG 881  
Db 20 GTAGTGGGATCAGACTATG 1

RESULT 188  
117161/c  
LOCUS 117161 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 16 from patent US 5484886.  
ACCESSION 117161  
VERSION 117161.1 GI:1252069  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 16 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1012 TTCTCTCGCCCTACATCAA 1031  
Db 20 TTCTCTCGCCCTACATCAA 1

RESULT 189  
117164  
LOCUS 117164 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 19 from patent US 5484886.  
ACCESSION 117164  
VERSION 117164.1 GI:1252072  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 19 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCTCT 1019  
Db 1 TTCACATCTTCTCTCTCT 20

RESULT 190  
117165  
LOCUS 117165 20 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 20 from patent US 5484886.  
ACCESSION 117165  
VERSION 117165.1 GI:1252073  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Fong,T.M. and Strader,C.D.

TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 20 16-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1023 CTACATCAACCCAGATCTCT 1042  
Db 1 CTACATCAACCCAGATCTCT 20

RESULT 191  
AX468706  
LOCUS AX468706 20 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 22 from Patent WO0213799.  
ACCESSION AX468706  
VERSION AX468706.1 GI:21901476  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 22 21-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1000 TTCACATCTTCTCTCTCT 1019  
Db 1 TTCACATCTTCTCTCTCT 20

RESULT 192  
AX468709/c  
LOCUS AX468709 20 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 25 from Patent WO0213799.  
ACCESSION AX468709  
VERSION AX468709.1 GI:21901479  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 25 21-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1012 TTCCCTCTGCGCCATACATCAA 1031  
|||||  
Db 20 TTCCCTCTGCGCCATACATCAA 1

RESULT 193  
AX468711/c 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 27 from Patent WO0213799.  
ACCESSION AX468711  
VERSION AX468711.1 GI:21901481  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL and therapeutic uses thereof  
McGILL UNIVERSITY (CA) Patent: WO 0213799-A 27 21-FEB-2002;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GTAGTGGGATCATCACTATG 881  
|||||  
Db 20 GTAGTGGGATCATCACTATG 1

RESULT 194  
AX468713/c 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 29 from Patent WO0213799.  
ACCESSION AX468713  
VERSION AX468713.1 GI:21901483  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL and therapeutic uses thereof  
McGILL UNIVERSITY (CA) Patent: WO 0213799-A 29 21-FEB-2002;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 TCAGCCACAGCCACCAAGT 656  
|||||  
Db 20 TCAGCCACAGCCACCAAGT 1

RESULT 195  
AX468714/c

LOCUS AX468714 20 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 30 from Patent WO0213799.  
ACCESSION AX468714  
VERSION AX468714.1 GI:21901484  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL and therapeutic uses thereof  
McGILL UNIVERSITY (CA) Patent: WO 0213799-A 30 21-FEB-2002;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 TACATGGGCATCATCATCC 620  
|||||  
Db 20 TACATGGGCATCATCATCC 1

RESULT 196  
AX468725/c 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 41 from Patent WO0213799.  
ACCESSION AX468725  
VERSION AX468725.1 GI:21901495  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL and therapeutic uses thereof  
McGILL UNIVERSITY (CA) Patent: WO 0213799-A 41 21-FEB-2002;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1000 TTCCACATCTCTCTCTCCT 1019  
|||||  
Db 20 TTCCACATCTCTCTCTCCT 1

RESULT 197  
AX468728 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 44 from Patent WO0213799.  
ACCESSION AX468728  
VERSION AX468728.1 GI:21901498  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
synthetic construct  
other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 44 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1012 TTCCTCTGCGCCCTACATCAA 1031  
|||||  
1 TTCCTCTGCGCCCTACATCAA 20

RESULT 198  
AX468730 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 46 from Patent WO0213799.  
DEFINITION AX468730  
ACCESSION AX468730.1 GI:21901500  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 46 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 GTAGTGGGAAATCACAATG 881  
|||||  
1 GTAGTGGGAAATCACAATG 20

RESULT 199  
AX468732 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 48 from Patent WO0213799.  
DEFINITION AX468732  
ACCESSION AX468732.1 GI:21901502  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 48 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 TCAGCCACAGCCACCAAGT 656  
|||||  
1 TCAGCCACAGCCACCAAGT 20

RESULT 200  
AX468733 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 49 from Patent WO0213799.  
DEFINITION AX468733  
ACCESSION AX468733.1 GI:21901503  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 49 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 TACATGGCCATCATCATCC 620  
|||||  
1 TACATGGCCATCATCATCC 20

RESULT 201  
AX616473 20 bp DNA linear PAT 20-FEB-2003  
LOCUS Sequence 34 from Patent EP1262565.  
DEFINITION AX616473  
ACCESSION AX616473.1 GI:28447516  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Affouric, J.P., Nelson, D.L., Seymour, A.B. and Webb, S.M.  
TITLE Genetic polymorphisms in the human neurokinin 1 receptor gene and their uses in diagnosis and treatment of diseases  
JOURNAL Patent: EP 1262565-A 34 04-DEC-2002;  
Pfizer Products Inc. (US)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 GGCACGTGTAGTATGTG 374  
|||||  
20 GGCACGTGTAGTATGTG 1

RESULT 202  
AX616485/c 20 bp DNA linear PAT 20-FEB-2003  
LOCUS  
DEFINITION Sequence 46 from Patent EP1262565.  
ACCESSION AX616485  
VERSION AX616485.1 GI:28447528  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
AFFOURTIC,J.P., NELSON,D.L., SEYMOUR,A.B. and WEBB,S.M.  
Genetic polymorphisms in the human neurokinin 1 receptor gene and  
their uses in diagnosis and treatment of diseases  
Patent: EP 1262565-A 46 04-DEC-2002;  
Pfizer Products Inc. (US)  
Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1483 CCCTTCATGCATGGAATTC 1502  
DB 20 CCCTTCATGCATGGAATTC 1

RESULT 203  
AX616486 20 bp DNA linear PAT 20-FEB-2003  
LOCUS  
DEFINITION Sequence 47 from Patent EP1262565.  
ACCESSION AX616486  
VERSION AX616486.1 GI:28447529  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
AFFOURTIC,J.P., NELSON,D.L., SEYMOUR,A.B. and WEBB,S.M.  
Genetic polymorphisms in the human neurokinin 1 receptor gene and  
their uses in diagnosis and treatment of diseases  
Patent: EP 1262565-A 47 04-DEC-2002;  
Pfizer Products Inc. (US)  
Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1417 TCCATGTCCTCTCTAGGC 1436  
DB 1 TCCATGTCCTCTCTAGGC 20

RESULT 204  
AX616487/c 20 bp DNA linear PAT 20-FEB-2003  
LOCUS  
DEFINITION Sequence 48 from Patent EP1262565.  
ACCESSION AX616487  
VERSION AX616487.1 GI:28447530  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
AFFOURTIC,J.P., NELSON,D.L., SEYMOUR,A.B. and WEBB,S.M.  
Genetic polymorphisms in the human neurokinin 1 receptor gene and  
their uses in diagnosis and treatment of diseases  
Patent: EP 1262565-A 48 04-DEC-2002;  
Pfizer Products Inc. (US)  
Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

other sequences; artificial sequences.

REFERENCE  
1  
AFFOURTIC,J.P., NELSON,D.L., SEYMOUR,A.B. and WEBB,S.M.  
Genetic polymorphisms in the human neurokinin 1 receptor gene and  
their uses in diagnosis and treatment of diseases  
Patent: EP 1262565-A 48 04-DEC-2002;  
Pfizer Products Inc. (US)  
Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

FEATURES  
SOURCE

Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1746 GCGAGTGCATTCAGGAT 1765  
DB 20 GCGAGTGCATTCAGGAT 1

RESULT 205  
117154/c 21 bp DNA linear PAT 03-APR-1996  
LOCUS  
DEFINITION Sequence 9 from patent US 5484886.  
ACCESSION 117154  
VERSION 117154.1 GI:1252062  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
Unknown.  
Unclassified.  
1 (bases 1 to 21)  
REFERENCE  
Fong,T.M. and Strader,C.D.  
Human neurokinin-1 receptor  
Patent: US 5484886-A 9 16-JAN-1996;  
Location/Qualifiers  
1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 56;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAAGTTCACAACTTCTT 542  
DB 21 TGCAAGTTCACAACTTCTT 2

RESULT 206  
AX468716/c 21 bp DNA linear PAT 16-JUL-2002  
LOCUS  
DEFINITION Sequence 32 from Patent WO0213799.  
ACCESSION AX468716  
VERSION AX468716.1 GI:21901486  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1  
HENRY,J.L., CAHILL,C.M. and YASHPAL,K.  
Oligonucleotides and other modulators of the nk-1 receptor pathway  
and therapeutic uses thereof  
Patent: WO 0213799-A 32 21-FEB-2002;  
MCGILL UNIVERSITY (CA)  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"



Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTTCACCACTCTT 542  
|||||  
21 TGCAGTTCACCACTCTT 2

RESULT 207  
AX468735  
LOCUS AX468735 21 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 51 from Patent WO2023799.  
ACCESSION AX468735  
VERSION AX468735.1 GI:21901505  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry,J.L., Cahill,C.M. and Yashpal,K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 51 21-FEB-2002;  
MCGILL UNIVERSITY (CA)  
FEATURES  
Source 1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 TGCAGTTCACCACTCTT 542  
|||||  
1 TGCAGTTCACCACTCTT 20

RESULT 208  
AR109816  
LOCUS AR109816 23 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 240 from patent US 6114139.  
ACCESSION AR109816  
VERSION AR109816.1 GI:12826092  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 240 05-SEP-2000;  
FEATURES  
Location/Qualifiers  
Source 1. .23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.8; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCCCTT 1001  
|||||  
1 TTGCCATCTGCTGCTGCCCTT 23

RESULT 209  
AX463104  
LOCUS AX463104 23 bp DNA linear PAT 15-JUL-2002  
DEFINITION Sequence 11 from Patent WO0250115.

ACCESSION AX463104  
VERSION AX463104.1 GI:21886095  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Hall,M.D., Suman-Chauhan,N., McNulty,S. and Murray,J.H.  
TITLE Modified tachykinin receptors  
JOURNAL Patent: WO 0250115-A 11 27-JUN-2002;  
WARNER LAMBERT CO (US)  
FEATURES  
Source 1. .23  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

Query Match 1.1%; Score 19.8; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 74;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 438 CGCGAGGCTTCATGCTGCAT 460  
|||||  
1 CGCGAGGCTTCATGCTGCAT 23

RESULT 210  
AR109833  
LOCUS AR109833 21 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 257 from patent US 6114139.  
ACCESSION AR109833  
VERSION AR109833.1 GI:12826109  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 257 05-SEP-2000;  
FEATURES  
Location/Qualifiers  
Source 1. .21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 68;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGCCATCTGCTGCTGCC 999  
|||||  
1 TTGCCATCTGCTGCTGCC 21

RESULT 211  
AR001364  
LOCUS AR001364 24 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 7 from patent US 5739118.  
ACCESSION AR001364  
VERSION AR001364.1 GI:3963431  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: US 5739118-A 7 14-APR-1998;  
FEATURES  
Location/Qualifiers  
Source 1. .24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908  
DB 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 212  
AR044849 24 bp DNA linear PAT 29-SEP-1999  
LOCUS AR044849  
DEFINITION Sequence 7 from patent US 5817637.  
ACCESSION AR044849  
VERSION AR044849.1 GI:5966314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.  
TITLE Genetic immunization  
JOURNAL Patent: US 5817637-A 7 06-OCT-1998;  
FEATURES Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908  
DB 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 213  
AR052235 24 bp DNA linear PAT 29-SEP-1999  
LOCUS AR052235  
DEFINITION Sequence 7 from patent US 5830876.  
ACCESSION AR052235  
VERSION AR052235.1 GI:5975599  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.  
TITLE Genetic immunization  
JOURNAL Patent: US 5830876-A 7 03-NOV-1998;  
FEATURES Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908  
DB 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 214  
AR078344 24 bp DNA linear PAT 31-AUG-2000  
LOCUS AR078344  
DEFINITION Sequence 7 from patent US 5962428.  
ACCESSION AR078344  
VERSION AR078344.1 GI:10005090  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: US 5962428-A 7 05-OCT-1999;  
FEATURES Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908  
DB 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 215  
AR085195 24 bp DNA linear PAT 01-SEP-2000  
LOCUS AR085195  
DEFINITION Sequence 7 from patent US 5981505.  
ACCESSION AR085195  
VERSION AR085195.1 GI:10011965  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Weiner,D.B., Williams,W.V. and Wang,B.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: US 5981505-A 7 09-NOV-1999;  
FEATURES Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908  
DB 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 216  
AR138115 24 bp DNA linear PAT 16-JUN-2001  
LOCUS AR138115  
DEFINITION Sequence 7 from patent US 6197755.  
ACCESSION AR138115  
VERSION AR138115.1 GI:14479624  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Carrano,R.A., Wang,B. and Weiner,D.B.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: US 6197755-A 7 06-MAR-2001;  
FEATURES Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGGAGACTCTC 908

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 217  
LOCUS ARI178989/c 24 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 13 from patent US 6320022.  
ACCESSION ARI178989  
VERSION ARI178989.1 GI:20220127  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
Cutlita,F., Martinez,A., Miller,M.Jean., Unsworth,E.J., Hook,W.,  
Walsh,T., Gray,K. and Macri,C.  
TITLE Adrenomedullin peptides  
JOURNAL Patent: US 6320022-A 13 20-NOV-2001;  
FEATURES Location/Qualifiers  
Source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 980 TCGCCATCTGCTGCTGCTCC 1003  
24 TTGTTCATCTGCTGCTGCTACC 1

Db 24 TTGTTCATCTGCTGCTGCTACC 1

RESULT 218  
LOCUS CO898470 24 bp DNA linear PAT 08-NOV-2004  
DEFINITION Sequence 7 from Patent EPI473369.  
ACCESSION CO898470  
VERSION CO898470.1 GI:55582783  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Weiner,D.B., Williams,W.V., Wang,B., Coney,L.R., Merva,M.J. and Zurawski,V.R.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: EP 1473369-A 7 03-NOV-2004;  
Weiner, David B. (US); WILLIAMS, William V. (US); WANG, Bin (US); CONEY, Leslie R. (US); MERVA, Michael J. (US); ZURAWSKI, Vincent R Jr. (US)  
FEATURES Location/Qualifiers  
Source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: Oligonucleotide"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGAGACTCTC 908  
1 CAGTGATATCCCGGAGACTCTC 24

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 219  
LOCUS CS252672 24 bp DNA linear PAT 25-JAN-2006  
DEFINITION Sequence 7 from Patent EPI616578.  
ACCESSION CS252672

VERSION CS252672.1 GI:85814972  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1  
AUTHORS Carriano,R.A.  
TITLE Compositions and methods for delivery of genetic material  
JOURNAL Patent: EP 1616578-A 7 18-JAN-2006;  
Myeln (US)  
FEATURES Location/Qualifiers  
Source 1..24  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGAGACTCTC 908  
1 CAGTGATATCCCGGAGACTCTC 24

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 220  
LOCUS I13899 24 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 7 from patent US 5593972.  
ACCESSION I13899  
VERSION I13899.1 GI:1824690  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
Weiner,D.B., Williams,W.V. and Wang,B.  
TITLE Genetic immunization  
JOURNAL Patent: US 5593972-A 7 14-JAN-1997;  
FEATURES Location/Qualifiers  
Source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 885 CAGTGAGATCCCGGAGACTCTC 908  
1 CAGTGATATCCCGGAGACTCTC 24

Db 1 CAGTGATATCCCGGAGACTCTC 24

RESULT 221  
LOCUS AR241150 24 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 7 from patent US 6468962.  
ACCESSION AR241150  
VERSION AR241150.1 GI:27286376  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 24)  
Weiner,D.B., Williams,W.V. and Wang,B.  
TITLE Genetic immunization  
JOURNAL Patent: US 6468962-A 7 22-OCT-2002;  
The Trustees of the University of Pennsylvania and The Wistar Institute; Philadelphia, PA  
FEATURES Location/Qualifiers  
Source 1..24  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 885 CAGTGAGATCCCGGGGACTCTC 908  
|||||  
1 CAGTGATATCCCGGAGACTCTC 24

RESULT 222  
CS128871 19 bp DNA linear PAT 02-AUG-2005  
LOCUS CS128871  
DEFINITION Sequence 52 from Patent WO2005063983.  
ACCESSION CS128871  
VERSION CS128871.1 GI:71790738  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE 1  
AUTHORS van Rompaey, L.J.  
JOURNAL Patent: WO 2005063983-A 52 14-JUL-2005;  
Galapagos Genomics N.V. (BE)  
LOCATION/Qualifiers

FEATURES 1..19  
source /organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1137 TGACAGGTTCCGCTGGGC 1155  
|||||  
1 TGACAGGTTCCGCTGGGC 19

RESULT 223  
CS132144 19 bp DNA linear PAT 02-AUG-2005  
LOCUS CS132144  
DEFINITION Sequence 53 from Patent WO2005063976.  
ACCESSION CS132144  
VERSION CS132144.1 GI:71790894  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS van Rompaey, L.J.  
JOURNAL Methods for inducing differentiation of undifferentiated mammalian  
cells into osteoblasts  
Patent: WO 2005063976-A 53 14-JUL-2005;  
Galapagos Genomics N.V. (BE)  
LOCATION/Qualifiers

FEATURES 1..19  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1137 TGACAGGTTCCGCTGGGC 1155  
|||||  
1 TGACAGGTTCCGCTGGGC 19

RESULT 224  
CS186498/c 19 bp DNA linear PAT 04-NOV-2005  
LOCUS CS186498  
DEFINITION Sequence 4 from Patent WO2005100986.  
ACCESSION CS186498  
VERSION CS186498.1 GI:80748370  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Golz, S.  
JOURNAL Diagnostics and therapeutics for diseases associated with  
tachykinin receptor 1 (tacr1)  
Patent: WO 2005100986-A 4 27-OCT-2005;  
Bayer Healthcare AG (DE)  
LOCATION/Qualifiers

FEATURES 1..19  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="reverse primer"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 322 GCCTACACGGTCATTTGTG 340  
|||||  
19 GCCTACACGGTCATTTGTG 1

RESULT 225  
CS207431 19 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207431  
DEFINITION Sequence 139 from Patent WO2005109000.  
ACCESSION CS207431  
VERSION CS207431.1 GI:83413738  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Spitael, K.F.  
JOURNAL Patent: WO 2005109000-A 139 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spitael, Koenraad Frederick F. (BE)  
LOCATION/Qualifiers

FEATURES 1..19  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 528 GTTCACAACCTTCTTCCC 546  
|||||  
1 GTTCACAACCTTCTTCCC 19

RESULT 226  
CS207432 19 bp DNA linear PAT 08-DEC-2005  
LOCUS CS207432  
DEFINITION Sequence 140 from Patent WO2005109000.  
ACCESSION CS207432  
VERSION CS207432.1 GI:83413739  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Spititaelis, K.F.  
JOURNAL Patent: WO 2005109000-A 140 17-NOV-2005;  
Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)  
FEATURES  
source 1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 799 CACATCTGTGTGACTGTGC 817  
DB 1 CACATCTGTGTGACTGTGC 19

RESULT 227  
LOCUS CS207433 19 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 141 from Patent WO2005109000.  
ACCESSION CS207433  
VERSION CS207433.1 GI:83413740  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.  
AUTHORS Patent: WO 2005109000-A 141 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)  
FEATURES  
source 1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATCAACCCAGATCTTACC 1045  
DB 1 ATCAACCCAGATCTTACC 19

RESULT 228  
LOCUS CS207434 19 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 142 from Patent WO2005109000.  
ACCESSION CS207434  
VERSION CS207434.1 GI:83413741  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.  
AUTHORS Patent: WO 2005109000-A 142 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)  
FEATURES  
source 1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 TGCACAGTTCCTCTGGCC 1155  
DB 1 TGCACAGTTCCTCTGGCC 19

RESULT 229  
LOCUS CS207722 19 bp DNA linear PAT 08-DEC-2005  
DEFINITION Sequence 430 from Patent WO2005109000.  
ACCESSION CS207722  
VERSION CS207722.1 GI:83413999  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 Spititaelis, K.F.  
AUTHORS Patent: WO 2005109000-A 430 17-NOV-2005;  
JOURNAL Galapagos Genomics N.V. (BE); Spititaelis, Koenraad Frederick F. (BE)  
FEATURES  
source 1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthetic oligonucleotide"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACACCGTAGTGGGAATCAC 875  
DB 1 ACACCGTAGTGGGAATCAC 19

RESULT 230  
LOCUS 117168/c 19 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 23 from patent US 5484886.  
ACCESSION 117168  
VERSION 117168.1 GI:1252076  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Fong, T.M. and Strader, C.D.  
JOURNAL Human neurokinin-1 receptor  
Patent: US 5484886-A 23 16-JAN-1996;  
FEATURES  
source 1. 19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGTT 1566  
DB 19 AAAAGGTCAGTATGGTT 1

RESULT 231  
LOCUS 117170 19 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 25 from patent US 5484886.  
ACCESSION 117170  
VERSION 117170.1 GI:1252078  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 Unclassified.  
1 (bases 1 to 19)

AUTHORS Rong, T.M. and Strader, C.D.

TITLE Human neurokinin-1 receptor

JOURNAL Patent: US 5484886-A 25 16-JUN-1996;

FEATURES Location/Qualifiers

source

1. .19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

1 GTGTACAGATAGTAGGCTT 19

RESULT 232

AX468719

LOCUS AX468719 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 35 from Patent WO0213799.

ACCESSION AX468719

VERSION AX468719.1 GI:21901489

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.

TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL Patent: WO 0213799-A 35 21-FEB-2002;

FEATURES MCGILL UNIVERSITY (CA)

source Location/Qualifiers

1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

1 GTGTACAGATAGTAGGCTT 19

RESULT 233

AX468721/c

LOCUS AX468721 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 37 from Patent WO0213799.

ACCESSION AX468721

VERSION AX468721.1 GI:21901491

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.

TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL Patent: WO 0213799-A 37 21-FEB-2002;

FEATURES MCGILL UNIVERSITY (CA)

source Location/Qualifiers

1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGCTT 1566

19 AAAAGGTCAGTATGGCTT 1

RESULT 234

AX468738/c

LOCUS AX468738 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 54 from Patent WO0213799.

ACCESSION AX468738

VERSION AX468738.1 GI:21901508

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.

TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL Patent: WO 0213799-A 54 21-FEB-2002;

FEATURES MCGILL UNIVERSITY (CA)

source Location/Qualifiers

1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GTGTACAGATAGTAGGCTT 194

19 GTGTACAGATAGTAGGCTT 1

RESULT 235

AX468740

LOCUS AX468740 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 56 from Patent WO0213799.

ACCESSION AX468740

VERSION AX468740.1 GI:21901510

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.

TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway

JOURNAL Patent: WO 0213799-A 56 21-FEB-2002;

FEATURES MCGILL UNIVERSITY (CA)

source Location/Qualifiers

1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAAAGGTCAGTATGGCTT 1566

1 AAAAGGTCAGTATGGCTT 19

RESULT 236  
LOCUS AR109799 22 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 223 from patent US 6114139.  
ACCESSION AR109799  
VERSION AR109799.1 GI:12826075  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
TITLE G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 223 05-SEP-2000;  
FEATURES  
source 1..22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 92;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 587 TGGCCTTGATGATGACATGAC 608  
|||||  
Db 1 TGGCCTTGACAGATACATGAC 22

RESULT 237  
LOCUS I60476 20 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 9 from patent US 5656462.  
ACCESSION I60476  
VERSION I60476.1 GI:2478921  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Keller,C., Mitsuhashi,M. and Akitaya,T.  
TITLE Method for synthesizing cDNA using a polynucleotide immobilized  
JOURNAL Patent: US 5656462-A 9 12-AUG-1997;  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 84;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GCCAGTATCTACTCCATGAC 581  
|||||  
Db 1 GCCAGCATCTACTCCATGAC 20

RESULT 238  
LOCUS AR098634 20 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 12 from patent US 6077666.  
ACCESSION AR098634  
VERSION AR098634.1 GI:12808400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Hadcock,J.Richard., Ozenberger,B.Alton. and Pausch,M.Henry.  
TITLE Receptor identification method  
JOURNAL Patent: US 6077666-A 12 20-JUN-2000;  
FEATURES  
Location/Qualifiers

source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 90;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGCTGCC 998  
|||||  
Db 1 TTGGCATCTGCTGCTGCC 20

RESULT 239  
LOCUS I65553 20 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 12 from patent US 5668006.  
ACCESSION I65553  
VERSION I65553.1 GI:2482123  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Hadcock,J.Richard., Ozenberger,B.Alton. and Pausch,M.Henry.  
TITLE Somatostatin receptors  
JOURNAL Patent: US 5668006-A 12 16-SEP-1997;  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 90;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 979 TTGGCATCTGCTGCTGCC 998  
|||||  
Db 1 TTGGCATCTGCTGCTGCC 20

RESULT 240  
LOCUS I17166 18 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 21 from patent US 548486.  
ACCESSION I17166  
VERSION I17166.1 GI:1252074  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Fong,T.M. and Strader,C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 548486-A 21 16-JAN-1996;  
FEATURES  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 TCTCTACCTGAAGAATT 1055  
|||||  
Db 1 TCTCTACCTGAAGAATT 18

RESULT 241  
LOCUS AX468723 18 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 39 from Patent W00213799.

ACCESSION AX468723  
VERSION AX468723.1 GI:21901493  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAGAGATT 1055  
Db 1 TCTCTACCTGAGAGATT 18

RESULT 242  
AX468742/c 18 bp DNA linear PAT 16-JUL-2002  
LOCUS  
DEFINITION Sequence 58 from Patent WO0213799.  
ACCESSION AX468742  
VERSION AX468742.1 GI:21901512  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAGAGATT 1055  
Db 1 TCTCTACCTGAGAGATT 1

RESULT 243  
AX616471/c 18 bp DNA linear PAT 20-FEB-2003  
LOCUS  
DEFINITION Sequence 32 from Patent EP1262565.  
ACCESSION AX616471  
VERSION AX616471.1 GI:28447514  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 TCTCTACCTGAGAGATT 1055  
Db 1 TCTCTACCTGAGAGATT 1

RESULT 244  
AR109832 21 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 256 from patent US 6114139.  
ACCESSION AR109832  
VERSION AR109832.1 GI:12826108  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 11e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCC 999  
Db 1 TTGACCTCTGCTGCTGCC 21

RESULT 245  
AR109843 21 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 267 from patent US 6114139.  
ACCESSION AR109843  
VERSION AR109843.1 GI:12826119  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 11e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCC 999  
Db 1 TTGACCTCTGCTGCTGCC 21

their uses in diagnosis and treatment of diseases  
Patent: EP 1262565-A 32 04-DEC-2002;  
Pfizer Products Inc. (US)  
Location/Qualifiers  
1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.0%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 CGCCAGTTGAGCTTTCAA 75  
Db 18 CGCCAGTTGAGCTTTCAA 1

RESULT 244  
AR109832 21 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 256 from patent US 6114139.  
ACCESSION AR109832  
VERSION AR109832.1 GI:12826108  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1 (bases 1 to 21)  
Hinnma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 256 05-SEP-2000;  
Location/Qualifiers  
1.21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 11e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCC 999  
Db 1 TTGACCTCTGCTGCTGCC 21

RESULT 245  
AR109843 21 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 267 from patent US 6114139.  
ACCESSION AR109843  
VERSION AR109843.1 GI:12826119  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1 (bases 1 to 21)  
Hinnma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 267 05-SEP-2000;  
Location/Qualifiers  
1.21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 11e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 979 TTGCGCATCTGCTGCTGCC 999  
Db 1 TTGACCTCTGCTGCTGCC 21



RESULT 246	ARI09845	21 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	ARI09845				
DEFINITION	Sequence 269 from patent US 6114139.				
ACCESSION	ARI09845				
VERSION	ARI09845.1	GI:12826121			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 21)				
TITLE	Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.				
JOURNAL	G-protein coupled receptor protein and a DNA encoding the receptor				
FEATURES	Patent: US 6114139-A 269 05-SEP-2000;				
source	location/Qualifiers				
	1..21				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	1.0%; Score 17.8; DB 1;	Length 21;			
Best Local Similarity	90.5%; Pred. No. 1,1e+02;				
Matches	19; Conservative 0; Mismatches 2;	Indels 0;	Gaps 0;		
Qy	979 TTGCGCATCTGCTGCTGCC 999				
Db	1 TTGCGCATCTGCTGCTGCC 21				
RESULT 247	ARI09846	21 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	ARI09846				
DEFINITION	Sequence 270 from patent US 6114139.				
ACCESSION	ARI09846				
VERSION	ARI09846.1	GI:12826122			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 21)				
TITLE	Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.				
JOURNAL	G-protein coupled receptor protein and a DNA encoding the receptor				
FEATURES	Patent: US 6114139-A 270 05-SEP-2000;				
source	location/Qualifiers				
	1..21				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	1.0%; Score 17.8; DB 1;	Length 21;			
Best Local Similarity	90.5%; Pred. No. 1,1e+02;				
Matches	19; Conservative 0; Mismatches 2;	Indels 0;	Gaps 0;		
Qy	979 TTGCGCATCTGCTGCTGCC 999				
Db	1 TTGCGCATCTGCTGCTGCC 21				
RESULT 248	CO976990	21 bp	DNA	linear	PAT 19-JAN-2005
LOCUS	CO976990/c				
DEFINITION	Sequence 38 from Patent WO2005008075.				
ACCESSION	CO976990				
VERSION	CO976990.1	GI:57975973			
KEYWORDS					
SOURCE					
ORGANISM	Synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	other sequences; artificial sequences.				
TITLE	1 Witamer,V., Communi,D., Dethaux,M., Parmentier,M., Loison,C. and				
JOURNAL	Ooms,F.D.				
	Compositions and methods comprising a ligand of chemerin				
	Patent: WO 2005008075-A 38 06-JAN-2005;				
	Euroscreen S.A. (BE)				

FEATURES	location/Qualifiers
source	1..21
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="Synthetic primer"
misc_feature	1..21
	/note="Synthetic primer"
Query Match	1.0%: Score 17.8; DB 1; Length 21;
Best Local Similarity	90.5%: Pred. No. 1.1e+02; Indels 2; Gaps 0;
Matches	19; Conservative 0; Mismatches 2;
QY	669 CATCTGGGCTCTGGCTCTCCT 689
Db	21 CATCTGGGCTCTGGCTTTCTT 1
RESULT 249	
AX720862/c	21 bp DNA linear PAT 15-APR-2003
LOCUS	AX720862
DEFINITION	Sequence 42 from Patent WO0300696.
ACCESSION	AX720862
VERSION	AX720862.1 GI:29892630
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
	Wiltamer V., Communi D., Vandembogaerde A., Detheux M. and
TITLE	Palmentier M.
JOURNAL	Natural ligand of gpccr chemr23 and uses thereof
	Patent: WO 0300696-A 42 23 -JAN-2003;
	Euroscreen S.A. (BE)
FEATURES	location/Qualifiers
source	1..21
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="oligonucleotide"
Query Match	1.0%: Score 17.8; DB 1; Length 21;
Best Local Similarity	90.5%: Pred. No. 1.1e+02; Indels 2; Gaps 0;
Matches	19; Conservative 0; Mismatches 2;
QY	669 CATCTGGGCTCTGGCTCTCCT 689
Db	21 CATCTGGGCTCTGGCTTTCTT 1
RESULT 250	
AR014600/c	21 bp DNA linear PAT 05-DEC-1998
LOCUS	AR014600
DEFINITION	Sequence 25 from patent US 5773691.
ACCESSION	AR014600
VERSION	AR014600.1 GI:3972054
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 21)
TITLE	Falco S. Carl., Keeler S. Jo. and Rice J. Ann.
JOURNAL	Chimeric genes and methods for increasing the lysine and threonine
	content of the seeds of plants
	Patent: US 5773691-A 25 30 -JUN-1998;
FEATURES	location/Qualifiers
source	1..21
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	1.0%: Score 17; DB 1; Length 21;
Best Local Similarity	100.0%: Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches	17; Conservative 0; Mismatches 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420  
|||||  
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 251  
AR014608/c 21 bp DNA linear PAT 05-DEC-1998  
LOCUS Sequence 41 from patent US 5773691.  
DEFINITION AR014608  
ACCESSION AR014608  
VERSION AR014608.1 GI:3972062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Falco,S.Carl., Keeler,S.Jo. and Rice,J.Ann.  
TITLE Chimeric genes and methods for increasing the lysine and threonine  
JOURNAL content of the seeds of plants  
FEATURES Patent: US 5773691-A 41 30-JUN-1998;  
source Location/Qualifiers  
1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420  
|||||  
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 252  
AR014610/c 21 bp DNA linear PAT 05-DEC-1998  
LOCUS Sequence 43 from patent US 5773691.  
DEFINITION AR014610  
ACCESSION AR014610  
VERSION AR014610.1 GI:3972064  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Falco,S.Carl., Keeler,S.Jo. and Rice,J.Ann.  
TITLE Chimeric genes and methods for increasing the lysine and threonine  
JOURNAL content of the seeds of plants  
FEATURES Patent: US 5773691-A 43 30-JUN-1998;  
source Location/Qualifiers  
1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420  
|||||  
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 253  
BD010392/c 21 bp DNA linear PAT 09-JAN-2004  
LOCUS Chimeric genes and methods for increasing the lysine content of the  
DEFINITION seeds of plants.  
ACCESSION BD010392  
VERSION BD010392.1 GI:18638765  
KEYWORDS JP 2001502923-A/24.  
SOURCE unidentified

ORGANISM unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.  
TITLE Chimeric genes and methods for increasing the lysine content of the  
JOURNAL seeds of plants  
PATENT: JP 2001502923-A 24 06-MAR-2001;  
COMMENT EI DU PONT DE NEMOURS AND CO  
OS Unidentified  
PN JP 2001502923-A/24  
PD 06-MAR-2001  
PF 27-MAR-1998 JP 1998543284  
PR 27-MAR-1997 US 08/824627  
PI SAVERIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI SABINE  
URSULA EPELBAUM  
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..21  
/organism='Unidentified'.  
/db\_xref="taxon:32644"

FEATURES  
source 1..21  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCTCTCCA 1420  
|||||  
Db 19 CTTGAGCTTCTCTCCA 3

RESULT 254  
BD010400/c 21 bp DNA linear PAT 09-JAN-2004  
LOCUS Chimeric genes and methods for increasing the lysine content of the  
DEFINITION seeds of plants.  
ACCESSION BD010400  
VERSION BD010400.1 GI:18638773  
KEYWORDS JP 2001502923-A/32.  
SOURCE unidentified  
ORGANISM Unclassified  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.  
TITLE Chimeric genes and methods for increasing the lysine content of the  
JOURNAL seeds of plants  
PATENT: JP 2001502923-A 32 06-MAR-2001;  
COMMENT EI DU PONT DE NEMOURS AND CO  
OS Unidentified  
PN JP 2001502923-A/32  
PD 06-MAR-2001  
PF 27-MAR-1998 JP 1998543284  
PR 27-MAR-1997 US 08/824627  
PI SAVERIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI SABINE  
URSULA EPELBAUM  
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..21  
/organism='Unidentified'.  
/db\_xref="taxon:32644"

FEATURES  
source 1..21  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 255  
BD010402/c 21 bp DNA linear PAT 09-JAN-2004  
LOCUS Chimeric genes and methods for increasing the lysine content of the  
DEFINITION seeds of plants.  
ACCESSION BD010402  
VERSION JP 2001502923-A/34.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Falco,S.C., Ili,R.E.M. and Epelbaum,S.U.  
TITLE Chimeric genes and methods for increasing the lysine content of the  
JOURNAL seeds of plants  
COMMENT Patent: JP 2001502923-A 34 06-MAR-2001;  
EI DU PONT DE NEMOURS AND CO  
OS Unidentified  
PN JP 2001502923-A/34  
PD 06-MAR-2001  
PF 27-MAR-1998 JP 1998543284  
PR 27-MAR-1997 US 08/824627  
PI SAVERIO CARL FALCO,RAYMOND ERVIN MCDEVITT III, PI SABINE  
URSTUA EPELBAUM  
PC C12N9/06,C12N9/12,C12N9/88,C12P13/08,C12N15/82 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..21  
Location/Qualifiers  
FEATURES  
source 1..21  
/organism="unclassified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 256  
I26729/c 21 bp DNA linear PAT 07-OCT-1996  
LOCUS Sequence 17 from patent US 5559223.  
ACCESSION I26729  
VERSION I26729.1 GI:1606599  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Synthetic storage proteins with defined structure containing  
FEATURES programmable levels of essential amino acids for improvement of the  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 259  
AR235402/c 21 bp DNA linear PAT 20-DEC-2002  
LOCUS

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 257  
I26731/c 21 bp DNA linear PAT 07-OCT-1996  
LOCUS Sequence 19 from patent US 5559223.  
DEFINITION I26731  
ACCESSION I26731  
VERSION I26731.1 GI:1606601  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Synthetic storage proteins with defined structure containing  
FEATURES programmable levels of essential amino acids for improvement of the  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 258  
I26733/c 21 bp DNA linear PAT 07-OCT-1996  
LOCUS Sequence 21 from patent US 5559223.  
DEFINITION I26733  
ACCESSION I26733  
VERSION I26733.1 GI:1606603  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Synthetic storage proteins with defined structure containing  
FEATURES programmable levels of essential amino acids for improvement of the  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 CTTGAGCTTCCTCCTCA 1420  
|||||  
19 CTTGAGCTTCCTCCTCA 3

Db 19 CTTGAGCTTCCTCCTCA 3

RESULT 259  
AR235402 21 bp DNA linear PAT 20-DEC-2002  
LOCUS

DEFINITION Sequence 25 from patent US 6459019.  
ACCESSION AR235402  
VERSION AR235402.1 GI:27278543  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Chimeric genes and methods for increasing the lysine and threonine  
E.I. du Pont de Nemours and Company; Wilmington, DE  
FEATURES  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCCTCCCA 1420  
DB 19 CTTGAGCTTCCTCCCA 3

RESULT 260  
LOCUS AR235410 21 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 41 from patent US 6459019.  
ACCESSION AR235410  
VERSION AR235410.1 GI:27278551  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Chimeric genes and methods for increasing the lysine and threonine  
E.I. du Pont de Nemours and Company; Wilmington, DE  
FEATURES  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCCTCCCA 1420  
DB 19 CTTGAGCTTCCTCCCA 3

RESULT 261  
LOCUS AR235412 21 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 43 from patent US 6459019.  
ACCESSION AR235412  
VERSION AR235412.1 GI:27278553  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 21)  
TITLE Falco,S.C., Keeler,S.J. and Rice,J.A.  
JOURNAL Chimeric genes and methods for increasing the lysine and threonine  
E.I. du Pont de Nemours and Company; Wilmington, DE

FEATURES  
source Location/Qualifiers  
1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCCTCCCA 1420  
DB 19 CTTGAGCTTCCTCCCA 3

RESULT 262  
LOCUS BD240830 21 bp DNA linear PAT 17-JUL-2003  
DEFINITION Isoforms of human calcium sensing receptor.  
ACCESSION BD240830  
VERSION BD240830.1 GI:33050600  
KEYWORDS JP 2002521052-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Yu,K.T., Labaudiniere,R.F. and Thrower,L.W.  
TITLE Isoforms of human calcium sensing receptor  
JOURNAL Patent: JP 2002521052-A 2 16-JUL-2002;  
COMMENT AVENTIS PHARMACEUTICALS PRODUCTS INC  
OS Homo sapiens (human)  
PN JP 2002521052-A/2  
PD 16-JUL-2002  
PF 28-JUL-1999 JP 2000562397  
PI 30-JUL-1998 US 60/094702  
PI KIN T YU,RICHARD F LABAUDINIERE,LARRY W THROWER PC  
C12N15/09,A61K31/7088,A61K35/74,A61K35/76,A61K38/00,A61K45/00,PC  
A61K48/00,A61K31/7088,A61K35/74,A61K35/76,A61K38/00,A61K45/00,PC  
PC A61P3/14,A61P5/18,A61P9/12,A61P19/10,A61P35/00,A61P43/00,PC  
C07K14/705,  
PC C07K16/28,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/PC  
15,  
PC G01N33/50//C12N5/10,C12R1:91,C12N15/00,C12N5/00,A61K37/02,PC  
C12N5/00,C12R1:91)  
CC Isoforms of human calcium sensing receptor  
FH Key Location/Qualifiers  
FT source 1..21  
/organism="Homo sapiens (human)".  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 656 TGGTCATCTGTCATCTGG 675  
DB 21 TTGTCACTGTGTATCTGG 2

RESULT 263  
LOCUS AR209863 21 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 7 from patent US 6387619.  
ACCESSION AR209863  
VERSION AR209863.1 GI:21511944  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Gottschling, D.E. and Singer, M.S.  
TITLE Telomerase compositions and methods  
JOURNAL Patent: US 6387619-A 7 14-MAY-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CGAGCAAGTCTTGCACAGC 940  
DB 21 CGAGCAAGTCTATGCAAGC 2

RESULT 264  
LOCUS 185799 21 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 7 from patent US 5698686.  
ACCESSION 185799  
VERSION 185799.1 GI:3205517  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Gottschling, D.E. and Singer, M.S.  
TITLE Yeast telomerase compositions  
JOURNAL Patent: US 5698686-A 7 16-DEC-1997;  
FEATURES Location/Qualifiers  
SOURCE 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CGAGCAAGTCTTGCACAGC 940  
DB 21 CGAGCAAGTCTATGCAAGC 2

RESULT 265  
LOCUS 117147 18 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 2 from patent US 5484886.  
ACCESSION 117147  
VERSION 117147.1 GI:1252055  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Fong, T.M. and Strader, C.D.  
TITLE Human neurokinin-1 receptor  
JOURNAL Patent: US 5484886-A 2 16-JAN-1996;  
FEATURES Location/Qualifiers  
SOURCE 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 448 TCCATGCGTGCATTCAT 465  
DB 1 TCCATGCGTGCATTCAT 18

DB 1 TCCATGCGTGCATTCAT 18

RESULT 266  
LOCUS AR190721/c 18 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6209 from patent US 6346398.  
ACCESSION AR190721  
VERSION AR190721.1 GI:20236686  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 6209 12-FEB-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTACG 641  
DB 18 CCAGCCCCGGCTGTACG 1

RESULT 267  
LOCUS AR325569/c 18 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 2971 from patent US 6566127.  
ACCESSION AR325569  
VERSION AR325569.1 GI:33711377  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 2971 20-MAY-2003;  
FEATURES Location/Qualifiers  
SOURCE 1..18  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGTACG 641  
DB 18 CCAGCCCCGGCTGTACG 1

RESULT 268  
LOCUS AR599029/c 18 bp RNA linear PAT 15-DEC-2004  
DEFINITION Sequence 2971 from patent US 6818447.  
ACCESSION AR599029  
VERSION AR599029.1 GI:56650043  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)

AUTHORS Pavco, P., McSwiggan, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 2971 16-NOV-2004;  
Sirma Therapeutics, Inc.; Boulder, CO  
FEATURES  
source  
1. .18  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 CCAGCCCCGGCTGCAGC 641  
Db 18 CCAGCCGGCGCTGCAGC 1

RESULT 269  
CQ778932 19 bp DNA linear PAT 11-MAR-2004  
LOCUS Sequence 4 from Patent WO2004015422.  
DEFINITION CQ778932  
ACCESSION CQ778932.1 GI:45381605  
VERSION CQ778932.1  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
1 Golz, S., Brueggemeier, U. and Summer, H.  
Diagnostics and therapeutics for diseases associated with  
ovariancancer g-protein coupled receptor 1 (ogr-1)  
Patent: WO 2004015422-A 4 19-FEB-2004;  
JOURNAL Bayer Healthcare AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 985 ATCTGCTGGCTGCCCTTC 1002  
Db 19 ATCTGCTGGCTGCCCTTC 2

RESULT 270  
AX958828 20 bp DNA linear PAT 14-JAN-2004  
LOCUS AX958828  
DEFINITION Sequence 3 from Patent WO03100059.  
ACCESSION AX958828  
VERSION AX958828.1 GI:40879621  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
TITLE  
1 Macaulay, V.M. and Schall, M.W.  
Molecular targeting of the igf-1 receptor  
Patent: WO 03100059-A 3 04-DEC-2003;  
JOURNAL ISIS INNOVATION LIMITED (GB)  
FEATURES  
source  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Antisense oligonucleotide"

Query Match 0.9%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCAAATGTGC 1426  
Db 3 GCTTCTCTCCAAATGTCC 20

RESULT 271  
CQ755471 20 bp DNA linear PAT 01-MAR-2004  
LOCUS CQ755471  
DEFINITION Sequence 3 from Patent WO2003100093.  
ACCESSION CQ755471  
VERSION CQ755471.1 GI:44846276  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS  
TITLE  
1 Schall, M. and Macaulay, V.M.  
Method of selecting targets for gene silencing by rna interference  
Patent: WO 2003100093-A 3 04-DEC-2003;  
JOURNAL Isis Innovation Limited (GB)  
FEATURES  
source  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Antisense oligonucleotide"

Query Match 0.9%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCAAATGTGC 1426  
Db 3 GCTTCTCTCCAAATGTCC 20

RESULT 272  
AR475720 20 bp DNA linear PAT 20-FEB-2004  
LOCUS AR475720  
DEFINITION Sequence 87 from patent US 6692960.  
ACCESSION AR475720  
VERSION AR475720.1 GI:42715203  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unknown.  
Unclassified.  
REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 20)  
Bennett, C.F. and Freier, S.M.  
Antisense modulation of sphingosine-1-phosphate lyase expression  
Patent: US 6692960-A 87 17-FEB-2004;  
JOURNAL Isis Pharmaceuticals, Inc.; Carlsbad, CA  
FEATURES  
source  
Location/Qualifiers  
1. .20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 963 TGTGCTGTGTGCACCTT 980  
Db 18 TGTGCTGTGTGCACCTT 1

RESULT 273  
AX218029 17 bp RNA linear PAT 07-SEP-2001  
LOCUS AX218029

DEFINITION Sequence 3471 from Patent WO0159103.  
ACCESSION AX218029  
VERSION AX218029.1 GI:15528090  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS 1 Blatt, L., Mcswigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3471 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
Mcswigen, James (US); Chowrira, Bharat M. (US)  
FEATURES  
source 1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.9%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 801 CATCTGTGACTGTG 816  
DB 2 CATCTGTGACTGTG 17  
RESULT 274  
LOCUS CQ815064 19 bp DNA linear PAT 24-MAY-2004  
CQ815064/c  
DEFINITION Sequence 10 from Patent WO2004039978.  
ACCESSION CQ815064  
VERSION CQ815064.1 GI:47604155  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS 1 Meder, W., Wendland, M., John, H., Richter, R., Meyer, M. and  
Forsmann, W.G.  
TITLE Hf-chondroosteomodulin, production, and use for the treatment or  
diagnosis of bone diseases, cartilage diseases, obesity,  
inflammatory diseases, and skin diseases  
JOURNAL Patent: WO 2004039978-A 10 13-MAY-2004;  
IPF Pharmaceuticals GmbH (DE)  
FEATURES  
source 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der k netlichen Sequenz: Primer  
MDEZ014"  
Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 671 TTGGGCTCTGCTCTCT 689  
DB 19 TCTGGGTCTCTGCTTTCTT 1  
RESULT 275  
LOCUS CQ815066 19 bp DNA linear PAT 24-MAY-2004  
CQ815066/c  
DEFINITION Sequence 12 from Patent WO2004039978.  
ACCESSION CQ815066  
VERSION CQ815066.1 GI:47604157  
KEYWORDS  
SOURCE synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
AUTHORS 1 Meder, W., Wendland, M., John, H., Richter, R., Meyer, M. and  
Forsmann, W.G.  
TITLE Hf-chondroosteomodulin, production, and use for the treatment or  
diagnosis of bone diseases, cartilage diseases, obesity,  
inflammatory diseases, and skin diseases  
JOURNAL Patent: WO 2004039978-A 12 13-MAY-2004;  
IPF Pharmaceuticals GmbH (DE)  
FEATURES  
source 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der k netlichen Sequenz: Primer  
HDEZ-a-0114"  
Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 671 TTGGGCTCTGCTCTCT 689  
DB 19 TCTGGGTCTCTGCTTTCTT 1  
RESULT 276  
LOCUS DQ6ADRB2B 19 bp DNA linear STS 09-APR-1996  
DQ6ADRB2B/c  
DEFINITION Canis familiaris Adrenergic Receptor Beta 2 (ADRB2) STS DNA, 3'  
primer, sequence tagged site.  
ACCESSION L77385  
VERSION L77385.1 GI:1256663  
KEYWORDS STS; Adrenergic Receptor Beta 2; PCR identification; PCR primer;  
sequence tagged site; universal mammalian STS.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
REFERENCE  
AUTHORS 1 (bases 1 to 19)  
Venter, P.J., Brownlie, J.A., Yuzbasyan-Gurkan, V. and Brewer, G.J.  
TITLE Gene-specific universal mammalian sequence-tagged sites:  
application to the canine genome  
JOURNAL Unpublished (1996)  
COMMENT Original source text: Canis familiaris DNA.  
Gene-specific universal mammalian sequence-tagged site for ADRB2.  
Primer for the 3' end is in exon 1. Human product is 360 bp. Canine  
product is 360 bp. PCR conditions: 1 min, 94 C, 2 min, 57 C, 3 min,  
94 C, 35 cycles.  
FEATURES  
source 1..19  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"  
1..19  
/experiment="experimental evidence, no additional details  
recorded"  
/note="PCR primer binding site"  
1..19  
primer\_bind  
STS  
Query Match 0.9%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 979 TTGGCATTCTGCTGCTG 997  
DB 19 TTACCTCTCTGCTGCTG 1  
RESULT 277  
LOCUS AR190056/c

LOCUS AR190056 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 5544 from patent US 6346398.  
ACCESSION AR190056  
VERSION AR190056.1 GI:20236021  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
METHOD and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 5544 12-FEB-2002;  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 716 CAACCAAGAGACCATG 732  
Db 17 CAACCAAGAGACCATG 1  
RESULT 278  
AR325033/c 17 bp RNA linear PAT 17-AUG-2003  
LOCUS AR325033  
DEFINITION Sequence 2435 from patent US 6566127.  
ACCESSION AR325033  
VERSION AR325033.1 GI:33710841  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
METHOD and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 2435 20-MAY-2003;  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 716 CAACCAAGAGACCATG 732  
Db 17 CAACCAAGAGACCATG 1  
RESULT 279  
AR398493/c 17 bp RNA linear PAT 15-DEC-2004  
LOCUS AR398493  
DEFINITION Sequence 2435 from patent US 6818447.  
ACCESSION AR398493  
VERSION AR398493.1 GI:56649507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
METHOD and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 2435 16-NOV-2004;  
Sirma Therapeutics, Inc.; Boulder, CO

FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 716 CAACCAAGAGACCATG 732  
Db 17 CAACCAAGAGACCATG 1  
RESULT 280  
AX216399 17 bp RNA linear PAT 07-SEP-2001  
LOCUS AX216399  
DEFINITION Sequence 1841 from Patent WO0159103.  
ACCESSION AX216399  
VERSION AX216399.1 GI:15526460  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1  
TITLE Blatt, L., McSwiggen, J., and Chowrira, B. M.  
METHOD and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 1841 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 619 CCCCTCAGCCCGGCT 635  
Db 1 CCCCTCAGCCCGGCT 17  
RESULT 281  
AR109819 18 bp DNA linear PAT 14-FEB-2001  
LOCUS AR109819  
DEFINITION Sequence 243 from patent US 6114139.  
ACCESSION AR109819  
VERSION AR109819.1 GI:12826095  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 18)  
TITLE Hinuma, S., Hosoya, M., Fujii, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.  
G-protein coupled receptor protein and a DNA encoding the receptor  
JOURNAL Patent: US 6114139-A 243 05-SEP-2000;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 427 AACCTGGCCTTGCGGA 443  
Db 1 AACCTGGCCTTGCGGA 17



RESULT 282  
LOCUS AR698481/c 18 bp DNA linear PAT 14-SEP-2005  
DEFINITION Sequence 19 from patent US 6919176.  
ACCESSION AR698481  
VERSION AR698481.1 GI:75203030  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Yang, J. and An, S.  
TITLE Polypeptides and nucleic acids associated with cancer  
JOURNAL Patent: US 6919176-A 19 19-JUL-2005;  
Amgen Inc.; Thousand Oaks, CA  
FEATURES  
source location/Qualifiers  
1. 18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 TCTGCTGCTGCTGCTTC 1002  
DB 18 TCTGCTGCTGCTGCTTC 2

RESULT 283  
LOCUS CQ876950/c 19 bp DNA linear PAT 04-OCT-2004  
DEFINITION Sequence 3 from Patent WO2004078981.  
ACCESSION CQ876950  
VERSION CQ876950.1 GI:53790337  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Bigot, Y., Auge-Gouillou, C., Hamelin, M.H. and Brillet, B.  
TITLE Hyperactive, non-phosphorylated, mutant transposases of mariner  
JOURNAL mobile genetic elements  
Patent: WO 2004078981-A 3 16-SEP-2004;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);  
Universite Francois Rabelais de Tours (FR)  
FEATURES  
source location/Qualifiers  
1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description de la s quence artificielle: Amoree  
Site consensus d'initiation de la traduction - Vecteur  
pBad18"

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 891 GATCCCCGGGATCTCT 907  
DB 19 GATCCCCGGGATCTCT 3

RESULT 284  
LOCUS CS096561 19 bp RNA linear PAT 03-JUN-2005  
DEFINITION Sequence 62 from Patent WO2005045038.  
ACCESSION CS096561  
VERSION CS096561.1 GI:66953025  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Richards, I., Polisky, B. and Mcswigen, J.  
TITLE RNA interference mediated inhibition of GPR4 and AA1 gene  
JOURNAL expression using short Nucleic Acid (siNA)  
Patent: WO 2005045038-A 62 19-MAY-2005;  
SiRNA Therapeutics, Inc. (US)  
FEATURES  
source location/Qualifiers  
1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: Target  
Sequence/siNA sense region"

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126  
DB 3 CAACCCCATCATCTACT 19

RESULT 285  
LOCUS CS096648/c 19 bp RNA linear PAT 03-JUN-2005  
DEFINITION Sequence 149 from Patent WO2005045038.  
ACCESSION CS096648  
VERSION CS096648.1 GI:66953112  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Richards, I., Polisky, B. and Mcswigen, J.  
TITLE RNA interference mediated inhibition of GPR4 and AA1 gene  
JOURNAL expression using short Nucleic Acid (siNA)  
Patent: WO 2005045038-A 149 19-MAY-2005;  
SiRNA Therapeutics, Inc. (US)  
FEATURES  
source location/Qualifiers  
1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: siNA antisense  
region"

Query Match 0.9%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1110 CAACCCCATCATCTACT 1126  
DB 17 CAACCCCATCATCTACT 1

RESULT 286  
LOCUS DD203034 19 bp DNA linear PAT 19-JAN-2006  
DEFINITION RNA Interference Mediated Inhibition of Vascular Endothelial Growth  
Factor and Vascular Endothelial Growth Factor Receptor Gene  
Expression Using Short Interfering RNA.  
ACCESSION DD203034  
VERSION DD203034.1 GI:85659126  
KEYWORDS JP 2005517436-A/1515.  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Beigelman, L., Mcswigen, J. and Pavco, P.

TITLE RNA Interference Mediated Inhibition of Vascular Endothelial Growth Factor and Vascular Endothelial Growth Factor Receptor Gene  
JOURNAL Expression Using Short Interfering RNA  
Patent: JP 200517436-A 1515 16-JUN-2005;  
Sirma Therapeutics Inc  
OS Artificial Sequence  
PN JP 200517436-A/1515  
PD 16-JUN-2005  
PR 15-JAN-2003 US 60/440129, 27-NOV-2002 US 10/306747, PR  
04-NOV-2002 US 10/287949, 09-SEP-2002 US 60/409293, PR  
05-SEP-2002 US 60/408378, 29-AUG-2002 US 60/406784, PR  
20-FEB-2002 US 60/358580, 29-MAY-2002 US T/US02/17674, PR  
11-MAR-2002 US 60/363124, 06-JUN-2002 US 60/386782, PR  
03-JUL-2002 US 60/393796, 29-JUL-2002 US 60/399348, PI  
beigelman,james mcswigen,pamela pavco CC Description of  
Artificial Sequence: Target Sequence/siNA CC sense  
region  
CC The type of this sequence is wrong in the original data. It is  
CC automatically modified by the JPO.  
FH Location/Qualifiers.  
Key  
1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 0.8%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 139 AGGCGCCAGCCACGGA 155  
Db 2 AGCGCCAGCCACCGGA 18  
|||||  
|||

RESULT 287  
DD203281/c 19 bp RNA linear PAT 19-JAN-2006  
LOCUS  
DEFINITION RNA Interference Mediated Inhibition of Vascular Endothelial Growth  
Factor and Vascular Endothelial Growth Factor Receptor Gene  
Expression Using Short Interfering RNA.  
DD203281  
ACCESSION DD203281.1 GI:85660056  
KEYWORDS JP 200517436-A/1762.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Beigelman, L., Mcswigen, J. and Pavco, P.  
TITLE RNA Interference Mediated Inhibition of Vascular Endothelial Growth  
Factor and Vascular Endothelial Growth Factor Receptor Gene  
Expression Using Short Interfering RNA  
JOURNAL Patent: JP 200517436-A 1762 16-JUN-2005;  
Sirma Therapeutics Inc  
OS Artificial Sequence  
PN JP 200517436-A/1762  
PD 16-JUN-2005  
PR 15-JAN-2003 US 60/440129, 27-NOV-2002 US 10/306747, PR  
04-NOV-2002 US 10/287949, 09-SEP-2002 US 60/409293, PR  
05-SEP-2002 US 60/408378, 29-AUG-2002 US 60/406784, PR  
20-FEB-2002 US 60/358580, 29-MAY-2002 US T/US02/17674, PR  
11-MAR-2002 US 60/363124, 06-JUN-2002 US 60/386782, PR  
03-JUL-2002 US 60/393796, 29-JUL-2002 US 60/399348, PI  
beigelman,james mcswigen,pamela pavco CC Description of  
Artificial Sequence: siNA antisense region FH Key  
Location/Qualifiers.  
1. 19  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"

FEATURES  
source

Query Match 0.8%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 139 AGGCGCCAGCCACGGA 155  
Db 18 AGCGCCAGCCACCGGA 2  
|||||  
|||

RESULT 288  
CO622226 17 bp DNA linear PAT 02-FEB-2004  
LOCUS  
DEFINITION Sequence 6966 from Patent WO0192524.  
CO622226  
ACCESSION CO622226.1 GI:41672444  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1  
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 6966 06-DEC-2001;  
Aeomica, Inc. (US)  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 CAGTGCATCCGAGG 42  
Db 3 CAGTGCATCCGAGG 17  
|||||  
|||

RESULT 289  
CO622227 17 bp DNA linear PAT 02-FEB-2004  
LOCUS  
DEFINITION Sequence 6967 from Patent WO0192524.  
CO622227  
ACCESSION CO622227.1 GI:41672445  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1  
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 6967 06-DEC-2001;  
Aeomica, Inc. (US)  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 CAGTGCATCCGAGG 42  
|||||  
|||

Db 2 CAGTGCATCCAGAAG 16

RESULT 290  
LOCUS C0622228  
DEFINITION Sequence 6966 from Patent WO0192524.  
ACCESSION C0622228  
VERSION C0622228.1 GI:41672446  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 6966 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
|||||  
1 CAGTGCATCCAGAAG 15

Db 1 CAGTGCATCCAGAAG 15

RESULT 291  
LOCUS AR463289  
DEFINITION Sequence 6966 from patent US 6686188.  
ACCESSION AR463289  
VERSION AR463289.1 GI:42698346  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 6966 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
|||||  
3 CAGTGCATCCAGAAG 17

Db 3 CAGTGCATCCAGAAG 17

RESULT 292  
LOCUS AR463290  
DEFINITION Sequence 6967 from patent US 6686188.  
ACCESSION AR463290

VERSION AR463290.1 GI:42698347  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 6967 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
|||||  
2 CAGTGCATCCAGAAG 16

Db 2 CAGTGCATCCAGAAG 16

RESULT 293  
LOCUS AR463291  
DEFINITION Sequence 6966 from patent US 6686188.  
ACCESSION AR463291  
VERSION AR463291.1 GI:42698348  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 6968 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;

FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGCATCCAGAAG 42  
|||||  
1 CAGTGCATCCAGAAG 15

Db 1 CAGTGCATCCAGAAG 15

RESULT 294  
LOCUS AX047386/c  
DEFINITION Sequence 2 from Patent WO006402.  
ACCESSION AX047386  
VERSION AX047386.1 GI:11876617  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS van den Ende,W., van Laere,A., de Roover,V. and Michiels,A.  
TITLE Manipulation of fructan catabolism in plants  
JOURNAL Patent: WO 006402-A 2 16-NOV-2000;



ACCESSION AR054536  
VERSION AR054536.1 GI:5980113  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
TITLE Hjelte,B. and Jensen,S.  
JOURNAL Hantavirus-associated respiratory distress virus antigens  
PATENT: US 5837441-A 45 17-NOV-1998;  
FEATURES  
source  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 CCTGAGCCCCGAGCCCA 146  
DB 18 CCTGAGCCCCGAGCACA 1

RESULT 300  
ARI38040/c 18 bp DNA linear PAT 16-JUN-2001  
LOCUS ARI38040 Sequence 50 from patent US 6197584.  
ACCESSION ARI38040  
VERSION ARI38040.1 GI:14479549  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Bennett,C.Frank. and Cowser,T.L.M.  
TITLE Antisense modulation of CD40 expression  
JOURNAL Patent: US 6197584-A 50 06-MAR-2001;  
FEATURES  
source  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 TCAGCTTCTCCCAATG 1423  
DB 18 TCGGCTTCTTCCCATG 1

RESULT 301  
BD064969/c 18 bp DNA linear PAT 27-AUG-2002  
LOCUS BD064969 Protein containing an SRCR domain.  
ACCESSION BD064969  
VERSION BD064969.1 GI:22610572  
KEYWORDS JP 2001509667-A/7.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
1 (bases 1 to 18)  
REFERENCE Mollenhauer,J. and Poustka,A.  
AUTHORS Mollenhauer,J. and Poustka,A.  
TITLE Protein containing an SRCR domain  
JOURNAL Patent: JP 2001509667-A 7 24-JUL-2001;  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS  
OS Artificial Sequence  
PN JP 2001509667-A/7  
PD 24-JUL-2001  
PF 09-JAN-1998 JP 1998530469  
PR 09-JAN-1997 DE 197 00 519.5,18-JUL-1997 DE 197 30 997.6 PI  
JAN MOLLENHAUER,ANNEMARIE POUSTKA

PC C12N15/12,C12N15/70,C12N1/21,C12Q1/68,C07K14/47,C07K16/18, PC  
A61K38/17,  
PC A61K48/00,G01N33/50  
CC Description of Artificial Sequence: primer sequence for CC  
amplifying a DNA  
CC encoding a protein containing SRCR domain.  
FH Key Location/Qualifiers  
FT source 1..18  
/organism='Artificial Sequence'.  
FEATURES  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAAACATCTCCAC 260  
DB 1 CTCGCCAAACATCTCTC 18

RESULT 303  
BD226591/c 18 bp DNA linear PAT 17-JUL-2003  
LOCUS BD226591

PC C12N15/12,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
00', C12P21/02,C12Q1/02,A61K48/00,A61K39/395,A61K45/00,A61P11/00 CC  
Description of Artificial Sequence: Artificially Synthesized CC  
Primer  
CC Sequence Location/Qualifiers  
FH Key 1..18  
FT source /organism='Artificial Sequence'.  
FEATURES  
source  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 243 CTCGCCAAACATCTCCAC 260  
DB 1 CTCGCCAAACATCTCTC 18

RESULT 303  
BD226591/c 18 bp DNA linear PAT 17-JUL-2003  
LOCUS BD226591

DEFINITION Antisense modulation of CD40 expression.  
ACCESSION BD226591  
VERSION BD226591.1 GI:33036361  
KEYWORDS JP 2002513593-A/50.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified sequences.  
1 (bases 1 to 18)  
AUTHORS Bennett,C.F. and Cowseert,I.M.  
TITLE Antisense modulation of CD40 expression  
JOURNAL Patent: JP 2002513593-A 50 14-MAY-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Unidentified  
PN JP 2002513593-A/50  
PD 14-MAY-2002  
PF 22-APR-1999 JP 2000547271  
PR 01-MAY-1998 US 09/071433  
PI C FRANK BENNETT, LEX M COMSERT  
PC C12N15/09,A61K9/10,A61K45/00,A61K48/00,A61P1/00,A61P11/06, PC  
A61P17/06,  
PC A61P29/00,A61P35/00,A61P37/02,A61P37/06,A61P43/00,C12P19/34,  
PC C12Q1/68,  
PC C12N15/00  
CC Strandedness: Single;  
CC Topology: linear;  
CC Antisense modulation of CD40 expression  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Unidentified'.  
FEATURES  
source 1..18  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1406 TCAGCTTCTCTCCATG 1423  
DB 18 TCGGCTTCTCTCCATG 1  
RESULT 304  
BD250496/c 18 bp DNA linear PAT 17-JUL-2003  
LOCUS Identification of genetic targets for modulation by  
DEFINITION oligonucleotides and generation of oligonucleotides for gene  
modulation.  
ACCESSION BD250496  
VERSION BD250496.1 GI:33060266  
KEYWORDS JP 2002511276-A/50.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
1 (bases 1 to 18)  
AUTHORS Cowseert,I.M., Baker,B.F., Mcneil,J., Freier,S.M., Saemor,H.M.,  
Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.  
TITLE Identification of genetic targets for modulation by  
JOURNAL oligonucleotides and generation of oligonucleotides for gene  
modulation  
PATENT: JP 2002511276-A 50 16-APR-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2002511276-A/50  
PD 16-APR-2002  
PF 13-APR-1999 JP 2000543647  
PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PT  
LEX M COMSERT, BRENDA F BAKER, JOHN MCNEILL, SUSAN M FREIER, HENRI PI  
M SASMOR,  
PI DOUGLAS G BROOKS, CARA OHASI, JACQUELINE R WYATT, ALEXANDER H PI  
BORCHERS,

PI TIMOTHY A VIKKARS  
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC  
C12N15/00  
CC Antisense Oligonucleotide  
FH Key Location/Qualifiers  
FT source 1..18  
FT /organism='Artificial Sequence'.  
FEATURES  
source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1406 TCAGCTTCTCTCCATG 1423  
DB 18 TCGGCTTCTCTCCATG 1  
RESULT 305  
AR193175/c 18 bp DNA linear PAT 20-APR-2002  
LOCUS AR193175  
DEFINITION Sequence 9 from patent US 6346606.  
ACCESSION AR193175  
VERSION AR193175.1 GI:20239140  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Mollenhauer,J. and Poustka,A.  
TITLE Protein containing a scavenger receptor cysteine rich domain  
JOURNAL Patent: US 6346606-A 9 12-FEB-2002;  
FEATURES  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1263 CAGCCGCTGAGACAC 1280  
DB 18 CAGCTGCTGACACAC 1  
RESULT 306  
AX146659 18 bp DNA linear PAT 31-MAY-2001  
LOCUS AX146659  
DEFINITION Sequence 1 from Patent WO0134834.  
ACCESSION AX146659  
VERSION AX146659.1 GI:14285052  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Leffers,H., Jorgensen,M. and Skakkebaek,K.N.E.  
TITLE Endogenous gene expression assay  
JOURNAL Patent: WO 0134834-A 1 17-MAY-2001;  
Rigshospitalet (DK)  
FEATURES  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer sequence"  
Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 105 CCTCTCTCTCTCTCTAG 122  
|||||  
Db 1 CCTCTCTCTCTCTAG 18

RESULT 307  
AX686022 18 bp DNA linear PAT 29-MAR-2003  
LOCUS Sequence 66 from Patent WO02064791.  
DEFINITION AX686022  
ACCESSION AX686022  
VERSION AX686022.1 GI:29371875  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1  
Alsebrook II, J.P., Anderson, D.W., Burgess, C.E., Boldog, F.L.,  
Caeman, S.J., Colman, S.D., Edinger, S.R., Ellerman, K., Gerlach, V.,  
Gorman, L., Grose, W.M., Guo, X., Herrmann, J.L., Kikuda, R.,  
Lepley, D.M., Li, L., Macdougall, J.R., Miller, I., Pena, C.E.,  
Peyman, J.A., Rastelli, L., Rieger, D.K., Shinkens, R.A., Smithson, G.,  
Spytek, K.A., Stone, D.J., Tchernev, V.T., Vernet, C.A., Voss, E.Z.,  
Zerhusen, B.D., Zhong, H. and Zhong, M.  
Proteins and nucleic acids encoding same  
Patent: WO 02064791-A 66 22-AUG-2002;  
Curagen Corporation (US)  
FEATURES  
SOURCE  
1. 18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide primer"

Query Match 0.8%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 315 GGCAGCTGCTTACACGGT 332  
|||||  
Db 1 GGCAGCGCTTACACGGT 18

RESULT 308  
AX468698 16 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468698  
DEFINITION Sequence 14 from Patent WO0213799.  
ACCESSION AX468698  
VERSION AX468698.1 GI:21901468  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1  
Henry, J.L., Cahill, C.M. and Yasbajal, K.  
Oligonucleotides and other modulators of the nk-1 receptor pathway  
and therapeutic uses thereof  
Patent: WO 0213799-A 14 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
SOURCE  
1. 16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="primer"

Query Match 0.8%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 207 CGAATGATACGTC 222

Db 16 CAATGATACGTC 1  
|||||

RESULT 309  
DD184677/c 17 bp DNA linear PAT 19-JAN-2006  
LOCUS DD184677  
DEFINITION Probe sets and methods for identifying HLA-B allele.  
ACCESSION DD184677  
VERSION DD184677.1 GI:85637624  
KEYWORDS JP 2005185172-A/103.  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1  
Tsuksada, M.  
1 (bases 1 to 17)  
Probe sets and methods for identifying HLA-B allele  
Patent: JP 2005185172-A 103 14-JUL-2005;  
CANON INC  
COMMENT  
OS Homo sapiens  
PN JP 2005185172-A/103  
PD 14-JUL-2005  
PF 25-DEC-2003 JP 2003430554  
PI mamoru tsuksada  
CC  
FH Key Location/Qualifiers.

FEATURES  
SOURCE  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 GCGGAGGCTTCATG 453  
|||||  
Db 17 GCGGAGGCTTCATG 2

RESULT 310  
DD188299/c 17 bp DNA linear PAT 19-JAN-2006  
LOCUS DD188299  
DEFINITION Probe set and method for identification of allele of HLA.  
ACCESSION DD188299  
VERSION DD188299.1 GI:85646382  
KEYWORDS WO 2005063985-A/740.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS

1  
Tsuksada, M.  
1 (bases 1 to 17)  
Probe set and method for identification of allele of HLA  
Patent: WO 2005063985-A 740 14-JUL-2005;  
CANON INC  
COMMENT  
OS Homo sapiens  
PN WO 2005063985-A/740  
PD 14-JUL-2005  
PR 24-DEC-2004 WO 2004JP019763  
PR 25-DEC-2003 JP 03P 430556, 25-DEC-2003 JP 03P 430555, PR  
25-DEC-2003 JP 03P 430559, 25-DEC-2003 JP 03P 430553, PR  
25-DEC-2003 JP 03P 430558, 25-DEC-2003 JP 03P 430557, PR  
25-DEC-2003 JP 03P 430554  
PI mamoru tsuksada  
CC  
FH Key Location/Qualifiers.

FEATURES  
SOURCE  
1. 17  
Location/Qualifiers.

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGAGGCTTCATG 453  
| | | | | | | | | | | | | | | | | |  
Db 17 CGCGAGGAGGCTTCATG 2

RESULT 311  
AX215478 17 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 920 from Patent WO0159103.  
DEFINITION AX215478  
ACCESSION AX215478  
VERSION AX215478.1 GI:15525521  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., Mcswigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 920 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
Mcswigen, James (US) ; Chowrira, Bharat M. (US)  
LOCATION/Qualifiers  
1. .17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCCCTCCAGCCCGGC 634  
| | | | | | | | | | | | | | | | | |  
Db 2 CCCCGCCAGCCCGGC 17

RESULT 312  
AX218028 17 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 3470 from Patent WO0159103.  
DEFINITION AX218028  
ACCESSION AX218028  
VERSION AX218028.1 GI:15528089  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., Mcswigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 3470 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
Mcswigen, James (US) ; Chowrira, Bharat M. (US)  
LOCATION/Qualifiers  
1. .17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 799 CACATCTGTGTGACTG 814  
| | | | | | | | | | | | | | | | | |  
Db 2 CCCATCTGTGTGACTG 17

RESULT 313  
AX468697 17 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 13 from Patent WO0213799.  
DEFINITION AX468697  
ACCESSION AX468697  
VERSION AX468697.1 GI:21901467  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
and therapeutic uses thereof  
JOURNAL Patent: WO 0213799-A 13 21-FEB-2002;  
MCGILL UNIVERSITY (CA)  
LOCATION/Qualifiers  
1. .17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.8%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CGAATGATPAACGTC 222  
| | | | | | | | | | | | | | | | | |  
Db 16 CAAATGATPAACGTC 1

RESULT 314  
AR096338 18 bp DNA linear PAT 08-SEP-2000  
LOCUS Sequence 9 from patent US 6007995.  
DEFINITION AR096338  
ACCESSION AR096338  
VERSION AR096338.1 GI:10025059  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
1 (bases 1 to 18)  
REFERENCE Baker, B.F. and Cowse, L.M.  
AUTHORS Antisense inhibition of TNF $\alpha$  expression  
TITLE Patent: US 6007995-A 9 28-DEC-1999;  
JOURNAL Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 105 CCCCTCTGTCTGCTT 120  
| | | | | | | | | | | | | | | | | |  
Db 3 CCCCTCTCTGTCTT 18

RESULT 315  
AX923497 18 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 22 from Patent WO03080663.  
DEFINITION AX923497  
ACCESSION AX923497  
VERSION AX923497.1 GI:40216543  
KEYWORDS



SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Chiquet-Ehrismann, R. and Scherberich, A.  
TITLE Tenascin-w compositions and uses thereof  
JOURNAL Patent: WO 03080663-A 22 OCT-2003;  
Novartis Forschungsbildung Zweigniederlassung (CH)  
Location/Qualifiers

FEATURES  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence:  
oligonucleotide"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1276 ACCACCATCTCCACAG 1291  
|||||  
Db 16 ACCACCTCTCCACAG 1

RESULT 316  
BD217386 18 bp DNA linear PAT 17-JUL-2003  
LOCUS Antisense modulation of TNFR1 expression.  
DEFINITION BD217386  
ACCESSION BD217386.1 GI:33027156  
VERSION JP 2002519015-A/9.  
KEYWORDS JP 2002519015-A/9.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Baker, B.F. and Cowse, L.M.  
TITLE Antisense modulation of TNFR1 expression  
JOURNAL Patent: JP 2002519015-A 9 OCT-2002;  
ISIS PHARMACEUTICALS INC  
OS Unidentified  
PN JP 2002519015-A/9  
PD 02-JUL-2002  
PR 17-JUN-1999 JP 2000557265  
PR 26-JUN-1998 US 09/106038  
PI BRENDA F BAKER, LEX M COWSE  
PC C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC  
C1201/68  
PC C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Antisense modulation of TNFR1 expression  
FH Key Location/Qualifiers  
FT source 1..18  
Location/Qualifiers  
1..18  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

QY 105 CCCTCCTGCTGCTTT 120  
|||||  
Db 3 CCCTCCTGCTGCTTT 18

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 317  
CQ799859

LOCUS CQ799859 18 bp DNA linear PAT 28-APR-2004  
DEFINITION Sequence 509 from Patent WO2004031413.  
ACCESSION CQ799859  
VERSION CQ799859.1 GI:4684806  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Nakamura, Y., Daigo, Y. and Nakatsu, S.  
TITLE Method for diagnosing non-small cell lung cancers  
JOURNAL Patent: WO 2004031413-A 509 15-APR-2004;  
Oncotherapy Science, Inc. (JP); Japan as  
president of the university of Tokyo (JP)  
Location/Qualifiers

FEATURES  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Artificially synthesized S-oligonucleotide sequence  
for antisense method"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 CCACCATCTCCACAGT 1292  
|||||  
Db 3 CCACCATCTCCACAGT 18

RESULT 318  
AR190767 18 bp DNA linear PAT 20-APR-2002  
LOCUS AR190767/c  
DEFINITION Sequence 6255 from patent US 6346398.  
ACCESSION AR190767  
VERSION AR190767.1 GI:20236732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Pavco, P., McSwiggen, J., Srincomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions  
JOURNAL related to levels of vascular endothelial growth factor receptor  
PATENT: US 6346398-A 6255 12-FEB-2002;  
Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

QY 662 TCTGTGTCATCTGGGT 677  
|||||  
Db 18 TCTGTGTCATCTGAGT 3

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 319  
AR299235 18 bp DNA linear PAT 12-JUN-2003  
LOCUS AR299235  
DEFINITION Sequence 10970 from patent US 6537751.  
ACCESSION AR299235  
VERSION AR299235.1 GI:3168519  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
TITLE Biallelic markers for use in constructing a high density

disequilibrium map of the human genome  
Patent: US 6537751-A 10970 25-MAR-2003;  
Genet S.A.;;

## FEATURES

source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1404 CTTGAGCTTCCTCC 1419  
Db 2 CTTGATCTTCTCTCC 17

RESULT 320  
AR325611/c AR325611 18 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 3013 from patent US 6566127.  
ACCESSION AR325611  
VERSION AR325611.1 GI:33711419  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 3013 20-MAY-2003;  
FEATURES  
source Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
1..18  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 662 TCTGTGTCATCTGGGT 677  
Db 18 TCTGTGTCATCTGAGT 3

RESULT 321  
I81946 I81946 18 bp DNA linear PAT 10-JUN-1998  
LOCUS Sequence 44 from patent US 5712094.  
DEFINITION I81946  
ACCESSION I81946  
VERSION I81946.1 GI:3210243  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Seidel,H.,Martin., Lamb,I.,Peter. and Chan,S.-S.,Tian.  
TITLE Methods for detecting modulators of cytokine action  
JOURNAL Patent: US 5712094-A 44 27-JAN-1998;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1717 TCCATTTCTGGAAGTG 1732  
|||||

Db 3 TCCATTTCTGGAATG 18

RESULT 322  
AR442143/c AR442143 18 bp DNA linear PAT 20-FEB-2004  
LOCUS Sequence 42 from patent US 6670124.  
DEFINITION AR442143  
ACCESSION AR442143  
VERSION AR442143.1 GI:42669400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS Chow,R. and Tonal,R.  
TITLE High throughput methods of HLA typing  
JOURNAL Patent: US 6670124-A 42 30-DEC-2003;  
StemCyle, Inc.; Arcadia, CA  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 438 CGCGAGGCTCTCATG 453  
Db 18 CGCGAGGCTCTCATG 3

RESULT 323  
AR599071/c AR599071 18 bp RNA linear PAT 15-DEC-2004  
LOCUS Sequence 3013 from patent US 6818447.  
DEFINITION AR599071  
ACCESSION AR599071  
VERSION AR599071.1 GI:56650085  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 3013 16-NOV-2004;  
Sigma Therapeutics, Inc.; Boulder, CO  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 662 TCTGTGTCATCTGGGT 677  
Db 18 TCTGTGTCATCTGAGT 3

RESULT 324  
AX115374/c AX115374 18 bp DNA linear PAT 11-MAY-2001  
LOCUS Sequence 497 from Patent WO0129262.  
DEFINITION AX115374  
ACCESSION AX115374  
VERSION AX115374.1 GI:14032316  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1

AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 497 26-APR-2001;  
Orchid Biosciences, Inc. (US)

FEATURES  
source  
1.18  
Location/Qualifiers

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1223 CCACCCGGTACTCCA 1238  
Db 18 CCACCCGGTCTCTCCA 3

RESULT 325  
AX468696/c 18 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468696  
DEFINITION Sequence 12 from Patent WO0213799.  
ACCESSION AX468696  
VERSION AX468696.1 GI:21901466  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 12 21-FEB-2002;  
MCGILL UNIVERSITY (CA)

FEATURES  
source  
1.18  
Location/Qualifiers

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.8%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 207 CGAATGATTAACCTC 222  
Db 16 CAAATGATTAACCTC 1

RESULT 326  
AR407912 14 bp RNA linear PAT 18-DEC-2003  
LOCUS AR407912  
DEFINITION Sequence 5 from patent US 6632057.  
ACCESSION AR407912  
VERSION AR407912.1 GI:40157899  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS Fauchet, C.R.J.  
TITLE Fixing unit with an end imprint in a threaded terminal portion  
JOURNAL Patent: US 6632057-A 5 14-OCT-2003;  
GRT Aerospace; Paris;  
FR;

FEATURES  
source  
1.14  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 689 TGCTGGCCTTCCCC 702  
Db 1 TGCTGGCCTTCCCC 14

RESULT 327  
E09069 15 bp DNA linear PAT 29-SEP-1997  
LOCUS E09069  
DEFINITION DNA encoding N-terminal fragment of recombinant bile  
salt-activating lipase.  
ACCESSION E09069  
VERSION E09069.1 GI:22025695  
KEYWORDS JP 1995111891-A/11.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.

REFERENCE  
AUTHORS Murasugi, A. and Asami, Y.  
TITLE EXPRESSION OF RECOMBINANT BILE SALT ACTIVATED LIPASE IN HIGH YIELD  
JOURNAL Patent: JP 1995111891-A 11 02-MAY-1995;  
MEIJI MILK PROD CO LTD

COMMENT  
OS None  
OC Artificial sequences.  
PN JP 1995111891-A/11  
PD 02-MAY-1995  
PF 30-SEP-1993 JP 1993245079  
PI MURASUGI AKIRA, ASAMI YUKIO  
PC C12N9/20, C12N1/19, C12N15/09, (C12N9/20, C12R1/84), (C12N1/19, PC  
C12R1/84);

CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
FH Key  
FH Location/Qualifiers

FT source 1.15  
FT /organism="Artificial sequences".

FEATURES  
source  
1.15  
Location/Qualifiers

/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1133 TCAATGACAGGTTTC 1146  
Db 1 TCAATGACAGGTTTC 14

RESULT 328  
AX468699/c 15 bp DNA linear PAT 16-JUL-2002  
LOCUS AX468699  
DEFINITION Sequence 15 from Patent WO0213799.  
ACCESSION AX468699  
VERSION AX468699.1 GI:21901469  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 15 21-FEB-2002;  
MCGILL UNIVERSITY (CA)

FEATURES  
source  
Location/Qualifiers

source

1. .15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 209 AAATGATACGTC 222  
| | | | | | | | | | | | | | | |  
Db 14 AAATGATACGTC 1

RESULT 329

AR043296 16 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 84 from patent US 5814457.  
ACCESSION AR043296  
VERSION AR043296.1 GI:5964304  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Kern,S.E. and Hahn,S.A.  
TITLE DPC4 polypeptide  
JOURNAL Patent: US 5814457-A 84 29-SEP-1998;  
FEATURES  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743  
| | | | | | | | | | | | | | | |  
Db 2 ATGCCACGACGAGT 15

RESULT 330

AR074951 16 bp DNA linear PAT 28-AUG-2000  
LOCUS AR074951  
DEFINITION Sequence 84 from patent US 5955292.  
ACCESSION AR074951  
VERSION AR074951.1 GI:10001703  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Kern,S.E. and Hahn,S.A.  
TITLE Tumor suppressor gene, DPC4  
JOURNAL Patent: US 5955292-A 84 21-SEP-1999;  
FEATURES  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743  
| | | | | | | | | | | | | | | |  
Db 2 ATGCCACGACGAGT 15

RESULT 331

182147

LOCUS 182147 16 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 84 from patent US 5712097.  
ACCESSION 182147  
VERSION 182147.1 GI:3210444  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Kern,S.E. and Hahn,S.A.  
TITLE Tumor suppressor gene, DPC4  
JOURNAL Patent: US 5712097-A 84 27-JUN-1998;  
FEATURES  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 ATGCCACGACGAGT 743  
| | | | | | | | | | | | | | | |  
Db 2 ATGCCACGACGAGT 15

RESULT 332

AR075054 17 bp DNA linear PAT 28-AUG-2000  
LOCUS AR075054  
DEFINITION Sequence 14 from patent US 5955306.  
ACCESSION AR075054  
VERSION AR075054.1 GI:10001806  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Gimeno,C.J. and Errada,P.R.  
TITLE Genes encoding proteins that interact with the tub protein  
JOURNAL Patent: US 5955306-A 14 21-SEP-1999;  
FEATURES  
Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 571 TACTCATGACGCG 584  
| | | | | | | | | | | | | | | |  
Db 3 TACTCATGACGCG 16

RESULT 333

AR141872 17 bp DNA linear PAT 08-AUG-2001  
LOCUS AR141872  
DEFINITION Sequence 14 from patent US 6147192.  
ACCESSION AR141872  
VERSION AR141872.1 GI:15101388  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Gimeno,C.J. and Errada,P.R.  
TITLE Tub interactor (TI) polypeptides and uses therefor  
JOURNAL Patent: US 6147192-A 14 14-NOV-2000;  
FEATURES  
Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACTCATGACGCG 584  
|||||  
Db 3 TACTCATGACGCG 16

RESULT 334  
LOCUS C0622225 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 6965 from Patent WO0192524.  
ACCESSION C0622225  
VERSION C0622225.1 GI:41672443  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNML Patent: WO 0192524-A 6965 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGTGATCCAGAA 41  
|||||  
Db 4 CAGTGATCCAGAA 17

RESULT 335  
LOCUS C0622229 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 6969 from Patent WO0192524.  
ACCESSION C0622229  
VERSION C0622229.1 GI:41672447  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNML Patent: WO 0192524-A 6969 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AGTGATCCAGAG 42  
|||||  
Db 1 AGTGATCCAGAG 14

RESULT 336  
LOCUS CQ931584/c 17 bp DNA linear PAT 23-NOV-2004  
DEFINITION Sequence 6617 from Patent WO2004083403.  
ACCESSION CQ931584  
VERSION CQ931584.1 GI:56220974  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Cargill,M., Begovich,A.B. and Alexander,H.C.  
TITLE Genetic polymorphisms associated with rheumatoid arthritis, methods  
JOURNML of detection and uses thereof  
Patent: WO 2004083403-A 6617 30-SEP-2004;  
Applera Corporation (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 TCCTGGCTTCCTG 690  
|||||  
Db 14 TCCTGGCTTCCTG 1

RESULT 337  
LOCUS AR404183 17 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 22 from patent US 6627739.  
ACCESSION AR404183  
VERSION AR404183.1 GI:40152223  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
Anderson,J.P., Basl,G., Doan,M.T., Frigon,N., John,V., Power,M.,  
Sinha,S., Tatsuno,G., Tung,J., Wang,S. and McConlogue,L.  
TITLE .beta.-secretase enzyme compositions and methods  
JOURNML Patent: US 6627739-A 22 30-SEP-2003;  
Elian Pharmaceuticals, Inc.; South San Francisco, CA  
FEATURES  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 2.4e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1306 GAGGAGGAGCCAGGA 1322  
|||||  
Db 1 GAYGARGAGCCGAGGA 17

RESULT 338  
LOCUS AR463288 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 6965 from patent US 6686188.  
ACCESSION AR463288  
VERSION AR463288.1 GI:42698345  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 6965 03-FEB-2004;  
Amer sham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 CAGTGCATCCAGAA 41  
|||||  
4 CAGTGCATCCAGAA 17

Db

RESULT 339  
AR463292 17 bp DNA linear PAT 20-FEB-2004  
LOCUS  
DEFINITION Sequence 6969 from patent US 6686188.  
AR463292  
ACCESSION  
VERSION AR463292.1 GI:42698349  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 6969 03-FEB-2004;  
Amer sham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 AGTGCATCCAGAG 42  
|||||  
1 AGTGCATCCAGAG 14

Db

RESULT 340  
AX218126 17 bp RNA linear PAT 07-SEP-2001  
LOCUS  
DEFINITION Sequence 3568 from Patent WO0159103.  
AX218126  
ACCESSION  
VERSION AX218126.1 GI:15528187  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,U., Mcswigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 3568 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Mcswigen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
source  
Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 803 TCTGTGACTGTG 816  
|||||  
1 TCTGTGACTGTG 14

Db

RESULT 341  
AR046956 17 bp DNA linear PAT 29-SEP-1999  
LOCUS  
DEFINITION Sequence 1749 from patent US 5817796.  
AR046956  
ACCESSION  
VERSION AR046956.1 GI:5968421  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T., Draper,K., Mcswigen,J. and Jarvis,T.  
TITLE C-myb ribozymes having 2'-5',-linked adenylate residues  
JOURNAL Patent: US 5817796-A 1749 06-OCT-1998;  
FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 441 GGAGGCTCCATGGCTG 457  
|||||  
1 GGAGGCTCCATGGCTG 17

Db

RESULT 342  
BD067403/C 17 bp RNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.  
BD067403  
ACCESSION  
VERSION BD067403.1 GI:22613006  
KEYWORDS  
SOURCE JP 2001511003-A/243.  
ORGANISM  
unidentified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Akhtar,S., Fell,P. and Mcswigen,J.A.  
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors  
JOURNAL Patent: JP 2001511003-A 243 07-AUG-2001;  
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV  
COMMENT  
OS Unidentified  
PN JP 2001511003-A/243  
PD 07-AUG-2001  
PF 14-JAN-1998 JP 1998532913  
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI  
SAGHIR AKHTAR, PATRICIA FELL,JAMES A MCSWIGEN PC  
CL2N9/00, C07K14/71  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Enzymatic nucleic acid treatment of diseases or conditions related to  
CC levels of epidermal growth factor receptors

FEATURES  
source  
Location/Qualifiers  
1. .17  
/organism='unidentified'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32644'

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1313 AGCCAGAGAGAGCCCC 1329  
DB 17 AGCAAGAGAGAGCCCC 1

RESULT 343  
BD104935  
LOCUS BD104935 17 bp DNA linear PAT 27-AUG-2002  
DEFINITION Kit and method for determining HLA type.  
ACCESSION BD104935  
VERSION BD104935.1 GI:22650509  
KEYWORDS WO 0192572-A/1039.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
TITLE Kit and method for determining HLA type  
JOURNAL Patent: WO 0192572-A 1039 06-DEC-2001;  
NISHIMBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA  
COMMENT OS Artificial Sequence  
PN WO 0192572-A/1039  
PD 06-DEC-2001  
PF 01-JUN-2001 WO 2001JP004662  
PR 01-JUN-2000 JP 00P 164798  
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,  
MORIYA,SHOGO  
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53  
CC Description of Artificial Sequence:capture  
FH Key Location/Qualifiers  
FT source 1. .17  
/organism='Artificial Sequence'.  
FEATURES  
source  
Location/Qualifiers  
1. .17  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1299 GGCCAGAGAGAGAGC 1315  
DB 1 GGCCATAGAGCGAGC 17

RESULT 344  
BD200869  
LOCUS BD200869/c 17 bp RNA linear PAT 17-JUL-2003  
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.  
ACCESSION BD200869  
VERSION BD200869.1 GI:33010639  
KEYWORDS JP 2002509721-A/3895.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.  
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response  
JOURNAL Patent: JP 2002509721-A 3895 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002509721-A/3895  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,  
JAMES A MCSWIGEN  
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC A61P29/00  
C12N5/00  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1. .17  
/organism='Homo sapiens (human)'.  
FEATURES  
source  
Location/Qualifiers  
1. .17  
/organism='Homo sapiens'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:9606'

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1720 ATTCTGTGAGTGAATT 1736  
DB 17 ACTTCTGGAAGTGAATT 1

RESULT 345  
CG618016  
LOCUS CG618016 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 2756 from Patent W00192524.  
ACCESSION CG618016  
VERSION CG618016.1 GI:41668234  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 2756 06-DEC-2001;  
Aecmica, Inc. (US)  
FEATURES  
source  
Location/Qualifiers  
1. .17  
/organism='Homo sapiens'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:9606'

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1196 GCGACTATGAGGGCTG 1212  
|||||

Db 1 GCGAGTATGAGGAGCTG 17

RESULT 346  
LOCUS DD185435 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Probe sets for detection of HLA-C allele and methods thereof.  
ACCESSION DD185435  
VERSION DD185435.1 GI:185638904  
KEYWORDS JP 2005185174-A/180.  
SOURCE synthetic construct  
ORGANISM Homo sapiens (human)  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 7674 06-DEC-2001;  
Aecomica, Inc. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 CTTGAGCTTCTCTCCA 1420  
Db 17 CTTGCTCTCTCTCCA 1

RESULT 347  
LOCUS DD184601 17 bp DNA linear PAT 19-JAN-2006  
DEFINITION Probe sets and methods for identifying HLA-B allele.  
ACCESSION DD184601  
VERSION DD184601.1 GI:85637235  
KEYWORDS JP 2005185172-A/27.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Tsukada,M.  
TITLE Probe sets and methods for identifying HLA-B allele  
JOURNAL Patent: JP 2005185172-A 27 14-JUL-2005;  
CANON INC  
COMMENT OS Homo sapiens  
PN JP 2005185172-A/27  
PD 14-JUL-2005  
PF 25-DEC-2003 JP 2003430554  
PI mamoru tsukada  
CC

FEATURES  
source FH Key Location/Qualifiers.  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 CAGGCGCCAGGCACAGG 154  
Db 1 CAAGCGCCAGGCACAGG 17

RESULT 348  
LOCUS DD185435 17 bp DNA linear PAT 19-JAN-2006  
DEFINITION Probe sets for detection of HLA-C allele and methods thereof.  
ACCESSION DD185435  
VERSION DD185435.1 GI:185638904  
KEYWORDS JP 2005185174-A/180.  
SOURCE synthetic construct  
ORGANISM Homo sapiens (human)  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Tsukada,M.  
TITLE Probe sets for detection of HLA-C allele and methods thereof  
JOURNAL Patent: JP 2005185174-A 180 14-JUL-2005;  
Canon Inc  
COMMENT OS artificial sequence  
PN JP 2005185174-A/180  
PD 14-JUL-2005  
PF 25-DEC-2003 JP 2003430556  
PI mamoru tsukada  
CC probe for detection  
FH Key Location/Qualifiers.  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 CAGGCGCCAGGCACAGG 154  
Db 1 CAAGCGCCAGGCACAGG 17

RESULT 349  
LOCUS DD188223 17 bp DNA linear PAT 19-JAN-2006  
DEFINITION Probe set and method for identification of allele of HLA.  
ACCESSION DD188223  
VERSION DD188223.1 GI:85646306  
KEYWORDS WO 2005063985-A/664.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Tsukada,M.  
TITLE Probe set and method for identification of allele of HLA  
JOURNAL Patent: WO 2005063985-A 664 14-JUL-2005;  
CANON INC  
COMMENT OS Homo sapiens  
PN WO 2005063985-A/664  
PD 14-JUL-2005  
PF 24-DEC-2004 WO 2004JP019763  
PR 25-DEC-2003 JP 03P 430556,25-DEC-2003 JP 03P 430553, PR  
25-DEC-2003 JP 03P 430558,25-DEC-2003 JP 03P 430557, PR  
25-DEC-2003 JP 03P 430554  
PI mamoru tsukada  
CC

FEATURES  
source FH Key Location/Qualifiers.  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"





REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 5545 12-FEB-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCCAGAGACCA 730  
DB 17 CACACCCAGAGACCA 1

RESULT 355  
AR190206/c  
LOCUS AR190206 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 5694 from patent US 6346398.  
ACCESSION AR190206  
VERSION AR190206.1 GI:20236171  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 5694 12-FEB-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGAACCATCA 1521  
DB 17 TTCATCTGATCCATGA 1

RESULT 356  
AR196300/c  
LOCUS AR196300 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 765 from patent US 6350934.  
ACCESSION AR196300  
VERSION AR196300.1 GI:20245737  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P., Ann Owens, G., L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.  
TITLE Nucleic acid encoding delta-9 desaturase  
JOURNAL Patent: US 6350934-A 765 26-FEB-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 GTCAGCCACAGCCACCA 652

DB 17 GTCAGCCAGAGCCACCA 1

RESULT 357  
AR324312/c  
LOCUS AR324312 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1714 from patent US 6566127.  
ACCESSION AR324312  
VERSION AR324312.1 GI:33710120  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1714 20-MAY-2003;  
FEATURES Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers  
SOURCE 1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 714 CTCACCCAGAGACCA 730  
DB 17 CACACCCAGAGACCA 1

RESULT 358  
AR324484/c  
LOCUS AR324484 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1886 from patent US 6566127.  
ACCESSION AR324484  
VERSION AR324484.1 GI:33710292  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1886 20-MAY-2003;  
FEATURES Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers  
SOURCE 1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1505 TTCATCTGGAACCATCA 1521  
DB 17 TTCATCTGATCCATGA 1

RESULT 359  
AR328943/c  
LOCUS AR328943 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 6345 from patent US 6566127.  
ACCESSION AR328943  
VERSION AR328943.1 GI:33714751  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 6345 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 ACTCAACACAGAGACC 729  
Db 17 ACACACACAGAGACC 1

RESULT 360  
LOCUS 154008 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1749 from patent US 5646042.  
ACCESSION 154008  
VERSION 154008.1 GI:2475211  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Stinchcomb, D. T., Draper, K., McSwiggen, J. and Jarvis, T.  
TITLE C-myc targeted ribozymes  
JOURNAL Patent: US 5646042-A 1749 08-JUL-1997;  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 441 GGAGCCTCCATGCGCTG 457  
Db 1 GGAGCCTCCATGCGCTG 17

RESULT 361  
LOCUS 160477 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 10 from patent US 5656462.  
ACCESSION 160477  
VERSION 160477.1 GI:2478922  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Keller, C., Mitsuhashi, M. and Akitaya, T.  
TITLE Method for synthesizing cDNA using a polynucleotide immobilized  
JOURNAL Supprot Patent: US 5656462-A 10 12-AUG-1997;  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CCATCTGCTGGCGCC 999  
Db 17 CCATCTGCTGGCGCC 1

RESULT 362  
LOCUS AR401903 17 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 243 from patent US 6623962.  
ACCESSION AR401903  
VERSION AR401903.1 GI:40149353  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Abhtar, S., Fell, P. and McSwiggen, J. A.  
TITLE Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors  
JOURNAL Patent: US 6623962-A 243 23-SEP-2003;  
Sirma Therapeutics, Inc. and Aston University; Boulder, CO  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1313 AGCCAGAGAGAGGCC 1329  
Db 17 AGCAGAGAGAGGCC 1

RESULT 363  
LOCUS AR459079 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 2756 from patent US 6686188.  
ACCESSION AR459079  
VERSION AR459079.1 GI:42694136  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and Shannon, M. E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2756 03-FEB-2004;  
Amerisham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source  
1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1196 GCGACTATGAGGGGCTG 1212  
Db 1 GCGAGTATGAGGAGCTG 17

RESULT 364  
LOCUS AR463997 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 7674 from patent US 6686188.  
ACCESSION AR463997  
VERSION AR463997.1 GI:42699054

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu.Y., Ji.Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 7674 03-FEB-2004;  
Amerisham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1404 CTCGAGCTTCCTCCCA 1420  
17 CTTCTGCTTCTTCCTCCA 1  
Db  
RESULT 365  
AR597772/c AR597772 17 bp RNA linear PAT 15-DEC-2004  
LOCUS Sequence 1714 from patent US 6818447.  
DEFINITION AR597772  
ACCESSION AR597772  
VERSION AR597772.1 GI:56648786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 1714 16-NOV-2004;  
Sirma Therapeutics, Inc.; Boulder, CO  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 714 CTCACCCAGAGACCA 730  
17 CACAACCCAGAGACCA 1  
Db  
RESULT 366  
AR597944/c AR597944 17 bp RNA linear PAT 15-DEC-2004  
LOCUS Sequence 1886 from patent US 6818447.  
DEFINITION AR597944  
ACCESSION AR597944  
VERSION AR597944.1 GI:56648958  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6818447-A 1886 16-NOV-2004;  
Sirma Therapeutics, Inc.; Boulder, CO  
FEATURES  
Location/Qualifiers

source 1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1505 TTCATCTGGAAACCATCA 1521  
17 TTCATCTGGATCCATGA 1  
Db  
RESULT 367  
AX216138 AX216138 17 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 1580 from Patent WO0159103.  
DEFINITION AX216138  
ACCESSION AX216138  
VERSION AX216138.1 GI:15526181  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., McSwigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 1580 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwigen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 545 CCATCGCCGCTGCTTC 561  
1 CCATCCCGCGCTGCTGC 17  
Db  
RESULT 368  
AX216915 AX216915 17 bp RNA linear PAT 07-SEP-2001  
LOCUS Sequence 2357 from Patent WO0159103.  
DEFINITION AX216915  
ACCESSION AX216915  
VERSION AX216915.1 GI:15526976  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt,L., McSwigen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 2357 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwigen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

OY 1003 CACATCTTCTCTCCT 1019  
Db 17 CTCTCTTCTCTCTCT 1

RESULT 369  
LOCUS AX216921 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2363 from Patent WO0159103.  
ACCESSION AX216921  
VERSION AX216921.1 GI:15526982  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Blact, L., Mcswigen, J. and Chowitra, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
PATENT: WO 0159103-A 2363 16-AUG-2001;  
MSWIGEN, JAMES (US) ; CHOWITRA, BHARAT M. (US)  
location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

FEATURES  
source

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1306 GAGGAGAGCCAGAGA 1322  
Db 1 GAGGAGAGAGAGAGGA 17

RESULT 370  
LOCUS AX226878 17 bp RNA linear PAT 10-SEP-2001  
DEFINITION Sequence 250 from Patent WO0157206.  
ACCESSION AX226878  
VERSION AX226878.1 GI:15556019  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Fattaey, A.R., Jarvis, T., Mcswigen, J., Bocher, R.N. and Holman, P.S.  
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk  
1) enzyme  
PATENT: WO 0157206-A 250 09-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)  
location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"

FEATURES  
source

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1369 TCTTCAGAGTGTGCTC 1385  
Db 17 TCTTCAGAGTGTGCTC 1

RESULT 371  
LOCUS AX475125 17 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 346 from Patent WO0224750.  
ACCESSION AX475125  
VERSION AX475125.1 GI:22214410  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Zhang, J.  
TITLE Human kidney tumor overexpressed membrane protein 1  
JOURNAL Patent: WO 0224750-A 346 28-MAR-2002;  
Aeomica, Inc. (US)  
location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1402 AGCTTCAGCTTCTCTC 1418  
Db 1 AGCTTCAGTTCCTCTC 17

RESULT 372  
LOCUS AX502961 17 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 4268 from Patent EP1229046.  
ACCESSION AX502961  
VERSION AX502961.1 GI:2385254  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 4268 07-AUG-2002;  
Aeomica, Inc. (US)  
location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1089 GGCATGAGCTCCACCA 1105  
Db 17 GGCATGAGCTGCCCA 1

RESULT 373  
LOCUS AX531944 17 bp DNA linear PAT 22-NOV-2002  
DEFINITION Sequence 1453 from Patent EP1239051.  
ACCESSION AX531944  
VERSION AX531944.1 GI:25255658  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1453 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1444 CCTTTGCGAGGTGCAGC 1460  
Db 17 CCTTTGCGAGGTCCAGC 1  
RESULT 374  
AX673572 17 bp DNA linear PAT 27-MAR-2003  
LOCUS Sequence 2017 from Patent WO03004526.  
DEFINITION AX673572  
ACCESSION AX673572.1 GI:29331920  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 2017 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1665 GAGCCTGFAAATAAAA 1681  
Db 1 GATCCTTAATAATAAAA 17  
RESULT 375  
AX674304 17 bp DNA linear PAT 27-MAR-2003  
LOCUS Sequence 2749 from Patent WO03004526.  
DEFINITION AX674304  
ACCESSION AX674304.1 GI:29332652  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 2749 16-JAN-2003;  
Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 806 GTGTGACTGTGCTGATC 822  
Db 17 GTGTGCTGTGTCAGATC 1  
RESULT 376  
AX688110 17 bp DNA linear PAT 31-MAR-2003  
LOCUS Sequence 842 from Patent EP1281758.  
DEFINITION AX688110  
ACCESSION AX688110.1 GI:29410808  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
mdz12  
JOURNAL Patent: EP 1281758-A 842 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 429 CCTGACCTTCGCGAGG 445  
Db 1 CTGACCTTCCTCGAGG 17  
RESULT 377  
AX692036 17 bp DNA linear PAT 31-MAR-2003  
LOCUS Sequence 4768 from Patent EP1281758.  
DEFINITION AX692036  
ACCESSION AX692036.1 GI:29414980  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
mdz12  
JOURNAL Patent: EP 1281758-A 4768 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 684 TCTCTGCTGCGCTTCC 700  
| | | | |  
Db 1 TCTTCTCTGCGCTTCC 17

RESULT 378  
AX722337 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 24 from Patent WO03025176.  
DEFINITION AX722337  
ACCESSION AX722337 GI:30422838  
VERSION  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murine; Mus.

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025176-A 24 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1.17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 GATCCCGGGGACTCCT 907  
| | | | |  
Db 1 GATCCCGGGGACTCCT 17

RESULT 379  
AX729053 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 687 from Patent WO03025175.  
DEFINITION AX729053  
ACCESSION AX729053 GI:30508396  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025175-A 687 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 AGAAGTGATCCAGATC 804  
| | | | |  
| | | | |

Db 17 AGAAGTGATCCAGATC 1

RESULT 380  
AX730414 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 2048 from Patent WO03025175.  
DEFINITION AX730414  
ACCESSION AX730414 GI:30509757  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025175-A 2048 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 806 GTGTGACTGTGCTGATC 822  
| | | | |  
Db 17 GTGTGACTGTGCTGATC 1

RESULT 381  
AX738266 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 3856 from Patent WO03025177.  
DEFINITION AX738266  
ACCESSION AX738266 GI:30517554  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 3856 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 806 GTGTGACTGTGCTGATC 822  
| | | | |  
Db 17 GTGTGACTGTGCTGATC 1

RESULT 382  
AX744431

LOCUS AX744431 17 bp DNA linear PAT 14-MAY-2003  
DEFINITION Sequence 396 from Patent WO03031621.  
ACCESSION AX744431  
VERSION AX744431.1 GI:30723098  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Zhang, J.  
TITLE A human G protein coupled receptor  
JOURNAL Patent: WO 03031621-A 396 17-APR-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1536 CTGGGACTGGCAAAAG 1552  
Db 1 CTGGGACTGGCAAAAG 17  
|||||

RESULT 383  
LOCUS AX744432 17 bp DNA linear PAT 14-MAY-2003  
DEFINITION Sequence 397 from Patent WO03031621.  
ACCESSION AX744432  
VERSION AX744432.1 GI:30723099  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Zhang, J.  
TITLE A human G protein coupled receptor  
JOURNAL Patent: WO 03031621-A 397 17-APR-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1537 TGGGACTGGCAAAAG 1553  
Db 1 TGGGACTGGCAAAAG 17  
|||||

RESULT 384  
LOCUS AX745037 17 bp DNA linear PAT 14-MAY-2003  
DEFINITION Sequence 1002 from Patent WO03031621.  
ACCESSION AX745037  
VERSION AX745037.1 GI:30723704  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE  
AUTHORS Homiidae; Homo.  
TITLE A human G protein coupled receptor  
JOURNAL Patent: WO 03031621-A 1002 17-APR-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 455 CTGCATTCAATACATG 471  
Db 1 CTGCATTCAATACATG 17  
|||||

RESULT 385  
LOCUS AX760000 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 3321 from Patent WO03040369.  
ACCESSION AX760000  
VERSION AX760000.1 GI:32254616  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Telerman, A., Anson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 3321 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 375 GATCATCTTAGCCACA 391  
Db 1 GATCATCAAGCCACA 17  
|||||

RESULT 386  
LOCUS AX782045 17 bp DNA linear PAT 17-JUL-2003  
DEFINITION Sequence 376 from Patent WO03050284.  
ACCESSION AX782045  
VERSION AX782045.1 GI:32949894  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Guo, J.  
TITLE Human prostate cancer candidate protein 1  
JOURNAL Patent: WO 03050284-A 376 19-JUN-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
Location/Qualifiers



source 1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 786 TGAGAAAGTGTACGACA 802  
|||||  
1 TGAGAAAGTGTCCACA 17

Db

RESULT 387  
AX783524 17 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Sequence 1855 from Patent WO03050284.  
ACCESSION AX783524  
VERSION AX783524.1 GI:32951373  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Guo,J.  
TITLE Human prostate cancer candidate protein 1  
JOURNML Patent: WO 03050284-A 1855 19-JUN-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
source 1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 987 CTGCTGCTGCTGCTTCC 1003  
|||||  
1 CTGCTGCTGCTCTCTCC 17

Db

RESULT 388  
AX783713 17 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Sequence 2044 from Patent WO03050284.  
ACCESSION AX783713  
VERSION AX783713.1 GI:32951562  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Guo,J.  
TITLE Human prostate cancer candidate protein 1  
JOURNML Patent: WO 03050284-A 2044 19-JUN-2003;  
Amersham Biosciences (SV) Corp. (US)  
FEATURES  
source 1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 255 CTCACATACACCTCCG 271  
|||||  
Db 17 CTCCTCTACACACCG 1

RESULT 389  
ARI09816/c 23 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 240 from patent US 6114139.  
ACCESSION ARI09816  
VERSION ARI09816.1 GI:12826092  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Unknown.  
TITLE 1 (bases 1 to 23)  
JOURNML Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.  
G-protein coupled receptor protein and a DNA encoding the receptor  
Patent: US 6114139-A 240 05-SEP-2000;  
Location/Qualifiers  
1.23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.6; DB 1; Length 23;  
Best Local Similarity 80.0%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1307 AGGAGAGCCAGAGACGCG 1326  
|||||  
Db 23 AGGGGAGCCAGCAGACGCG 4

RESULT 390  
A09447/c 15 bp DNA linear PAT 09-NOV-1993  
LOCUS  
DEFINITION Oligonucleotide (es).  
ACCESSION A09447  
VERSION A09447.1 GI:490550  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Ueda,I., Niwa,M., Satoh,Y., Satoh,S. and Yamada,H.  
TITLE Process for production of somatostatin  
JOURNML Patent: EP 0197558-A 53 15-OCT-1986;  
FUJISAWA PHARMACEUTICAL CO., LTD  
FEATURES  
source 1.15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 759 ATGCCAGAGCATCC 773  
|||||  
Db 15 ATGACGAGAGCATCC 1

RESULT 391  
A10650/c 15 bp DNA linear PAT 02-DEC-1993  
LOCUS  
DEFINITION Oligonucleotide (es).  
ACCESSION A10650  
VERSION A10650.1 GI:490776  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNML  
FEATURES  
source  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

[illegible]

Query Match	0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity	93.3%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches	14; Conservative 0; Mismatches 1;
Oy	759 ATGGCAGAGCATCC 773
Db	15 ATGACGAGCATCC 1
RESULT 394	
LOCUS	AR133675 15 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 2100 from patent US 6194150.
ACCESSION	AR133675
VERSION	AR133675.1 GI:14122580
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Stinchcomb D.T., Jarvis T. and McSwiggen,J.
TITLE	Nucleic acid based inhibition of CD40
JOURNAL	Patent: US 6194150-A 2100 27-FEB-2001;
FEATURES	Location/Qualifiers
source	1..15
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity	93.3%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches	14; Conservative 0; Mismatches 1;
Oy	1409 GCTTCTCCTCCAGT 1423
Db	1 GCTTCTTCCCATG 15
RESULT 395	
LOCUS	AR133676 15 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 2101 from patent US 6194150.
ACCESSION	AR133676
VERSION	AR133676.1 GI:14122581
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Stinchcomb D.T., Jarvis T. and McSwiggen,J.
TITLE	Nucleic acid based inhibition of CD40
JOURNAL	Patent: US 6194150-A 2101 27-FEB-2001;
FEATURES	Location/Qualifiers
source	1..15
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity	93.3%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches	14; Conservative 0; Mismatches 1;
Oy	1411 TTCTCTCCATGTG 1425
Db	1 TTCTTCTCCATGTG 15
RESULT 396	
LOCUS	DD184741 15 bp DNA linear PAT 19-JAN-2006
DEFINITION	Probe sets and methods for identifying HLA-B allele.
ACCESSION	DD184741
VERSION	DD184741.1 GI:85637688
KEYWORDS	UP 2005185172-A/167.
SOURCE	Homo sapiens (human)

RESULT	398
BUILD	BD184657/c
LOCUS	BD184657
DEFINITION	Method and detector for identifying subtypes of human papilloma viruses.
ACCESSION	BD184657.1 GI:31876857
VERSION	BD184657
KEYWORDS	JP 2002360271-A/636.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 16)
TITLE	Huang,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
JOURNAL	Lin,Y.J., Fan,C.C., Heu,H.C., Shih,C.W., Yen,C.H., Kao,Y.F.,
COMMENT	Method and detector for identifying subtypes of human papilloma Patent: JP 2002360271-A 636 17-DEC-2002;
PATENT	KING CAR FOOD INDUSTRIAL CO LTD
OS	Artificial Sequence
PN	JP 2002360271-A/636
PD	17-DEC-2002
PF	28-NOV-2001 JP 2001362595
PR	04-MAY-2001 TW 90110785
PI	CHING-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSIUAN HUANG, BOW-HAENG LEE,
PI	SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHIANG HSU, CHA-MEN SHI,
PI	CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN
PC	C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC
CC	, C12Q1/70, G01N33/574, G01N33/58, G01N37/00//C12M1/34, C12R1.93), G01N33/53, G01N33/574, G01N33/58, G01N37/00//C12M1/34, C12R1.93), PC (C12Q1/70, C12R1.93), C12N15/00, C12N15/00 Oligonucleotide MM71 for identifying HPV MM7. FH Key CC location/Qualifiers
FT	1..16
FT	/Organism='Artificial Sequence'.
FEATURES	
source	location/Qualifiers
	1..16
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
Query Match	0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity	93.3%; Pred. No. 2.5e+02;
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	601 TACATGGCATCATTA 615
Db	16 TACAAGGCATCATTA 2
RESULT	399
BUILD	AX742804/c
LOCUS	AX742804
DEFINITION	Sequence 607 from Patent EP1302550.
ACCESSION	AX742804
VERSION	AX742804
KEYWORDS	AX742804.1 GI:30576793
SOURCE	
ORGANISM	synthetic construct
REFERENCE	synthetic construct
AUTHORS	other sequences; artificial sequences.
TITLE	1
JOURNAL	Liu,C.Y., Liu,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
FEATURES	Lin,Y.J., Fan,C.C., Heu,H.C., Shih,C.W., Yen,C.H., Kao,Y.F.,
source	Pan,C.L., and Chan,P.
	Method and detector for identifying subtypes of human papilloma viruses
	Patent: EP 1302550-A 607 16-APR-2003;
	King Car Food Industrial Co., Ltd. (TW)
	Location/Qualifiers
	1..16
	/organism="synthetic construct"
	/mol_type="genomic DNA"

```
/db_xref="taxon:32630"  
/note="Oligonucleotide for Identifying HPV MM7"
```

Query Match	0.8%	Score 13.4;	DB 1;	length 16;
Best Local Similarity	93.3%;	Pred. No. 2.5e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

```

QY      601 TACATGGCCATCATA 615
        |||||
Db      16 TACAAGGCATCATA 2

```

**RESULT 400**

LOCUS	A35619	15 bp	DNA	linear	PAT 02-DEC-1996
DEFINITION	Synthetic human IFN-alpha 2 gene oligo.				
ACCESSION	A35619				
VERSION	A35619.1	GI:1927001			

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences: artificial sequences.
AUTHORS	1 (bases 1 to 15)
TITLE	Camble,R. and Edge,M.D.
JOURNAL	Analogous interferon polypeptides, process for their preparation
FEATURES	and pharmaceutical compositions containing them
SOURCE	Patent: EP 0194006-A 64 10-SEP-1986;
	IMPERIAL CHEMICAL INDUSTRIES PLC
	location/Qualifiers
	1..15

```

source      1..15
            /organism="synthetic_construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match:      0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 ATCAGTTGTCGCA 290
|||||
db      1 ATCAGTTGTCGCA 13

```

RESULT	401
A35677	
LOCUS	A35677 15 bp DNA linear PAT 02-DEC-1996
DEFINITION	Synthetic human IFN-alpha 2 gene oligo.
ACCESSION	A35677
VERSION	A35677.1 GI:1927059
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 15)
TITLE	Candle,R. and Edge,M.D.
JOURNAL	Analogous interferon polypeptides, process for their preparation and pharmaceutical compositions containing them
FEATURES	Patent: EP 0194006-A 122 10-SEP-1986;
SOURCE	IMPERIAL CHEMICAL INDUSTRIES PLC
	location/Qualifiers
	1..15
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"

Query	March	Similarity	0.7%	Score	13	DB	1	Length	15
Best	Local	Similarity	100.0%	Pred. No.	2.5e+02				
Matches	13	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	278	ATCAGTTCGTGCA	290						
db	1	ATCAGTTCGTGCA	13						

RESULT 402  
AR037371

LOCUS	AR037371	15 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence	16	from patent	US 5801156.	
ACCESSION	AR037371				
VERSION	AR037371.1	GI:5955227			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				

REFERENCE	1 (bases 1 to 15)
AUTHORS	Robinson, G. S. and Smith, L. Elaine, Hodgson,
TITLE	Inhibition of neovascularization using VEGF-specific
JOURNAL	oligonucleotides
FEATURES	Patent: US 5801156-A 16 01-SEP-1998;
SOURCE	Location/Qualifiers
	1..15

QY	1011	CTTCCTCCTGCC	1023
Db	1	CTTCCTCCTGCC	13

## RESULT 403

LOCUS	AR043852	15 bp	DNA	PAT 29-SEP-1999
DEFINITION	Sequence 16 from patent US 5814620.			
ACCESSION	AR043852			
VERSION	AR043852.1	GI:5964860		
KEYWORDS				
SOURCE	Unknown.			

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 15)
TITLE	Robinson,G.S. and Smith,J.Elaine.Hodgson. Inhibition of neovascularization using vegf-specific oligonucleotides
JOURNAL	Patent: US 5814620-A 16 29-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1. .15

Query Match	0.74	Score 13	DB 1	Length 15
Best Local Similarity	100.0%	Pred. No. 2	5e+02	
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1011	CTTCCTCTGCC	1023	
Db	1	CTTCCTCTGCC	13	

FEATURES	RESULT
source	404
Location/Qualifiers	
1. .15	Q0848325

LOCUS	CO848325	15 bp	DNA	
DEFINITION	Sequence 16 from Patent EP1443110.		linear	PAT 19-AUG-2004
ACCESSION	CO848325			
VERSION	CO848325.1	GI:51469826		
KEYWORDS				
SOURCE				
ORGANISM				
	synthetic construct			
	synthetic construct			
	other sequences/ artificial sequences.			

REFERENCE  
1  
AUTHORS Robinson, G.S.  
TITLE Human VEGF-specific antisense oligonucleotides  
JOURNAL Patent: EP 1443110-A 16 04-AUG-2004;

REFERENCE  
1  
AUTHORS Robinson, G.S.  
TITLE Human VEGF-specific antisense oligonucleotides  
JOURNAL Patent: EP 1443110-A 16 04-AUG-2004;

HYBRIDON, INC. (US)  
Location/Qualifiers

FEATURES  
source  
1. .15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:33630"  
/note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match  
0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023  
DB 1 CTTCCTCTGCCC 13

RESULT 405  
LOCUS 147003 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 16 from patent US 5639736.  
ACCESSION 147003  
VERSION 147003.1 GI:2470968  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Robinson,G.S.  
TITLE Human VEGF-specific oligonucleotides  
JOURNAL Patent: US 5639736-A 16 17-JUN-1997;  
FEATURES  
source  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023  
DB 1 CTTCCTCTGCCC 13

RESULT 406  
LOCUS 147651 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 16 from patent US 5639872.  
ACCESSION 147651  
VERSION 147651.1 GI:2471616  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Robinson,G.S.  
TITLE Human VEGF-specific oligonucleotides  
JOURNAL Patent: US 5639872-A 16 17-JUN-1997;  
FEATURES  
source  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023  
DB 1 CTTCCTCTGCCC 13

RESULT 407  
LOCUS 163152 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 16 from patent US 5661135.  
ACCESSION 163152  
VERSION 163152.1 GI:2480860  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Robinson,G.S.  
TITLE Human VEGF-specific oligonucleotides  
JOURNAL Patent: US 5661135-A 16 26-AUG-1997;  
FEATURES  
source  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023  
DB 1 CTTCCTCTGCCC 13

RESULT 408  
LOCUS 181409 15 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 16 from patent US 5710136.  
ACCESSION 181409  
VERSION 181409.1 GI:3209706  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Robinson,G.S. and Smith,L.Elaine,Hodgson.  
TITLE Inhibition of neovascularization using VEGF-specific oligonucleotides  
JOURNAL Patent: US 5710136-A 16 20-JAN-1998;  
FEATURES  
source  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match  
0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CTTCCTCTGCCC 1023  
DB 1 CTTCCTCTGCCC 13

RESULT 409  
LOCUS 193800 15 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 16 from patent US 5731294.  
ACCESSION 193800  
VERSION 193800.1 GI:3938270  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Robinson,G.S. and Hodgson Smith,L.Elaine.  
TITLE Inhibition of neovascularization using VEGF-specific oligonucleotides  
JOURNAL Patent: US 5731294-A 16 24-MAR-1998;

FEATURES  
source  
location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1011 CTTCTCTCTGCC 1023  
1 CTTCTCTCTGCC 13

Db 1 CTTCTCTCTGCC 13

RESULT 410  
LOCUS CQ881957 16 bp DNA linear PAT 11-OCT-2004  
DEFINITION Sequence 9 from Patent WO2004083441.  
ACCESSION CQ881957  
VERSION CQ881957.1 GI:54034727  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Kleinschmidt J., Mueller O., Trepel M., Kaul F. and Leder C.  
Random peptide library displayed on aav vectors  
Patent: WO 2004083441-A 9 30-SEP-2004;  
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts  
(DB); Albert-Ludwigs-Universitaet Freiburg (DB)  
location/Qualifiers  
1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Second strand primer"

Query Match 0.7%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1261 GTCAGCCGCGCTGG 1273  
4 GTCAGCCGCGCTGG 16

Db 4 GTCAGCCGCGCTGG 16

RESULT 411  
LOCUS CQ800306 30 bp DNA linear PAT 28-APR-2004  
DEFINITION Sequence 5 from Patent WO2004030695.  
ACCESSION CQ800306  
VERSION CQ800306.1 GI:46849172  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Gibbins J.M., Lowry P.J., Graham G.J. and Page N.M.  
Treatment of vascular diseases  
Patent: WO 2004030695-A 5 15-APR-2004;  
University of Reading (GB)  
location/Qualifiers  
1..30  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.7%; Score 13; DB 1; Length 30;  
Best Local Similarity 65.5%; Pred. No. 5.9e+02;  
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 11 CACCGCGGCGAGCGGCGAGTGATCCAG 39

Db 1 CCCTGGGGAGAGGCCAGAGAGGCCAG 29

RESULT 412  
LOCUS AR131573 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 66 from patent US 6194149.  
ACCESSION AR131573  
VERSION AR131573.1 GI:14120476  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 16)  
Neri, B., Dong, F., Lyamichev, V., Brow, M., Ann, D. and Fors, L.  
Target-dependent reactions using structure-bridging  
oligonucleotides  
Patent: US 6194149-A 66 27-FEB-2001;  
location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1436 CCACAGGCGCTTGGC 1451  
16 CCACAGGCGCTTGGC 1

Db 16 CCACAGGCGCTTGGC 1

RESULT 413  
LOCUS AX927925 16 bp DNA linear PAT 19-DEC-2003  
DEFINITION Sequence 11 from Patent WO03085110.  
ACCESSION AX927925  
VERSION AX927925.1 GI:40250727  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Thue, C.A., h G.A.M. and Kristjansen P.E.  
Oligomeric compounds for the modulation hlf-1alpha expression  
Patent: WO 03085110-A 11 16-OCT-2003;  
Cureon A/S (DK)  
location/Qualifiers  
1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence:antisense  
oligonucleotide to human HIF-1a"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 73 CAAAAGAGTGCTGCC 88  
1 CAAAAGAGTGCTGCC 16

Db 1 CAAAAGAGTGCTGCC 16

RESULT 414  
LOCUS BD084991/c 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION Target-dependent reactions using structure-bridging  
oligonucleotides.  
ACCESSION BD084991  
VERSION BD084991.1 GI:22630601  
KEYWORDS  
JP 2001523111-A/66.

SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified sequences.  
AUTHORS 1 (bases 1 to 16)  
TITLE DONG, F., LYAMICHEV, V.I., Prudent, J.R., Forc, L., Neri, B.P.,  
Brow, M.A.D., Anderson, T.A. and Dahlberg, J.E.  
JOURNAL Target-dependent reactions using structure-bridging  
oligonucleotides  
Patent: JP 2001523111-A 66 20-NOV-2001;  
THIRD WAVE TECHNOLOGIES INC  
COMMENT OS Unidentified  
PN JP 2001523111-A/66  
PD 20-NOV-2001  
PF 05-MAY-1998 JP 1998548047  
PR 05-MAY-1997 US 08/851588, 19-SEP-1997 US 08/934097 PR  
03-MAR-1998 US 09/034205  
PI FANG DONG, VICTOR I LYAMICHEV, JAMES R PRUDENT, LANCE FORC, BRUCE  
PI P NERI,  
PI MARY ANN D BROW, TODD A ANDERSON, JAMES E DAHLBERG PC  
C07H21/04, C07H21/02, C12Q1/68  
CC Strandedness: Single;  
CC Topology: Linear;  
CC /desc = 'DNA'  
FH Key Location/Qualifiers  
FT source 1..16 Location/Qualifiers  
1..16 /organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451  
DB 16 CCACAGGCGCTTGGC 1

RESULT 415  
BD104692  
LOCUS BD104692 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION Kit and method for determining HLA type.  
ACCESSION BD104692.1 GI:22650266  
VERSION WO 0192572-A/796.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and  
Nishida, M.  
TITLE Kit and method for determining HLA type  
JOURNAL Patent: WO 0192572-A 796 06-DEC-2001;  
NISHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDEOTOSHI INOKO, TAEKO  
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO  
NISHIDA  
COMMENT OS Artificial Sequence  
PN WO 0192572-A/796  
PD 06-DEC-2001  
PF 01-JUN-2001 WO 2001JP004662  
PR 01-JUN-2000 JP 00P 164798  
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI  
MATSUMURA,  
PI SHOGO MORIYA, MICHIO NISHIDA  
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53  
CC Description of Artificial Sequence: capture  
FH Key Location/Qualifiers  
FT source 1..16 Location/Qualifiers  
1..16 /organism='Artificial Sequence'.

FEATURES  
source Location/Qualifiers  
1..16 /organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

SOURCE 1..16  
ORGANISM /organism="synthetic construct"  
REFERENCE /mol\_type="genomic DNA"  
AUTHORS /db\_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 GGGGTGTGTACAGAT 185  
DB 1 GGGGTGTGTACAGAT 16

RESULT 416  
BD104794  
LOCUS BD104794 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION Kit and method for determining HLA type.  
ACCESSION BD104794.1 GI:22650368  
VERSION WO 0192572-A/898.  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and  
Nishida, M.  
TITLE Kit and method for determining HLA type  
JOURNAL Patent: WO 0192572-A 898 06-DEC-2001;  
NISHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDEOTOSHI INOKO, TAEKO  
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO  
NISHIDA  
COMMENT OS Artificial Sequence  
PN WO 0192572-A/898  
PD 06-DEC-2001  
PF 01-JUN-2001 WO 2001JP004662  
PR 01-JUN-2000 JP 00P 164798  
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI  
MATSUMURA,  
PI SHOGO MORIYA, MICHIO NISHIDA  
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53  
CC Description of Artificial Sequence: capture  
FH Key Location/Qualifiers  
FT source 1..16 Location/Qualifiers  
1..16 /organism='Artificial Sequence'.

FEATURES  
source Location/Qualifiers  
1..16 /organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 GGGGTGTGTACAGAT 185  
DB 1 GGGGTGTGTACAGAT 16

RESULT 417  
BD106365  
LOCUS BD106365 16 bp DNA linear PAT 18-SEP-2002  
DEFINITION Novel LDI-receptor.  
ACCESSION BD106365  
VERSION BD106365.1 GI:23201183  
KEYWORDS JP 2002501376-A/380.  
SOURCE Chlamydia sp.  
ORGANISM Chlamydia sp.  
REFERENCE Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H.

TITLE Novel LDL-receptor  
JOURNAL Patent: JP 2002501376-A 380 15-JAN-2002;  
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO  
INC  
COMMENT JP 2002501376-A/380  
PD 15-JAN-2002  
PF 15-APR-1998 JP 1998543635  
PR 15-APR-1997 US 60/043553,05-JUN-1997 US 60/048740 PI  
JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES  
THOMAS CASKEY,ROGER  
PI DAVID COX,  
PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY  
PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,  
PC A61K39/395,  
PC A61K48/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1..16  
/organism="Chlamydia sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:35827"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 13 CCGCGGCGAGCGGCGC 28  
DB 1 CCGCGGCGAGCGGCGC 16

RESULT 418  
BD233314 16 bp DNA linear PAT 17-JUN-2003  
LOCUS BD233314 Method of detecting mutation selected by drug in HIV protease gene.  
ACCESSION BD233314.1 GI:33043084  
VERSION JP 2002518065-A/410.  
KEYWORDS Aids-associated retrovirus  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Stuyver,L.  
TITLE Method of detecting mutation selected by drug in HIV protease gene  
JOURNAL Patent: JP 2002518065-A 410 25-JUN-2002;  
INNOGENETICS NV  
COMMENT OS Aids-associated retrovirus  
PN JP 2002518065-A/410  
PD 25-JUN-2002  
PF 22-JUN-1999 JP 2000556068  
PR 24-JUN-1998 EP 98870143.9  
PI LIEVEN STUYVER  
PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00  
CC Method of detecting mutation selected by drug in HIV protease  
CC gene  
FH Key Location/Qualifiers  
FT source 1..16  
/organism="Aids-associated retrovirus".  
/location/Qualifiers  
1..16  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1586 TGAGTCAAAATCTC 1601  
DB 16 TGAGTCAAAATCTC 1

RESULT 419  
CO808460/c 16 bp DNA linear PAT 10-MAY-2004  
LOCUS CO808460 Sequence 1910 from Patent WO2004035803.  
DEFINITION CO808460  
ACCESSION CO808460  
VERSION CO808460.1 GI:47113854  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Roekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,  
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and  
Marx,A.  
TITLE Method and nucleic acids for the improved treatment of breast cell  
proliferative disorders  
JOURNAL Patent: WO 2004035803-A 1910 29-APR-2004;  
EpiGenomics AG (DE)  
FEATURES  
source 1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for TGB3"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1001 TCCACATCTTCCT 1016  
DB 16 TCCACATCTTCATCT 1

RESULT 420  
CO828744 16 bp DNA linear PAT 05-JUL-2004  
LOCUS CO828744 Sequence 462 from Patent WO2004053120.  
DEFINITION CO828744  
ACCESSION CO828744  
VERSION CO828744.1 GI:49732227  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 462 24-JUN-2004;  
Gruenthal GmbH (DE)  
FEATURES  
source 1..16  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
/note="V\$TH1E47 01"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1534 CACTGGGACTTGCAA 1549  
DB 1 CACTGGGCTCTGGCAA 16

RESULT 421  
CS124427 16 bp DNA linear PAT 21-JUL-2005  
LOCUS CS124427 Sequence 113 from Patent WO2005059172.  
DEFINITION



ACCESSION CS124427  
VERSION CS124427.1 GI:71057582  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1.16  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 640 GCCACAGCCACCAAG 655  
DB 1 GCCACAGCCACCAAG 16

RESULT 422  
LOCUS DD186098 16 bp DNA linear PAT 19-JAN-2006  
DEFINITION Probe sets for detection of HLA-A allele and methods thereof.  
ACCESSION DD186098.1 GI:85641213  
VERSION JP 2005185176-A/498.  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
OS artificial sequence  
PN JP 2005185176-A/498  
PD 14-JUL-2005  
PF 25-DEC-2003 JP 2003430558  
PI mamoru tsukada  
CC probe for detection  
FH Key Location/Qualifiers.  
FEATURES  
source  
1.16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1299 GGGCCACGAGGAG 1314  
DB 1 GGGCCATGAGCGAG 16

RESULT 423  
LOCUS DD188057 16 bp DNA linear PAT 19-JAN-2006  
DEFINITION Probe set and method for identification of allele of HLA.  
ACCESSION DD188057  
VERSION DD188057.1 GI:85645665  
KEYWORDS  
MO 2005063985-A/498.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
OS Homo sapiens  
PN WO 2005063985-A/498  
PD 14-JUL-2005  
PF 24-DEC-2004 WO 2004JP019763  
PR 25-DEC-2003 JP 03P 430556, 25-DEC-2003 JP 03P 430555, PR  
25-DEC-2003 JP 03P 430559, 25-DEC-2003 JP 03P 430553, PR  
25-DEC-2003 JP 03P 430558, 25-DEC-2003 JP 03P 430557, PR  
25-DEC-2003 JP 03P 430554  
PI mamoru tsukada  
CC  
FH Key Location/Qualifiers.  
FEATURES  
source  
1.16  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1299 GGGCCACGAGGAG 1314  
DB 1 GGGCCATGAGCGAG 16

RESULT 424  
LOCUS E39143 16 bp DNA linear PAT 18-JUN-2001  
DEFINITION Improved PCR method for primer elongation pre-amplification.  
ACCESSION E39143  
VERSION E39143.1 GI:13017705  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
OS Artificial Sequence  
PN JP 199318498-A/9  
PD 24-NOV-1999  
PF 26-MAR-1998 JP 1999084967  
PR 26-MAR-1998 DE 19813317.0  
PI URUFUGANKU DIETOMAIYA, JOSEPH RUSSHOFU  
PC C1201/68, C12N15/09, C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source 1.16  
/organism="Artificial Sequence".  
FEATURES  
source  
1.16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1061 AGCAGGTCTACTGCGC 1076

Db 16 ATCAGGTC TACCTGTC 1

RESULT	425				
LOCUS	AR199507/c				
DEFINITION	Sequence 66 from patent US 6355437.	16 bp	DNA	linear	PAT 20-APR-2002
ACCESSION	AR199507				
VERSION	AR199507.1				
KEYWORDS	GI:20249581				
SOURCE	Unknown.				

Query Match	0.7%	Score 12.8	DB 1	length 16
Best Local Similarity	87.5%	Pred. No. 3e+02		
Matches 14	Conservative	0	Mismatches	2
			Indels	0
			Gaps	0

QY 1436 CCACAGGGCCTTGGC 1451  
||| |||  
Db 16 CCACAAGGCTTTCGC 1

RESULT	426			
LOCUS	AR200978/c			
DEFINITION	Sequence 66 From patent US 6358691.	16 bp	DNA	PAT 20-APR-2002
ACCESSION	AR200978			
VERSION	AR200978.1			
KEYWORDS	GI:20251866			
SOURCE	Unknown.			

Query Match	0.7%	Score 12.8	DB 1	Length 16
Best Local Similarity	87.5%	Pred. No. 3e+02		
Matches 14	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

```

QY      1436 CCACAGGCGCTTTGGC 1451
          ||||| ||||| ||
Db      16 CCACAAGGCTTTGCG 1

```

RESULT 427	AR203388/c	16 bp	DNA	linear	PAT 20-JUN-2001
LOCUS	AR203388				
DEFINITION	Sequence 9 from patent US 635575.				
ACCESSION	AR203388				
VERSION	AR203388.1	GI:21499764			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 16)				
	Unclassified.				

**AUTHORS** Dietmaier W. and Ruschoff J.  
**TITLE** Method of primer extension Preamplification PCR  
**JOURNAL** Patent: US 653375-A 9 02-APR-2002;  
**FEATURES** location/Qualifiers  
**Source** 1. 16

Query Match	0.7%;	Score 12.8;	DB 1;	Length 16;
Best Local Similarity	87.5%;	Pred. No. 3e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0;

Qy	1061	AGCAGGCTACCTGGC	1076
Db	16	ATCAGGCTACCTGTC	1

RESULT	428
AR305454	
LOCUS	AR305454
DEFINITION	Sequence 412 from patent US 6545137.
ACCESSION	AR305454
VERSION	AR305454.1 GI:31694764
KEYWORDS	
SOURCE	Unknown.

Query Match	0.7%;	Score 12.8;	DB 1;	length 16;
Best Local Similarity	87.5%;	Pred. No. 3e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0

Qy	13	CCGCGGCGAGCGGGC	28
Db	1	CCGCGGCTAGGTGGCC	16

RESULT 429	AR309558	LOCUS	AR309558	16 bp	DNA	linear	PAT 12-JUN-2001
DEFINITION	Sequence	412	from patent	US 6555654.			
ACCESSION	AR309558						
VERSION	AR309558.1			GI:31701563			

**JOURNAL**  
Patent: US 6555654-A 412 29-APR-2003;  
The Wellcome Trust Limited as Trustee for the Wellcome Trust,  
London;  
WOX;

Query Match	0.7%;	Score 12.8;	DB 1;	Length 16
Best Local Similarity	87.5%;	Pred. No. 3e+02;		

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCGCGGCGAGCGCGGC 28  
|||||  
Db 1 CCGCGGCGTGGTGGGC 16

RESULT 430  
AR328448/c 16 bp RNA linear PAT 17-AUG-2003  
LOCUS Sequence 5850 from patent US 6566127.  
ACCESSION AR328448  
VERSION AR328448.1 GI:33714256  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Payco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5850 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1594 AAAATCTCAATCTTC 1609  
|||||  
Db 16 AAAATCACAATCTTC 1

RESULT 431  
AR328461 16 bp RNA linear PAT 17-AUG-2003  
LOCUS Sequence 5863 from patent US 6566127.  
ACCESSION AR328461  
VERSION AR328461.1 GI:33714269  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Payco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5863 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 ACAAAAGATGAGAC 404  
|||||  
Db 1 ACAATGATGAGAC 16

RESULT 432  
AR435791/c 16 bp RNA linear PAT 18-DEC-2003  
LOCUS Sequence 50 from patent US 6656731.  
ACCESSION AR435791  
VERSION AR435791.1 GI:40198875

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.  
TITLE Nucleic acid catalysts with endonuclease activity  
JOURNAL Patent: US 6656731-A 50 02-DEC-2003;  
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and  
Sirta Therapeutics; Munich;  
DEX;  
FEATURES  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 527 AGTTCCACAACTTCTT 542  
|||||  
Db 16 AATTCATACTTCTT 1

RESULT 433  
AR488737/c 16 bp DNA linear PAT 15-MAY-2004  
LOCUS Sequence 66 from patent US 6709815.  
ACCESSION AR488737  
VERSION AR488737.1 GI:47254935  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Dong, F., Lyamichov, V.I., Prudent, J.R., Fors, L., Neri, B.P.,  
Brow, M.A.D., Anderson, T.A. and Dahlberg, J.E.  
TITLE Target-dependent reactions using structure-bridging  
oligonucleotides  
JOURNAL Patent: US 6709815-A 66 23-MAR-2004;  
Third Wave Technologies, Inc.; Madison, WI  
FEATURES  
source 1..16  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451  
|||||  
Db 16 CCACAGGCGCTTGGC 1

RESULT 434  
AR589824/c 16 bp DNA linear PAT 15-DEC-2004  
LOCUS Sequence 410 from patent US 6803187.  
ACCESSION AR589824  
VERSION AR589824.1 GI:56637132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Stuyver, L.  
TITLE Method for detection of drug-selected mutations in the HIV protease  
gene  
JOURNAL Patent: US 6803187-A 410 12-OCT-2004;  
Imogenetics N.V.; Ghent;  
EPX;

FEATURES  
source  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 TGAGTCAAAAATCTC 1601  
16 TGAGTCACAAATTC 1

Db 16 TGAGTCACAAATTC 1

RESULT 435  
AX007868/c 16 bp DNA linear PAT 06-SEP-2000

LOCUS AX007868  
DEFINITION Sequence 410 from Patent WO967428.  
ACCESSION AX007868  
VERSION AX007868.1 GI:9995565

KEYWORDS  
Aids-associated retrovirus  
Aids-associated retrovirus  
viruses; Retro-transcribing viruses; Retroviridae.

REFERENCE  
1 Stuyver, L.  
Method for detection of drug-selected mutations in the hiv protease gene  
Patent: WO 9967428-A 410 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)

JOURNAL  
Location/Qualifiers  
1..16  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

FEATURES  
source

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 TGAGTCAAAAATCTC 1601  
16 TGAGTCACAAATTC 1

Db 16 TGAGTCACAAATTC 1

RESULT 436  
AX011286/c 16 bp DNA linear PAT 06-SEP-2000

LOCUS AX011286  
DEFINITION Sequence 9 from Patent EP0957177.  
ACCESSION AX011286  
VERSION AX011286.1 GI:9997837

KEYWORDS  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Dietmaier, W.D. and Rueschoff, J.P.  
Improved method for primer extension preamplification-per  
Patent: EP 0957177-A 9 17-NOV-1999;  
ROCHE DIAGNOSTICS GMBH (DE)

JOURNAL  
Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1061 AGCAGGTCTACTGCG 1076

Db 16 ATCAGGTCTACTGCTC 1

RESULT 437  
AX419729/c 16 bp DNA linear PAT 18-JUN-2002

LOCUS AX419729  
DEFINITION Sequence 66 from Patent WO0198537.  
ACCESSION AX419729  
VERSION AX419729.1 GI:21524096

KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Lyamichev, V., Allawi, H., Dong, F., Neri, B. P. and Vener, I. T.  
Nucleic acid accessible hybridization sites  
Patent: WO 0198537-A 66 27-DEC-2001;  
THIRD WAVE TECHNOLOGIES, INC. (US)

JOURNAL  
Location/Qualifiers  
1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

FEATURES  
source

Query Match 0.7%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1436 CCACAGGCGCTTGGC 1451  
16 CCACAGGCGCTTGGC 1

Db 16 CCACAGGCGCTTGGC 1

RESULT 438  
I17159 20 bp DNA linear PAT 03-APR-1996

LOCUS I17159  
DEFINITION Sequence 14 from patent US 5484886.  
ACCESSION I17159  
VERSION I17159.1 GI:1252067

KEYWORDS  
Unknown.  
Unknown.

SOURCE  
Unknown.

ORGANISM  
Unclassified.

REFERENCE  
1 (bases 1 to 20)  
Fong, T.M. and Strader, C.D.  
Human neurokinin-1 receptor  
Patent: US 5484886-A 14 16-JAN-1996;  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

FEATURES  
source

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.7e+02; 4; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 861 CGTAGTGGAAATCACCTA 879  
1 CATAGTGTATTCACCTA 19

Db 1 CATAGTGTATTCACCTA 19

RESULT 439  
AX468711 20 bp DNA linear PAT 16-JUL-2002

LOCUS AX468711  
DEFINITION Sequence 27 from Patent WO0213799.  
ACCESSION AX468711  
VERSION AX468711.1 GI:21901481

KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

SOURCE  
synthetic construct

ORGANISM  
other sequences; artificial sequences.

REFERENCE  
1

AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 27 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source  
1. 20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 861 CCTAGTGGGATCCACTA 879  
Db 1 CATAGTGTGATCCCACTA 19

RESULT 440  
AX468730 20 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 46 from Patent WO0213799.  
DEFINITION AX468730  
ACCESSION AX468730  
VERSION AX468730.1 GI:21901500  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Henry, J.L., Cahill, C.M. and Yashpal, K.  
TITLE Oligonucleotides and other modulators of the nk-1 receptor pathway  
JOURNAL Patent: WO 0213799-A 46 21-FEB-2002;  
McGILL UNIVERSITY (CA)  
FEATURES  
source  
1. 20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.7%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.7e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 861 CGTAGTGGGATCCACTA 879  
Db 20 CATAGTGTGATCCCACTA 2

RESULT 441  
A06948 14 bp DNA linear PAT 14-OCT-1993  
LOCUS Nucleotide sequence 6 from patent number EP0246864.  
DEFINITION A06948  
ACCESSION A06948  
VERSION A06948.1 GI:489034  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 14)

REFERENCE  
AUTHORS Carr, P.J.  
TITLE Hybridisation probes  
JOURNAL Patent: EP 0246864-A 6 25-NOV-1987;  
IMPERIAL CHEMICAL INDUSTRIES PLC  
FEATURES  
source  
1. 14  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1752 GCTCATTTCAGGAT 1765  
Db 14 GCTCATTTCAGGAT 1

RESULT 442  
A89425 14 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 1573 from Patent WO9833904.  
DEFINITION A89425  
ACCESSION A89425  
VERSION A89425.1 GI:6737995  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified  
unidentified  
unclassified sequences.

REFERENCE  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1573 06-AUG-1998;  
BIOGENSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source  
1. 14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1145 TCCGCTGGGCTTC 1158  
Db 1 TCCGCTGGGCTTC 14

RESULT 443  
AR027912 14 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1 from patent US 5858351.  
DEFINITION AR027912  
ACCESSION AR027912  
VERSION AR027912.1 GI:5939885  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
1 (bases 1 to 14)

REFERENCE  
AUTHORS Podsakoff, G.M., Kessler, P.D., Byrne, B.J. and Kurtzman, G.J.  
TITLE Methods for delivering DNA to muscle cells using recombinant  
JOURNAL Patent: US 5858351-A 1 12-JAN-1999;  
FEATURES  
source  
1. 14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 444  
AR063256 14 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 2 from patent US 5846528.  
DEFINITION

ACCESSION AR063256  
VERSION AR063256.1 GI:5992564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Podsakoff,G.M., and Kurtzman,G.J.  
TITLE Treating anemia using recombinant adeno-associated virus virions  
JOURNAL Patent: US 5846528-A 2 08-DEC-1998;  
FEATURES  
source 1.14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 445  
LOCUS AR073886 14 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 1 from patent US 5952221.  
ACCESSION AR073886  
VERSION AR073886.1 GI:10000646  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kurtzman,G.J., Colosi,P.C., Yoshida,J., Mizuno,M. and Okada,H.  
TITLE Adeno-associated virus vectors comprising a first and second  
nucleic acid sequence  
JOURNAL Patent: US 5952221-A 1 14-SEP-1999;  
FEATURES  
source 1.14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 446  
LOCUS AR078208 14 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 1 from patent US 5962313.  
ACCESSION AR078208  
VERSION AR078208.1 GI:10004954  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Podsakoff,G.M., Keesler,P.D., Byrne,B.J. and Kurtzman,G.J.  
TITLE Adeno-associated virus vectors comprising a gene encoding a  
lysosomal enzyme  
JOURNAL Patent: US 5962313-A 1 05-OCT-1999;  
FEATURES  
source 1.14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 447  
LOCUS AR095650 14 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 1 from patent US 6004797.  
ACCESSION AR095650  
VERSION AR095650.1 GI:10023714  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Colosi,P.C.  
TITLE Adenovirus helper-free recombinant AAV virion production  
JOURNAL Patent: US 6004797-A 1 21-DEC-1999;  
FEATURES  
source 1.14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 448  
LOCUS AR118998 14 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 124 from patent US 6150092.  
ACCESSION AR118998  
VERSION AR118998.1 GI:14100908  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.  
TITLE Antisense nucleic acid compound targeted to VEGF  
JOURNAL Patent: US 6150092-A 124 21-NOV-2000;  
FEATURES  
source 1.14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 468 AGTGTGAAGTCTCA 481  
Db 14 AGTGTGAAGTCTCA 1

RESULT 449  
LOCUS AR145148 14 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6211163.  
ACCESSION AR145148  
VERSION AR145148.1 GI:15107015  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Podsakoff,G.M., Kessler,P.D., Byrne,B.J. and Kurtzman,G.J.  
TITLE Methods for delivering DNA to the bloodstream using recombinant  
JOURNAL Patent: US 6211163-A 1 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 450  
LOCUS ARI48600 14 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 17 from patent US 6225291.  
ACCESSION ARI48600  
VERSION ARI48600.1 GI:15112690  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Lewin,A.S., Hauswirth,W.W. and Drenser,K.  
TITLE Rod opsin mRNA-specific ribozyme compositions and methods for the  
JOURNAL Patent: US 6225291-A 17 01-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388  
Db 14 CGAAGTACTCCGA 1

RESULT 451  
LOCUS ARI79014 14 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2 from patent US 6325998.  
ACCESSION ARI79014  
VERSION ARI79014.1 GI:20220569  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Podsakoff,G.M. and Kurtzman,G.J.  
TITLE Methods of treating disease using recombinant adeno-associated  
JOURNAL Patent: US 6325998-A 2 04-DEC-2001;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 452  
LOCUS AX934402 14 bp DNA linear PAT 05-JAN-2004  
DEFINITION Sequence 5 from Patent EP1359223.  
ACCESSION AX934402  
VERSION AX934402.1 GI:40641665  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Natsoolis,G.  
TITLE Recombinant AAV preparation substantially free of wt aav virus  
JOURNAL Patent: EP 1359223-A 5 05-NOV-2003;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTGCA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 453  
LOCUS BD064896 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting the extent of binding of transcriptional  
ACCESSION BD064896  
VERSION BD064896.1 GI:22610499  
KEYWORDS JP 2001275678-A/108.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and  
TITLE Nishikawa,K.  
JOURNAL Method for detecting the extent of binding of transcriptional  
COMMENT regulatory protein to oligodNA  
PATENT: JP 2001275678-A 108 09-OCT-2001;  
SUMITOMO ELECTRIC INDUSTRIES LTD  
OS Artificial Sequence  
PN JP 2001275678-A/108  
PD 09-OCT-2001  
PF 31-MAR-2000 JP 2000096306  
PI TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI  
MIMAKI,REI FUKUSHIMA,  
PI KAZUOKO NISHIKAWA,  
PC C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC  
SYNTHETIC DNA  
FT Key source Location/Qualifiers  
FT source 1..14  
/organism="Artificial Sequence".  
FEATURES Location/Qualifiers  
source 1..14  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1491 GCATGGAATTC 1504  
14 GCACGGAATTC 1

Db

RESULT 454  
BD066938 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066938  
VERSION BD066938.1 GI:22612541  
KEYWORDS JP 2001511000-A/1573.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
AUTHORS 1 (bases 1 to 14)  
TITLE Schlingensiepen, K.H. and Brysch, W.  
JOURNAL An antisense oligonucleotide preparation method  
PATENT: JP 2001511000-A 1573 07-AUG-2001;  
BIOLOGISTIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/1573  
PD 07-AUG-2001  
PR 30-JAN-1998 JP 1998532533  
PI 31-JAN-1997 EP 97101531.8  
PC KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH  
PC C12N15/11, C07H21/04, A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
Location/Qualifiers  
FT source 1. .14  
/organism='Unknown'.  
1. .14  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

FEATURES  
source  
1. .14  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1145 TCCGCTGGGCTTC 1158  
1 TCCCTCTGGGCTTC 14

Db

RESULT 455  
BD082683/c 14 bp RNA linear PAT 27-AUG-2002  
LOCUS BD082683  
DEFINITION Material and method for ribozyme treatment of disease.  
ACCESSION BD082683  
VERSION BD082683.1 GI:22628293  
KEYWORDS JP 2001523959-A/17.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
1 (bases 1 to 14)  
REFERENCE Lewin, A.S., Hauswirth, W.W. and Dresner, K.  
AUTHORS Material and method for ribozyme treatment of disease  
JOURNAL Patent: JP 2001523959-A 17 27-NOV-2001;  
UNIVERSITY OF FLORIDA  
OS Artificial Sequence  
PN JP 2001523959-A/17  
PD 27-NOV-2001  
PR 21-APR-1998 JP 1998546254  
PI 21-APR-1997 US 60/044492, 09-MAY-1997 US 60/046147  
ALFRED S LEWIN, WILLIAM W HAUWSWIRTH, KIMBERLY DRENSER  
C12N15/11, C12N9/00, A61K31/70, C12N15/86  
CC Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

FEATURES FH Key Location/Qualifiers.  
source  
1. .14  
/organism='synthetic construct'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1375 CGAAGTACTCCAA 1388  
14 CGAAGTACTCCGA 1

Db

RESULT 456  
BD209328 14 bp RNA linear PAT 17-JUL-2003  
LOCUS BD209328  
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
ACCESSION BD209328  
VERSION BD209328.1 GI:33019098  
KEYWORDS JP 2002512791-A/2918.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
AUTHORS 1 (bases 1 to 14)  
TITLE Blatt, L., Mewsigen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.  
JOURNAL Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
PATENT: JP 2002512791-A 2918 08-MAY-2002;  
RIBOZYME PHARMACEUTICALS INC  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/2918  
PD 08-MAY-2002  
PR 26-APR-1999 JP 2000545991  
PI 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842  
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553  
LAWRENCE BLATT, JAMES A MCSWIGEN, ELISABETH ROBERTS, PAMELA A PAVCO,  
PI DENNIS MACEJAK  
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions CC  
related to  
CC hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1. .14  
/organism='Hepatitis virus (hepatitis C virus)'.  
1. .14  
/organism='unidentified'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32644'

FEATURES  
source  
1. .14  
/organism='unidentified'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32644'

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 685 CTCCTGCTGGCCTT 698  
1 CTCCTGCTGGCCTT 14

Db

RESULT 457  
BD235049 14 bp DNA linear PAT 17-JUL-2003  
LOCUS BD235049  
DEFINITION A method for stimulating the immune system.  
ACCESSION BD235049  
VERSION BD235049.1 GI:33044819



KEYWORDS JP 2002517434-A/153.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 14)  
Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.  
REFERENCE  
AUTHORS  
TITLE A method for stimulating the immune system  
JOURNAL Patent: JP 2002517434-A 153 18-JUN-2002;  
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/153  
PD 18-JUN-2002  
PP 10-JUN-1998 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI  
BRYSCH  
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/  
PC 00, A61P35/00  
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A  
method for stimulating the immune system  
FH Key Location/Qualifiers  
FT source 1..14  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source  
1..14  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1008 CTCTCTCCTCCTGC 1021  
DB 1 CTCCTCTCCTCCTGC 14  
RESULT 458  
LOCUS CS062891 14 bp DNA linear PAT 19-APR-2005  
DEFINITION Sequence 1 from Patent EP1522588.  
ACCESSION CS062891  
VERSION CS062891.1 GI:62750877  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1  
AUTHORS Colosi, P.C.  
TITLE Accessory functions for use in recombinant AAV virion production  
JOURNAL Patent: EP 1522588-A 1 13-APR-2005;  
Avigen, Inc. (US)  
FEATURES  
source  
1..14  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 315 GGCAGCTGCCTACA 328  
DB 1 GGCAGCTGCCTGCA 14  
RESULT 459  
LOCUS CS123773 14 bp DNA linear PAT 16-JUL-2005

DEFINITION Sequence 124 from Patent WO2005059133.  
ACCESSION CS123773  
VERSION CS123773.1 GI:70912266  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..14  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: human VEGF antisense oligonucleotide"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1008 CTCTCTCCTCCTGC 1021  
DB 1 CTCCTCTCCTCCTGC 14  
RESULT 460  
LOCUS AR181054 14 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1 from patent US 6335011.  
ACCESSION AR181054  
VERSION AR181054.1 GI:20223268  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Podaskoff, G.M., Kessler, P.D., Byrne, B.J. and Kurtzman, G.J.  
TITLE Methods for delivering DNA to muscle cells using recombinant adeno-associated virus virions to treat lysosomal storage disease  
JOURNAL Patent: US 6335011-A 1 01-JAN-2002;  
FEATURES  
source  
1..14  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 315 GGCAGCTGCCTACA 328  
DB 1 GGCAGCTGCCTGCA 14  
RESULT 461  
LOCUS AR255917 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 1 from patent US 6482633.  
ACCESSION AR255917  
VERSION AR255917.1 GI:27305176  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Colosi, P.C.  
TITLE Accessory functions for use in recombinant AAV virion production  
JOURNAL Patent: US 6482633-A 1 19-NOV-2002;

Avigen, Inc.; Alameda, CA  
FEATURES  
source  
1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 462  
AR381782 14 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 1 from patent US 6610290.  
DEFINITION AR381782  
ACCESSION AR381782.1 GI:4009043  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Unkown.  
Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Podsakoff,G.M., Kessler,P.D., Byrne,B.J. and Kurtzman,G.J.  
TITLE Adeno associated virus vectors for the treatment of a  
cardiomyopathy  
JOURNAL Patent: US 6610290-A 1 26-AUG-2003;  
Avigen, Inc. and Johns Hopkins University; Alameda, CA  
FEATURES  
source  
1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 463  
AR407913 14 bp RNA linear PAT 18-DEC-2003  
LOCUS Sequence 6 from patent US 6632057.  
DEFINITION AR407913  
ACCESSION AR407913  
VERSION AR407913.1 GI:40157900  
KEYWORDS  
SOURCE  
ORGANISM  
Unkown.  
Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Faucher,C.R.J.  
TITLE Fixing unit with an end imprint in a threaded terminal portion  
JOURNAL Patent: US 6632057-A 6 14-OCT-2003;  
GPI Aerospace; Paris;  
FRX;  
FEATURES  
source  
1. .14  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 689 TGCTGCGCTTCCCC 702  
Db 1 TGCTGCTTCCCC 14

AR658576 14 bp DNA linear PAT 13-JUN-2005  
LOCUS Sequence 1 from patent US 6897063.  
DEFINITION AR658576  
ACCESSION AR658576  
VERSION AR658576.1 GI:67593355  
KEYWORDS  
SOURCE  
ORGANISM  
Unkown.  
Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Colosi,P.C.  
TITLE Accessory functions for use in recombinant AAV virion production  
JOURNAL Patent: US 6897063-A 1 24-MAY-2005;  
Avigen, Inc.; Alameda, CA  
FEATURES  
source  
1. .14  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 315 GGCAGCTGCCTACA 328  
Db 1 GGCAGCTGCCTGCA 14

RESULT 465  
AR775644 14 bp DNA linear PAT 08-DEC-2005  
LOCUS Sequence 1573 from patent US 6972171.  
DEFINITION AR775644  
ACCESSION AR775644  
VERSION AR775644.1 GI:83352908  
KEYWORDS  
SOURCE  
ORGANISM  
Unkown.  
Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingsensiepen,K.-H. and Brysch,W.  
TITLE Antisense oligonucleotide preparation method  
JOURNAL Patent: US 6972171-A 1573 06-DEC-2005;  
Biagnostik Ges. fur Biomolekulare Diagnostik mbH; Gottingen;  
EPX;  
FEATURES  
source  
1. .14  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1145 TCCGCTCGGGCTTC 1158  
Db 1 TCCCTCGGGCTTC 14

RESULT 466  
AX009120 14 bp DNA linear PAT 06-SEP-2000  
LOCUS Sequence 153 from patent WO9963975.  
DEFINITION AX009120  
ACCESSION AX009120  
VERSION AX009120.1 GI:9936494  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,K.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: WO 9963975-A 153 16-DEC-1999;  
BIOGOSTRIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL  
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
FEATURES  
source 1.14  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1008 CTTCTTCTCTCTGC 1021  
Db 1 CTCCTTCTCTCTGC 14  
RESULT 467  
A88048/c A88048 15 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 196 from Patent WO9833904.  
DEFINITION A88048  
ACCESSION A88048.1 GI:6736618  
VERSION A88048.1 GI:6736618  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 196 06-AUG-1998;  
BIOGOSTRIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
source 1.15  
/organism="unassigned DNA"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 936 CAAGCCGACAGTGG 949  
Db 14 CAAGCCGACAGTGG 1  
RESULT 468  
A90015/c A90015 15 bp DNA linear PAT 22-JAN-2000  
LOCUS Sequence 196 from Patent EP0856579.  
DEFINITION A90015  
ACCESSION A90015  
VERSION A90015.1 GI:6738529  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 196 05-AUG-1998;  
BIOGOSTRIK GES (DE)  
FEATURES  
source 1.15  
/organism="unassigned DNA"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 936 CAAGCCGACAGTGG 949  
Db 14 CAAGCCGACAGTGG 1  
RESULT 469  
AR086102/c AR086102 15 bp DNA linear PAT 07-SEP-2000  
LOCUS Sequence 13 from patent US 5985554.  
DEFINITION AR086102  
ACCESSION AR086102  
VERSION AR086102.1 GI:10012868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Tanimura,H. and Hosoya,M.  
TITLE Method of probing the function of proteins or peptides encoded by  
JOURNAL partially sequenced cDNAs by inhibiting protein synthesis with  
antense oligonucleotides  
Patent: US 5985554-A 13 16-NOV-1999;  
FEATURES  
source 1.15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 910 GACCGTACCACGA 923  
Db 14 GACCGTACCACGA 1  
RESULT 470  
AR126545/c AR126545 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 2 from patent US 6180347.  
DEFINITION AR126545  
ACCESSION AR126545  
VERSION AR126545.1 GI:14113138  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Iida,Y., Koshimoto,H., Kondo,S. and Tsuji,A.  
TITLE Method for monitoring transcriptional synthesis of RNA  
JOURNAL Patent: US 6180347-A 2 30-JAN-2001;  
FEATURES  
source 1.15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1155 CTTCAAGCATGCCT 1168  
Db 14 CTTCAAGCATGCCT 1  
RESULT 471  
AR13372/c AR13372 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 797 from patent US 6194150.  
DEFINITION AR13372  
ACCESSION AR13372  
VERSION AR13372.1 GI:14121277  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 797 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CCTGGCAAAATTGTC 309  
Db 15 CCTGGCAAAATTGTC 2

RESULT 472  
ARI32373/c 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 798 from patent US 6194150.  
DEFINITION ARI32373  
ACCESSION ARI32373  
VERSION ARI32373.1 GI:14121278  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 798 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 296 CCTGGCAAAATTGTC 309  
Db 14 CCTGGCAAAATTGTC 1

RESULT 473  
ARI33674 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 2099 from patent US 6194150.  
DEFINITION ARI33674  
ACCESSION ARI33674  
VERSION ARI33674.1 GI:14122579  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 2099 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422

Db 2 GCTTCTCTCCCAAT 15

RESULT 474  
ARI33870 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 2295 from patent US 6194150.  
DEFINITION ARI33870  
ACCESSION ARI33870  
VERSION ARI33870.1 GI:14122775  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 2295 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422  
Db 2 GCTTCTCTCCCAAT 15

RESULT 475  
ARI33871 15 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 2296 from patent US 6194150.  
DEFINITION ARI33871  
ACCESSION ARI33871  
VERSION ARI33871.1 GI:14122776  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 2296 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 GCTTCTCTCCCAAT 1422  
Db 1 GCTTCTCTCCCAAT 14

RESULT 476  
BD065561/c 15 bp DNA linear PAT 27-AUG-2002  
LOCUS An antisense oligonucleotide preparation method.  
DEFINITION BD065561  
ACCESSION BD065561  
VERSION BD065561.1 GI:22611164  
KEYWORDS JP 2001511000-A/196.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Schlingensiefen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: JP 2001511000-A 196 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/196  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH  
PC C12N15/11, C07H21/04, A61K31/70  
CC An antisense oligonucleotide preparation method FH Key

FEATURES FT source  
1. .15  
Location/Qualifiers /organism='Unknown'

source 1. .15  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 936 CAAGCCAGAGTGG 949  
Db 14 CAAGCCAGAGTGG 1

RESULT 477  
LOCUS CQ875812/c 15 bp DNA linear PAT 04-OCT-2004  
DEFINITION Sequence 6 from Patent EP1462527.  
ACCESSION CQ875812  
VERSION CQ875812.1 GI:53789557  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Costello, C., Ma, N., Schreiber, S. and Seeger, D.  
TITLE Novel markers for inflammatory bowel disease  
JOURNAL Patent: EP 1462527-A 6 29-SEP-2004;  
CONARIS research institute AG (DE)  
Location/Qualifiers

FEATURES source  
1. .15  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 134 GCCCGAGCGCCAG 147  
Db 14 GCCCGAGCGCCAG 1

RESULT 478  
LOCUS CQ889695/c 15 bp DNA linear PAT 19-OCT-2004  
DEFINITION Sequence 6 from Patent WO2004085677.  
ACCESSION CQ889695  
VERSION CQ889695.1 GI:54305544  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Costello, C., Ma, N., Schreiber, S. and Seeger, D.  
TITLE Novel markers for inflammatory bowel disease  
JOURNAL Patent: WO 2004085677-A 6 07-OCT-2004;  
CONARIS research institute AG (DE)

FEATURES Location/Qualifiers  
source 1. .15  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'  
/note='Primer'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 134 GCCCGAGCGCCAG 147  
Db 14 GCCCGAGCGCCAG 1

RESULT 479  
LOCUS CS052672 15 bp DNA linear PAT 23-MAR-2005  
DEFINITION Sequence 13 from Patent WO2005021796.  
ACCESSION CS052672  
VERSION CS052672.1 GI:61891467  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Aerssens, J., Athanasiou, M., Brain, C., Cohen, N., Dain, B., Denton, R.R., Judson, R.S., Ozdemir, V. and Reed, C.R.  
TITLE Chn2 genetic markers associated with galantamine response  
JOURNAL Patent: WO 2005021796-A 13 10-MAR-2005;  
Genaisance Pharmaceuticals, Inc. (US)  
Location/Qualifiers

FEATURES source  
1. .15  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'  
/note='ASO Reverse Primer for Detecting Alleles at P58 in Haplotypes Comprising Preferred Embodiments of Response Markers I and Response Markers II'

misc\_feature 14  
/note='r is 'g' or 'a''

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 671 TCTGGTCTCTGCT 684  
Db 2 TCTGGTCTCTGCT 15

RESULT 480  
LOCUS CS125878 15 bp DNA linear PAT 21-JUL-2005  
DEFINITION Sequence 22 from Patent WO2005061545.  
ACCESSION CS125878  
VERSION CS125878.1 GI:71058918  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1  
AUTHORS Husain, I.  
TITLE Nogo antibodies for the treatment of alzheimer disease  
JOURNAL Patent: WO 2005061545-A 22 07-JUL-2005;  
Glaxo Group Limited (GB)  
Location/Qualifiers

FEATURES source  
1. .15  
/organism='Mus musculus'  
/mol\_type='unassigned DNA'

```
/db_xref="taxon:10090"
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
|||||
15 GTGCATCCAGTAGC 2

RESULT 481
CS126163/c 15 bp DNA linear PAT 21-JUL-2005
DEFINITION Sequence 22 from Patent WO2005061544.
ACCESSION CS126163
VERSION CS126163.1 GI:71059142
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 Ellis, J.H.
TITLE Nogo-a neutralising immunoglobulins for treatment of neurological
diseases
PATENT: WO 2005061544-A 22 07-JUL-2005;
JOURNAL Glaxo Group Limited (GB)
FEATURES
source 1. .15
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 GTGCATCCAGAGC 43
|||||
15 GTGCATCCAGTAGC 2

RESULT 482
CS249550 15 bp DNA linear PAT 18-JAN-2006
LOCUS CS249550
DEFINITION Sequence 37 from Patent WO2005121359.
ACCESSION CS249550
VERSION CS249550.1 GI:85361754
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hinmah, S.C.
TITLE A method for detecting analytes in a sample
JOURNAL Patent: WO 2005121359-A 37 22-DEC-2005;
FEATURES
source Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: FRET quencher
oligonucleotide for the detection of c-fos mRNA"
```

```
Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1449 GGCAGGTGCGAGCC 1462
|||||
```

```
Db 1 GGCTGTGTCAGCCC 14

RESULT 483
E11984/c 15 bp DNA linear PAT 29-SEP-1997
LOCUS E11984
DEFINITION Oligonucleotide.
ACCESSION E11984
VERSION E11984.1 GI:22025605
KEYWORDS JP 1996228798-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Tanimura, H. and Hosoya, M.
TITLE ELUCIDATION OF FUNCTION OF PROTEIN
JOURNAL Patent: JP 1996228798-A 13 10-SEP-1996;
COMMENT TAKEDA CHEM IND LTD
OS None
OC Artificial sequences.
FN JP 1996228798-A/13
PD 10-SEP-1996
PF 01-NOV-1995 JP 1995306423
PR 02-NOV-1994 JP 94P 269417
PI TANIMURA HIROSHI, HOSoya MASARI
PC C1201/68, C07H21/04, C12N15/09//C1201/02;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
FH Key
FT source 1. .15
Location/Qualifiers
1. .15
/organism="Artificial sequences".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 GACCGTACCACGA 923
|||||
14 GACCGTACCACGA 1

RESULT 484
E31959/c 15 bp DNA linear PAT 18-JUN-2001
LOCUS E31959
DEFINITION Method for assaying biological activity of drug, method for
screening the same and automatic screening device.
ACCESSION E31959
VERSION E31959.1 GI:13021575
KEYWORDS JP 2000041700-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Yukari, I., Satoshi, A. and Yoshiaki, Y.
TITLE Method for assaying biological activity of drug, method for
screening the same and automatic screening device
JOURNAL Patent: JP 2000041700-A 2 15-FEB-2000;
COMMENT BUNSHI BIO HOTONIKUSU KENKUTSHO
OS Artificial Sequence
FN JP 2000041700-A/2
PD 15-FEB-2000
PR 31-JUL-1998 JP 1998218025
PI YUKARI IDA, SATOSHI ABE, YOSHIKI YAMADA
PC C1201/68, G01N21/78//C12N15/09, C12N15/00
CC
```

PH Key Location/Qualifiers  
 FT source 1. .15 /organism='Artificial Sequence'  
 FEATURES  
 source Location/Qualifiers  
 1. .15 /organism='synthetic construct'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1155 CTTCAAGCATGCT 1168  
 DB 14 CTTCAAGTATGCT 1

RESULT 485  
 LOCUS AR180099/c 15 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 167 from patent US 6333152.  
 ACCESSION AR180099  
 VERSION AR180099.1 GI:20222132  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 1 (bases 1 to 15)  
 AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.  
 TITLE Gene expression profiles in normal and cancer cells  
 JOURNAL Patent: US 6333152-A 167 25-DEC-2001;  
 FEATURES  
 source Location/Qualifiers  
 1. .15 /organism='unknown'  
 /mol\_type='unassigned DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 367 GTGATGTGATCAT 380  
 DB 15 GCGATGTGATCAT 2

RESULT 486  
 LOCUS AR580858 15 bp DNA linear PAT 15-DEC-2004  
 DEFINITION Sequence 4 from patent US 6790616.  
 ACCESSION AR580858  
 VERSION AR580858.1 GI:56611528  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 1 (bases 1 to 15)  
 AUTHORS Moribe,T. and Kaneshige,T.  
 TITLE Method for typing of HLA class I alleles  
 JOURNAL Patent: US 6790616-A 4 14-SEP-2004;  
 Shionogi & Co., Ltd.; Osaka;  
 MOX;

FEATURES  
 source Location/Qualifiers  
 1. .15 /organism='unknown'  
 /mol\_type='genomic DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AGGAGAGCCGAG 1320  
 |||||

DB 2 AGGAGAGCCGAG 15

RESULT 487  
 LOCUS AR774267/c 15 bp DNA linear PAT 08-DEC-2005  
 DEFINITION Sequence 196 from patent US 6972171.  
 ACCESSION AR774267  
 VERSION AR774267.1 GI:83351531  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 1 (bases 1 to 15)  
 AUTHORS Schlingensiepen,K.-H. and Brysch,W.  
 TITLE Antisense oligonucleotide preparation method  
 JOURNAL Patent: US 6972171-A 196 06-DEC-2005;  
 Diagnostik Ges. fur biomolekulare Diagnostik mbH; Gettingen;  
 EPX;

FEATURES  
 source Location/Qualifiers  
 1. .15 /organism='unknown'  
 /mol\_type='genomic DNA'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 CAAGCCGAGGTG 949  
 DB 14 CAAGCCGAGGTG 1

RESULT 488  
 LOCUS AX419939 15 bp DNA linear PAT 18-JUN-2002  
 DEFINITION Sequence 276 from Patent WO0198537.  
 ACCESSION AX419939  
 VERSION AX419939.1 GI:21524306  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE  
 1 Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.  
 AUTHORS Nucleic acid accessible hybridization sites  
 TITLE Patent: WO 0198537-A 276 27-DEC-2001;  
 JOURNAL THIRD WAVE TECHNOLOGIES, INC. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. .15 /organism='synthetic construct'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:32630'

Query Match 0.7%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 669 CATCTGCTCTCTG 682  
 DB 2 CATCTGCTCTCTG 15

Search completed: June 12, 2006, 06:10:03  
 Job time : 12 secs

THIS PAGE BLANK (USPTO)

**THIS PAGE BLANK (USPTO)**





C 107	7.4	0.4	9	1	CF312817	ACCESSION:CF312817
C 108	7.4	0.4	9	1	CF313414	ACCESSION:CF313414
C 109	7.4	0.4	9	1	CF318771	ACCESSION:CF318771
C 110	7.4	0.4	9	1	CF330649	ACCESSION:CF330649
C 111	7.4	0.4	9	1	CO818814	ACCESSION:CO818814
C 112	7.4	0.4	9	1	CV933314	ACCESSION:CV933314
C 113	7.4	0.4	9	1	CO005921	ACCESSION:CO005921
C 114	7.4	0.4	9	1	DT904968	ACCESSION:DT904968
C 115	7.4	0.4	9	1	DT909435	ACCESSION:DT909435
C 116	7.4	0.4	9	1	DV571332	ACCESSION:DV571332
C 117	7.4	0.4	9	1	CV985814	ACCESSION:CV985814
C 118	7.4	0.4	9	1	CL663701	ACCESSION:CL663701
C 119	7.4	0.4	9	1	CL672804	ACCESSION:CL672804
C 120	7.4	0.4	9	1	CL682372	ACCESSION:CL682372
C 121	7.4	0.4	10	1	DM058225	ACCESSION:DM058225
C 122	7.4	0.4	10	1	BM396011	ACCESSION:BM396011
C 123	7.4	0.4	10	1	BM398849	ACCESSION:BM398849
C 124	7.4	0.4	10	1	CF311011	ACCESSION:CF311011
C 125	7.4	0.4	10	1	CL694809	ACCESSION:CL694809
C 126	7.4	0.4	10	1	AJ592517	ACCESSION:AJ592517
C 127	7.4	0.4	10	1	AJ587026	ACCESSION:AJ587026
C 128	7.4	0.4	11	1	AJ679435	ACCESSION:AJ679435
C 129	7.4	0.4	11	1	AJ681247	ACCESSION:AJ681247
C 130	7.4	0.4	11	1	AJ683713	ACCESSION:AJ683713
C 131	7.4	0.4	11	1	AJ686459	ACCESSION:AJ686459
C 132	7.4	0.4	11	1	BM396384	ACCESSION:BM396384
C 133	7.4	0.4	11	1	BM397892	ACCESSION:BM397892
C 134	7.4	0.4	12	1	BM398341	ACCESSION:BM398341
C 135	7.4	0.4	13	1	AJ666341	ACCESSION:AJ666341
C 136	7.4	0.4	13	1	CF297970	ACCESSION:CF297970
C 137	7.4	0.4	8	1	CF305141	ACCESSION:CF305141
C 138	7.4	0.4	8	1	CF306116	ACCESSION:CF306116
C 139	7.4	0.4	8	1	CF306762	ACCESSION:CF306762
C 140	7.4	0.4	8	1	CF322514	ACCESSION:CF322514
C 141	7.4	0.4	8	1	CF322653	ACCESSION:CF322653
C 142	7.4	0.4	8	1	CF323889	ACCESSION:CF323889
C 143	7.4	0.4	8	1	CF324406	ACCESSION:CF324406
C 144	7.4	0.4	8	1	CF325379	ACCESSION:CF325379
C 145	7.4	0.4	8	1	CF325469	ACCESSION:CF325469
C 146	7.4	0.4	8	1	CF325485	ACCESSION:CF325485
C 147	7.4	0.4	8	1	CF330558	ACCESSION:CF330558
C 148	7.4	0.4	8	1	CF339091	ACCESSION:CF339091
C 149	7.4	0.4	8	1	CV933358	ACCESSION:CV933358
C 150	7.4	0.4	8	1	CV933304	ACCESSION:CV933304
C 151	7.4	0.4	8	1	CK001098	ACCESSION:CK001098
C 152	7.4	0.4	8	1	CK001172	ACCESSION:CK001172
C 153	7.4	0.4	8	1	CK001200	ACCESSION:CK001200
C 154	7.4	0.4	8	1	CK001601	ACCESSION:CK001601
C 155	7.4	0.4	8	1	CK001811	ACCESSION:CK001811
C 156	7.4	0.4	8	1	CK001864	ACCESSION:CK001864
C 157	7.4	0.4	8	1	CK001954	ACCESSION:CK001954
C 158	7.4	0.4	8	1	CK001980	ACCESSION:CK001980
C 159	7.4	0.4	8	1	CK002359	ACCESSION:CK002359
C 160	7.4	0.4	8	1	CK002747	ACCESSION:CK002747
C 161	7.4	0.4	8	1	CK003296	ACCESSION:CK003296
C 162	7.4	0.4	8	1	DR025726	ACCESSION:DR025726
C 163	7.4	0.4	8	1	DT909735	ACCESSION:DT909735
C 164	7.4	0.4	8	1	CL659535	ACCESSION:CL659535
C 165	7.4	0.4	8	1	CL675700	ACCESSION:CL675700
C 166	7.4	0.4	8	1	CL676755	ACCESSION:CL676755
C 167	7.4	0.4	8	1	CL677992	ACCESSION:CL677992
C 168	7.4	0.4	8	1	CL681141	ACCESSION:CL681141
C 169	7.4	0.4	8	1	CL682011	ACCESSION:CL682011
C 170	7.4	0.4	8	1	DM753265	ACCESSION:DM753265
C 171	7.4	0.4	9	1	DM021589	ACCESSION:DM021589
C 172	7.4	0.4	9	1	CNS06E5N	ACCESSION:CNS06E5N
C 173	7.4	0.4	9	1	CF307008	ACCESSION:CF307008

## ALIGNMENTS

RESULT 1

AJ598266/c	15 bp	DNA	linear	GSS 15-JAN-2004
LOCUS				
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 465A07, genomic survey sequence.			
ACCESSION	AJ598266			
VERSION	AJ598266.1	GI:37947894		
KEYWORDS	GSS; left border; T-DNA flanking sequence.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE				
AUTHORS	Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Crnaud, C., Dehose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Lecharny, A.			
TITLE	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites			
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)			
PubMed	12446565			
REFERENCE				
AUTHORS	2 (bases 1 to 15)			
TITLE	Balzerque, S.			
JOURNAL	Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE			
COMMENT	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsag.versailles.inra.fr/publiclines/">http://dbsag.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ). Location/Qualifiers			
FEATURES				
SOURCE	1..15			
	/organism="Arabidopsis thaliana"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:3702"			
	/clone="465A02"			
	/clone_lib="Arabidopsis thaliana T-DNA insertion lines"			
	/ecotype="Wassilewskij"			
	1..15			
	/note="T-DNA flanking sequence			
	left border"			
misc_feature				
Query Match	0.8%; Score 13.4; DB 1; Length 15;			
Best Local Similarity	93.3%; Pred. No. 2.5;			
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1687 GACCACTTTTCCTC 1701			
Db	15 GAGCAGCTTTCCTC 1			
RESULT 2				
AM075254/c	14 bp	mRNA	linear	EST 14-SEP-2005
LOCUS				
DEFINITION	AM075254 Chicken immune 1 - CSEGRB08 Gallus gallus CDNA clone C0000222R05_T7, mRNA sequence.			
ACCESSION	AM075254			
VERSION	AM075254.1	GI:75475695		
KEYWORDS	EST.			
SOURCE	Gallus gallus (chicken)			
ORGANISM	Gallus gallus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
AUTHORS	1 (bases 1 to 14)			
	Smith, J., Speed, D., Hocking, P., Talbot, R. T., Degen, W., Schijns, V., Glass, E. J. and Butt, D.			

TITLE  
JOURNAL  
COMMENT

Development of a chicken 5k array  
Unpublished (2005)  
Contact: Smith J  
Genetics and Genomics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Vector pBluescript II KS(+), R. Site1: EcoRI R. Site2: NotI 5' Seq  
Primer T7 Strain Lohman Brown layer/Ross 308 broiler cross CDNA  
synthesis was initiated using an oligo(dT) primer, using methylated  
C in the first strand synthesis reaction. Following this first  
strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI  
adapters, digested with EcoRI, size-selected, and cloned into the  
NotI and EcoRI compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. Clones available from the ARK-Genomics  
Centre for Functional Genomics in Farm Animals, Roslin Institute,  
Midlothian, EH25 9PS, UK see [www.ark-genomics.org](http://www.ark-genomics.org).

FEATURES  
source

1. 14  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Lohman Brown layer/Ross 308 broiler cross"  
/db\_xref="taxon:9031"  
/clone="C0000222E05.T7"  
/issue\_type="Bursa\_spleen, Peyer's patch (pooled)"  
/clone\_lib="Chicken immune 1 - CSRR08108"  
/note="Vector: pBluescript II KS(+); Site\_1: EcoRI;  
Site\_2: NotI"  
Query Match 0.7%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 4.4;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GCCACCGCGGCGAG 22  
14 GCCACCGCGGCGAG 1

RESULT 3  
LOCUS  
DEFINITION

CFJ24040 15 bp mRNA linear EST 18-AUG-2003  
HDN--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
clone HDN--05-H11, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CFJ24040  
CFJ24040.1 GI:33796346  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
JOURNAL  
COMMENT

1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nam, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nam B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

FEATURES  
source

1. 15  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN--05-H11"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"

/clone\_lib="OSHDAC1-overexpressing transgenic rice lambda  
phage cDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Qy 1223 CGGCCCAAGGCCA 1336  
1 CGGCCCAAGGCCA 14  
Query Match 0.7%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 6.9;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
LOCUS  
DEFINITION

ATH521816 15 bp DNA linear GSS 08-FEB-2006  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
279D04, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

ATH521816  
AJ521816.1 GI:26790052  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Crnaud, C., DeRose, R., Pelletier, G.,  
Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 15)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program "Genoplante" (<http://www.genoplante.com> and  
<http://genoplante-info.inbio.gen.fr>).

FEATURES  
source

1. 15  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="MassillaewskiJa"  
/db\_xref="taxon:3702"  
/clone="279D04"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="MassillaewskiJa"  
1. 15  
/note="T-DNA flanking sequence  
left border"

Qy 1045 CTGAGAGAGTT 1056  
Query Match 0.7%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 CTGAAGAAGTTT 14

RESULT 5  
AM075481/c

LOCUS  
DEFINITION AM075481 Chicken immune 5 - CSEQRBN30 Gallus gallus CDNA clone

ACCESSION  
VERSION AM075481

KEYWORDS  
SOURCE AM075481.1 GI:75476052

ORGANISM  
Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
Smith, J., Speed, D., Hocking, P., Talbot, R.T., Degen, W., Schijns, V., Glass, E.J. and Burt, D.

TITLE  
JOURNAL Development of a chicken 5k array

COMMENT  
Unpublished (2005)  
Contact: Smith J  
Genetics and Genomics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Vector: Bluescript II KS(+)  
R. Site1, ECORI R. Site2, NotI 5' Seq  
Primer T7 Strain Lohman Brown Layer/Ross 308 Prolifer cross This  
normalized library was constructed from 1 million independent  
clones. cDNA synthesis was initiated using an oligo(dT) primer,  
using methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA was  
blunted, ligated to NotI adapters, digested with EcoRI,  
size-selected, and cloned into the NotI and EcoRI compatible sites  
of a custom modified MCS of the Bluescript (KS+) vector. The  
library was normalized in 2 rounds using conditions adapted from  
Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldi et al., Genome  
Research 6 (1996): 791, except that a significantly longer  
reannealing hybridization was used. Clones available from the  
ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin  
Institute, Midlothian, EH25 9PS, UK see [www.ark-genomics.org](http://www.ark-genomics.org).

FEATURES  
source  
1..13  
/organism="Gallus gallus"  
/mol\_type="RNA"  
/db\_xref="taxon:9031"  
/clone="C0000798E15\_77"  
/tissue="thymus"  
/clone\_id="Chicken immune 5 - CSEQRBN30"

Query Match 0.6%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 7.3;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 GCCACCGCGGCA 21  
13 GCCACCGCGGGA 1

Db 13 GCCACCGCGGGA 1

RESULT 6  
BM396557/c

LOCUS  
DEFINITION BM396557 13 bp mRNA linear EST 17-JAN-2002

ACCESSION  
VERSION BM396557

KEYWORDS  
SOURCE BM396557.1 GI:18196625

ORGANISM  
Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.

TITLE  
JOURNAL  
COMMENT  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: [apturkew@midway.uchicago.edu](mailto:apturkew@midway.uchicago.edu)  
Seq primer: T3.

FEATURES  
source  
1..13  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript 2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.6%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 7.3;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 8 AGCCACCGCGGC 20  
13 AGCCACCGCGGTC 1

Db 13 AGCCACCGCGGTC 1

RESULT 7  
AJ587382/c

LOCUS  
DEFINITION AJ587382 13 bp DNA linear GSS 15-JAN-2004

ACCESSION  
VERSION AJ587382

KEYWORDS  
SOURCE GSS: left border; T-DNA flanking sequence.

ORGANISM  
Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS 1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Denose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.

TITLE  
JOURNAL T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

COMMENT  
EMBO Rep. 3 (12), 1152-1157 (2002)  
12446565  
2 (bases 1 to 13)  
Balzerque, S.  
Direct Submision  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publications/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1..13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="270B03"

```
misc_feature
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Maslilewskija"
1..13
/notes="T-DNA flanking sequence
left border"

Query Match      0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 7.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      716 CAACACAGAGAC 728
Db      13 CAACACAGAGTC 1

RESULT 8
AJ679435/c
LOCUS
DEFINITION AJ679435 CSEORAN04 Sus scrofa cDNA clone C0001779_B18, mRNA
ACCESSION
VERSION AJ679435.1 GI:49412022
KEYWORDS
SOURCE
ORGANISM Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcotRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_B18"
/issue_type="uterus"
/clone_lib="CSEORAN04"
/notes="Vector: pb1uescriptII(KS+); Site 1: EcotRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

FEATURES
source

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      9 GCCACCGCGGG 19
Db      11 GCCACCGCGGG 1

RESULT 9
AJ681247/c
LOCUS
DEFINITION AJ681247 CSEORAN04 Sus scrofa cDNA clone C0001795_I24, mRNA
ACCESSION
VERSION AJ681247
KEYWORDS
EST.
AJ681247.1 GI:49413837
```

```
SOURCE
ORGANISM Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcotRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11

FEATURES
source

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      9 GCCACCGCGGG 19
Db      11 GCCACCGCGGG 1

RESULT 10
AJ683713/c
LOCUS
DEFINITION AJ683713 CSEORAN04 Sus scrofa cDNA clone C0001802_O06, mRNA
ACCESSION
VERSION AJ683713
KEYWORDS
EST.
AJ683713.1 GI:49416303
SOURCE
ORGANISM Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcotRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arxgenomics.org.
Location/Qualifiers
1..11

FEATURES
source
```

/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001802\_006"  
/tissue\_type="uterus"  
/clone\_id="CSEQRAN04"  
/note="Vector: pBluescriptII (KS+), Site\_1: EcoRI, Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 0.6%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GCCACCGCGGG 19  
|||||  
DB 11 GCCACCGCGGG 1

RESULT 11  
AJ686459 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811\_K23, mRNA  
DEFINITION sequence.  
ACCESSION AJ686459.1 GI:49419049  
VERSION AJ686459.1  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBluescriptII (KS+), R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.

FEATURES  
source location/Qualifiers

1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001811\_K23"  
/tissue\_type="uterus"  
/clone\_id="CSEQRAN04"  
/note="Vector: pBluescriptII (KS+), Site\_1: EcoRI, Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

Query Match 0.6%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GCCACCGCGGG 19  
|||||  
DB 11 GCCACCGCGGG 1

RESULT 12  
CF337407 12 bp mRNA linear EST 18-AUG-2003  
LOCUS CF337407  
DEFINITION JMT--07-N08.D1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--07-N08, mRNA sequence.

ACCESSION CF337407  
VERSION CF337407.1 GI:33823214  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers

1..12  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT--07-N08"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_id="AtJMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.6%; Score 10.4; DB 1; Length 12;  
Best Local Similarity 91.7%; Pred. No. 12;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1393 ATGCAGAGAGC 1404  
|||||  
DB 12 ATGCAGAGAGC 1

RESULT 13  
AJ666341 13 bp mRNA linear EST 28-JUN-2004  
LOCUS AJ666341 CSEQRAN09 Sus scrofa cDNA clone C0000033\_C09, mRNA  
DEFINITION sequence.  
ACCESSION AJ666341  
VERSION AJ666341.1 GI:49350792  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBluescriptII (KS+) R. Site 1:

ECORI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

## FEATURES

source

1. 13  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0000033\_C09"  
/issue\_type="Placenta"  
/clone\_lib="GSEORAN09"  
/note="Vector: pBluescriptII(KS+); Site 1: EcorI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match  
Best Local Similarity 91.7%; Pred. No. 19;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1495 GGAATTCCTT 1506  
|||||  
Db 2 GGAATTCCTT 13

RESULT 14  
AJ590935/c 13 bp DNA linear GSS 15-JAN-2004  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577B08, genomic survey sequence.

ACCESSION  
AJ590935.1 GI:37940559  
VERSION  
GSS; left border; T-DNA flanking sequence.  
KEYWORDS  
Arabidopsis thaliana (chale cress)  
SOURCE  
Arabidopsis thaliana

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1

Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pellecier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-integration sites

JOURNAL  
EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 13)

Balzergue, S.

Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr/>).

Location/Qualifiers

## FEATURES

source

1. 13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="577B08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Massilewska"  
1. 13  
/note="T-DNA flanking sequence  
left border"

Query Match  
Best Local Similarity 91.7%; Pred. No. 19;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 952 AAATGATGATT 963  
|||||  
Db 13 AAAAGATGATT 2

RESULT 15  
CF324040/c 15 bp mRNA linear EST 18-AUG-2003  
LOCUS  
DEFINITION  
HDN-05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN-05-H11, mRNA sequence.

ACCESSION  
CF324040.1 GI:33796346  
VERSION  
EST.

## KEYWORDS

Oryza sativa (japonica cultivar-group)

## SOURCE

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

## CONTACT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

source

1. 15  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN-05-H11"  
/issue\_type="cDNA"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E. coli SOLR"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site 1: EcorI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcorI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match  
Best Local Similarity 80.0%; Pred. No. 49;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 305 TTGTCTTTGGCGAG 319  
|||||  
Db 15 TTGGCTTTGGGCGG 1

## RESULT 16

BM396011/c

LOCUS

DEFINITION

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM396011

VERSION

BM396011.1 GI:18196064

KEYWORDS

EST.

Tetrahymena thermophila

Tetrahymena thermophila

Tetrahymena thermophila

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hyenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 10)  
 Turkewitz A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E., Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 CONTACT: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
 1..10  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
 Query Match 0.6%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 9 GCCACCGCGG 18  
 Db 10 GCCACCGCGG 1  
 RESULT 17 10 bp mRNA linear EST 17-JAN-2002  
 BM398849/c  
 LOCUS 5009-0-5-g06.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM398849  
 VERSION BM398849.1 GI:18198902  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hyenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena. 1 (bases 1 to 10)  
 Turkewitz A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E., Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 CONTACT: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
 1..10  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
 Query Match 0.6%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 9 GCCACCGCGG 18  
 Db 10 GCCACCGCGG 1  
 RESULT 19 10 bp DNA linear GSS 09-JUL-2004  
 CL659790/c  
 LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.  
 ACCESSION CL659790  
 VERSION CL659790.1 GI:50144248  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 9 GCCACCGCGG 18  
 Db 10 GCCACCGCGG 1  
 RESULT 18 10 bp DNA linear GSS 28-DEC-2004  
 CW979862  
 LOCUS KBxH003N20F KBxH, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBxH003N20, genomic survey sequence.  
 ACCESSION CW979862  
 VERSION CW979862.1 GI:56811149  
 KEYWORDS GSS.  
 SOURCE Brassica rapa subsp. pekinensis  
 ORGANISM Brassica rapa subsp. pekinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 10)  
 Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.  
 End sequence of Brassica rapa HindIII BAC library (KBxH) Unpublished (2004)  
 CONTACT: Beom-Seok Park  
 Brassica Genomics Team  
 National Institute of Agricultural Biotechnology  
 225 Seodun-Dong, Suwon, 441-707, Korea  
 Tel: +82-31-299-1672  
 Fax: +82-31-299-1670  
 Email: pbeom@da.90.kr  
 BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone KBxH003N20  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers  
 1..10  
 /organism="Brassica rapa subsp. pekinensis"  
 /mol\_type="genomic DNA"  
 /cultiivar="Chilfu"  
 /sub\_species="pekinensis"  
 /db\_xref="taxon:51351"  
 /clone="KBxH003N20"  
 /tissue\_type="young leaves"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="KBxH, Brassica rapa HindIII BAC library"  
 /note="Vector: pCUGBac1; Site 1: HindIII; Brassica rapa ssp. pekinensis indred line Chilfu BAC library (KBxH BAC) is provided by Yong-Pyo Lim."  
 Query Match 0.6%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 531 CCACAATTC 540  
 Db 1 CCACAATTC 10  
 RESULT 19 10 bp DNA linear GSS 09-JUL-2004  
 CL659790  
 LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.  
 ACCESSION CL659790  
 VERSION CL659790.1 GI:50144248  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;



REFERENCE 1 (bases 1 to 10)  
AUTHORS Sriinivasan,J., Otto,G.W., Kahlow,U., Gelsler,R. and Sommer,R.J.  
TITLE Appabi: an Acedb database for the nematode satellite organism  
JOURNAL Pristionchus pacificus  
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT 14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..10  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.6%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 891 GATCCCGCGG 900  
|||||  
10 GATCCCGCGG 1

RESULT 20  
AJ686546/c 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686546 CSEQRAN04 Sus scrofa cDNA clone C0001812\_C13, mRNA  
DEFINITION  
ACCESSION AJ686546  
VERSION AJ686546.1 GI:49419136  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.  
1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site1: EcoRI  
R. Site2: NotI 5' Seg Primer M13P Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
Location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001812\_C13"  
/issue\_type="uterns"  
/tissue\_type="uterus"

FEATURES  
source

/clone\_lib="CSEQRAN04"  
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.6%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCACCGCGG 18  
|||||  
11 GCCACCGCGG 2

RESULT 21  
AJ686590/c 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686590 CSEQRAN04 Sus scrofa cDNA clone C0001812\_E11, mRNA  
DEFINITION  
ACCESSION AJ686590  
VERSION AJ686590.1 GI:49419180  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.  
1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI  
R. Site2: NotI 5' Seg Primer M13P Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
Location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001812\_E11"  
/issue\_type="uterns"  
/tissue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

FEATURES  
source

Query Match 0.6%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCACCGCGG 18  
|||||  
11 GCCACCGCGG 2

RESULT 22  
AJ655540/c 12 bp mRNA linear EST 28-JUN-2004  
LOCUS AJ655540 KN277 Sus scrofa cDNA clone C0005190\_G13, mRNA sequence.  
DEFINITION  
ACCESSION AJ655540  
VERSION AJ655540.1 GI:49339572  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 12)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
Unpublished (2004)  
CONTACT: Anderson ST  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the minscore 20 and -mismatch 12 options. Vector:PB1uescriptII(SK+) R. Site1: EcorI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org

FEATURES  
source  
1..12  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005190.G13"  
/issue\_type="embryo"  
/clone\_lib="KN277"  
/note="Vector: pBluescriptII(SK+); Site\_1: EcorI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1283 TCTCCACGAT 1292  
|||||  
10 TCTCCACGAT 1

RESULT 23  
BM395918/c 12 bp mRNA linear EST 17-JAN-2002  
LOCUS 5009-0-14-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM395918  
VERSION BM395918.1 GI:18195971  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 12)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
CONTACT: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1..12  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES  
source  
1..12  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCCACCGCG 18  
|||||  
10 GCCACCGCG 1

RESULT 25  
AJ655617/c 11 bp mRNA linear EST 28-JUN-2004  
LOCUS AJ655617 KN277 Sus scrofa cDNA clone C0005190\_J23, mRNA sequence.  
DEFINITION AJ655617  
ACCESSION AJ655617.1 GI:49339649  
VERSION AJ655617.1 GI:49339649  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCCACCGCG 17  
|||||  
11 AGCCACCGCG 2

RESULT 24  
BM398341/c 12 bp mRNA linear EST 17-JAN-2002  
LOCUS BM398341  
DEFINITION 5009-0-44-D05.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM398341  
VERSION BM398341.1 GI:18198394  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 12)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
CONTACT: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1..12  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCCACCGCG 18  
|||||  
10 GCCACCGCG 1

RESULT 25  
AJ655617/c 11 bp mRNA linear EST 28-JUN-2004  
LOCUS AJ655617 KN277 Sus scrofa cDNA clone C0005190\_J23, mRNA sequence.  
DEFINITION AJ655617  
ACCESSION AJ655617.1 GI:49339649  
VERSION AJ655617.1 GI:49339649  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.



```

ACCESSION      CX000541
VERSION        CX000541.1  GI:56271958
KEYWORDS       EST.
SOURCE         Canis familiaris (dog)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE      1 (bases 1 to 11)
AUTHORS       Ballja,V.S., Nasclimento,L.U. and McCombie,W.R.
TITLE         ESTs from Canis familiaris right cardiac ventricle (dog)
JOURNAL       Unpublished (2004)
COMMENT       Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mccombie@cshl.org.

FEATURES
  source
    1..11
      /organism="Canis familiaris"
      /mol_type="mRNA"
      /db_xref="taxon:9615"
      /sex="unknown"
      /tissue_type="Cardiac muscle"
      /dev_stage="3 month old normal canine"
      /lab_host="XL10 Gold"
      /clone_idb="Right Cardiac Ventricle (DOGEST6)"
      /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
             XhoI; Site 2: XhoI; Library constructed using pBluescript
             XR kit from Stratagene. Cloned cDNA was size selected
             between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
             Pathology and Medical Genetics, School of Veterinary
             Medicine, University of Pennsylvania, 3800 Spruce Street,
             Philadelphia, PA 19104-6051"

Query Match      0.5%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1337 CACCCTGCTCC 1347
        |||||
        11 CACCTGCTGC 1

Db
RESULT 29
AJ592230/c
LOCUS       AJ592230
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
              609B09, genomic survey sequence.
ACCESSION   AJ592230
VERSION     AJ592230.1  GI:37941854
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
             Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
             Lepointec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
             of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED     12446565
REFERENCE   2 (bases 1 to 11)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
             Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana

```

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

```

FEATURES
  source
    1..11
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /db_xref="taxon:3702"
      /clone_idb="609B09"
      /clone_idb="Arabidopsis thaliana T-DNA insertion lines"
      /ecotype="Wassilewskija"
      /note="T-DNA flanking sequence
             right border"

misc_feature
    1..11
      /note="T-DNA flanking sequence
             right border"

Query Match      0.5%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1594 AAAATCTCAT 1604
        |||||
        11 AAAATCTCAT 1

Db
RESULT 30
AJ587382
LOCUS       AJ587382
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
              270B03, genomic survey sequence.
ACCESSION   AJ587382
VERSION     AJ587382.1  GI:37937006
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
             Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
             Lepointec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
             of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED     12446565
REFERENCE   2 (bases 1 to 13)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
             Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
             plants from INRA (Versailles). The DNA fragment(s) resulting from
             the PCR were directly sequenced from the left or the right border
             to determine the genomic sequence flanking the insertion. T-DNA
             derived sequences were removed. Information to order the
             corresponding mutant line and a link to a database providing a
             graphical display of the insertion site are available at
             http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
             been generated in the framework of the French plant genomics
             program "Genoplante" (http://www.genoplante.com and
             http://genoplante-info.infobiogen.fr).
FEATURES
  source
    1..13
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /db_xref="taxon:3702"

```

```

misc_feature
/clone="270B03"
/ecotype="Arabidopsis thaliana T-DNA insertion lines"
1..13
/notes="T-DNA flanking sequence
left border"

Query Match      0.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      345  CTCGTGTGGTGG 355
Db      3    CTCGTGTGGTTG 13

RESULT 31
CA850899/c
LOCUS
DEFINITION CA850899 9 bp mRNA linear EST 01-AUG-2003
CA850899
VERSION CA850899
KEYWORDS
SOURCE
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
Alkharouf, N., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
15060591
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D07H02"
/tissue_type="Roots"
/dev_stage="Seedling8"
/clone.lib="CDNA Peking library 2, 4 day SCN3"
/notes="Vector: pJuncscript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days post invasion."

Query Match      0.5%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1; 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1114 CCCATCATC 1122
Db      9    CCCATCATC 1

RESULT 32
CF311011/c
LOCUS
DEFINITION CF311011 10 bp mRNA linear EST 15-AUG-2003
ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-B02, mRNA sequence.
CF311011
ACCESSION
```

```

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 10)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..10
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-B02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOP0, Site 1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.5%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1306 GAGGAGGAG 1314
Db      10 GAGGAGGAG 2

RESULT 33
AJ591555/c
LOCUS
DEFINITION AJ591555 10 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
587C11, genomic survey sequence.
AJ591555
ACCESSION AJ591555.1 GI:37941179
VERSION
KEYWORDS GSS: left border; T-DNA flanking sequence.
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsie.
1
Brunaud, V., Balergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Gruaud, C., Denose, R., Pelleter, G.,
Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 10)
Balzergue, S.
Direct Submmission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRs, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
```



KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:BluescriptII(KS+). R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
Location/Qualifiers

FEATURES  
source  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001800\_K12"  
/tissue\_type="uterus"  
/clone\_id="CSEORAN04"  
/note="Vector: pBluescriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."  
Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 18  
|||||  
1 CCACCGCG 9

Db

RESULT 37  
AJ685455 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ685455 CSEORAN04 Sus scrofa cDNA clone C0001808\_P05, mRNA  
DEFINITION sequence.  
ACCESSION AJ685455  
VERSION AJ685455.1 GI:49418045  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:BluescriptII(KS+). R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
Location/Qualifiers

FEATURES

source  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001808\_P05"  
/tissue\_type="uterus"  
/clone\_id="CSEORAN04"  
/note="Vector: pBluescriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."  
Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 18  
|||||  
1 CCACCGCG 9

Db

RESULT 38  
BM396384 11 bp mRNA linear EST 17-JAN-2002  
LOCUS BM396384/c  
DEFINITION 5009-0-2-H08.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM396384  
VERSION BM396384.1 GI:18196422  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orise,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

FEATURES  
source  
1..11  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCCACCGCG 17  
|||||  
11 GCCACCGCG 3

Db

RESULT 39  
BM397892 11 bp mRNA linear EST 17-JAN-2002  
LOCUS BM397892/c  
DEFINITION 5009-0-38-F04.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM397892  
VERSION BM397892.1 GI:18197945  
KEYWORDS EST.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenotomastix; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 11)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

1..11  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCCACCGCG 17  
Db 11 GCCACCGCG 3

RESULT 40  
CF300559 11 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--05-B09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B09, mRNA  
sequence.  
ACCESSION CF300559  
VERSION CF300559.1 GI:33672320  
KEYWORDS EST  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 11)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Yonsei University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

1..11  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone\_lib="7LEAF--05-B09"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"

FEATURES  
source

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1673 AAAATATAA 1681  
Db 3 AAAATATAA 11

RESULT 41  
CF543159 11 bp mRNA linear EST 22-SEP-2003  
LOCUS S014678-024-030-006-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
DEFINITION 024-030-006 5-PRIME, mRNA sequence.  
ACCESSION CF543159  
VERSION CF543159.1 GI:34891599  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 11)  
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
12472698  
Contact: Weishaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert length: 11 Std Error: 0.00  
Plate: 30 row: 0 column: 06  
Seq primer: SP6.  
Location/Qualifiers

1..11  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:936619"  
/db\_xref="taxon:161934"  
/clone="024-030-006"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP12-ADIS-024-leaf"  
/note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleimanzelebener Saatnucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCGTCGCG-SP6-prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-BEET  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES  
source

Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 788 AGAAAGTGT 796  
|||||||



Db 10 AGAAGTCT 2

RESULT 42  
LOCUS DU733106/c  
DEFINITION DU733106 11 bp DNA linear GSS 27-JAN-2006  
ACCESSION ABK12073.g3 HF70\_10-07-02 uncultured marine microorganism  
VERSION DU733106  
KEYWORDS HF70\_10-07-02 genomic clone HF0070\_029A08, genomic survey sequence.  
SOURCE DU733106.1 GI:85742940  
GSS.  
ORGANISM uncultured marine microorganism HF70\_10-07-02  
KEYWORDS uncultured marine microorganism HF70\_10-07-02  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Delong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,  
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.  
and Karl,D.M.

TITLE Comparative genomics reveals ecological trends in stratified  
JOURNAL microbial communities in the ocean's interior  
COMMENT Science (2006) in press  
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,  
Kerrie Barry, Tijana Glavinadelirio, David Bruce, Paul Richardson  
and Edward Delong  
US DOE Joint Genome Institute  
US DOE Joint Genome Institute  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA  
Tel: 617-253-5271  
Fax: 617-253-2679  
Email: pmrichardson@lbl.gov; delong@mit.edu  
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m  
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/Kg  
Class: foamid ends.

FEATURES  
source  
1..11  
/organism="uncultured marine microorganism HF70\_10-07-02"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:361144"  
/clone="HF0070\_029A08"  
/cell\_type="marine picoplankton, less than 1.8 um, greater  
than 0.22 um fraction"  
/clone\_lib="HF70\_10-07-02"  
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre  
(Hawaii) picoplankton genomic formid DNA library prepared  
from marine picoplankton in the less than 1.6 um, greater  
than 0.22 um fraction. Picoplankton collected at 70 m  
depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample  
Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m  
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4  
umol/Kg"

Query Match 0.5%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 947 TGTGCAAA 955  
10 TGTGCAAAA 2

RESULT 43  
LOCUS CF337407  
DEFINITION CF337407 12 bp mRNA linear EST 18-AUG-2003  
JMT--07-N08.b1 AlJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa (Japonica cultivar-group) cDNA clone  
JMT--07-N08, mRNA sequence.  
ACCESSION CF337407  
VERSION CF337407.1 GI:33823214  
KEYWORDS EST.  
SOURCE Oryza sativa (Japonica cultivar-group)  
ORGANISM Oryza sativa (Japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE  
AUTHORS clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..12  
/organism="Oryza sativa (Japonica cultivar-group)"  
/mol\_type="mRNA"  
/culivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT--07-N08"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AlJMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis thaliana jasmonic acid Carboxyl  
methyltransferase overexpression line."

Query Match 0.5%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 929 TCTCTGCCA 937  
3 TCTCTGCCA 11

RESULT 44  
LOCUS AM075481  
DEFINITION AM075481 13 bp mRNA linear EST 14-SEP-2005  
AM075481 Chicken immune 5 - CSEGRBN30 Gallus gallus cDNA clone  
C0000798B15.T7, mRNA sequence.  
ACCESSION AM075481  
VERSION AM075481.1 GI:75476052  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 13)  
Smith,J., Speed,D., Hocking,P., Talbot,R.T., Degen,W., Schjns,V.,  
Glass,E.J. and Burt,D.  
TITLE Development of a chicken 5k array  
JOURNAL Unpublished (2005)  
COMMENT Contact: Smith J  
Genetics and Genomics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Vector pBluescript II KS(+).R. Site1:EcoRI.R. Site2:NotI.5'. Seg  
Primer T7 Strain Lohman Brown layer/Ross 308 broiler cross This  
normalized library was constructed from 1 million independent  
clones. cDNA synthesis was initiated using an oligo(dT) primer,  
using methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA was  
blunted, ligated to NotI adapters, digested with EcoRI,  
size-selected, and cloned into the NotI and EcoRI compatible sites  
of a custom modified MCS of the pBluescript (KS+) vector. The  
library was normalized in 2 rounds using conditions adapted from  
Scores et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome  
Research 6 (1996): 791, except that a significantly longer

reannealing hybridization was used. Clones available from the ARK-Genomics Centre for Functional Genomics in Farm Animals, Roslin Institute, Midlothian, EH25 9PS, UK see [www.ark-genomics.org](http://www.ark-genomics.org).

#### FEATURES

source

```
1..13
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="C0000798E15_T7"
/tissue_type="thymus"
/clone_lib="Chicken immune 5 - CSEQRBN30"
```

Query Match 0.5%; Score 8.8; DB 1; Length 13;  
Best Local Similarity 83.3%; Pred. No. 70;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 221 TCCTCCCGGTGG 232

Db 1 TCCCGCGGTGG 12

#### RESULT 45

BM396557

LOCUS

DEFINITION 5009-0-22-F07.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM396557

VERSION BM396557.1 GI:18196625

KEYWORDS

EST.

ORGANISM

Tetrahymena thermophila

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 13)

Turkewitz A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: [apturkew@midway.uchicago.edu](mailto:apturkew@midway.uchicago.edu)

Seq primer: T3.

Location/Qualifiers

```
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone="Vector: Bluescript SK+" Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

Query Match 0.5%; Score 8.8; DB 1; Length 13;  
Best Local Similarity 83.3%; Pred. No. 70;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 579 GACGCGTGTGGC 590

Db 1 GACGCGGTGGC 12

#### RESULT 46

AM075254

LOCUS

DEFINITION 14 bp mRNA linear EST 14-SEP-2005

AM075254 Chicken immune 1 - CSEQRBL08 Gallus gallus cDNA clone

C0000222E05\_T7, mRNA sequence.

ACCESSION

AM075254

VERSION AM075254.1 GI:75475695

#### KEYWORDS

SOURCE

ORGANISM

EST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 14)

Smith, J.J., Speed, D., Hocking, P., Talbot, R.T., Degen, W., Schijns, V.,

Glass, E.J., and Burr, D.

Development of a chicken 5k array

Unpublished (2005)

Contact: Smith J

Genetics and Genomics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Vector pBluescript II KS(+)

Primer T7 Strain Lohman Brown layer/Ross 308 broiler cross cDNA

synthesis was initiated using an oligo(dT) primer, using methylated

C in the first strand synthesis reaction. Following this first

strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI

adapters, digested with EcoRI, size-selected, and cloned into the

NotI and EcoRI compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. Clones available from the ARK-Genomics

Centre for Functional Genomics in Farm Animals, Roslin Institute,

Midlothian, EH25 9PS, UK see [www.ark-genomics.org](http://www.ark-genomics.org).

Location/Qualifiers

```
1..14
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Lohman Brown layer/Ross 308 broiler cross"
/db_xref="taxon:9031"
/clone="C0000222E05_T7"
/tissue_type="Burra spleen, Peyer's patch (pooled)"
/clone_lib="Chicken immune 1 - CSEQRBL08"
/clone="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: NotI"
```

Query Match 0.5%; Score 8.8; DB 1; Length 14;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 221 TCCTCCCGGTGG 232

Db 2 TCCCGCGGTGG 13

#### RESULT 47

ATH521816/c

LOCUS

DEFINITION 15 bp DNA linear GSS 08-FEB-2006

Arabidopsis thaliana T-DNA flanking sequence, left border, clone

279D04, genomic survey sequence.

ACCESSION AJ521816

VERSION AJ521816.1 GI:26790052

GSS; left border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,

Chauvin, S., Bechtold, N., Cruaud, C., Denose, R., Pelletier, G.,

Lepoint, L., Caboche, M., and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 15)

Balzerque, S.

Direct Submission

Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

source

```
1..15
  /organism="Arabidopsis thaliana"
  /mol_type="genomic DNA"
  /cultivar="Wassilewskija"
  /db_xref="taxon:3702"
  /clone="279D04"
  /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
  /ecotype="Wassilewskija"
misc_feature
  1..15 "T-DNA flanking sequence"
  /note="T-DNA flanking sequence"
  left border"
```

Query Match 0.5%; Score 8.6; DB 1; Length 15;  
Best Local Similarity 73.3%; Pred. No. 98;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1004 ACATCTTCTCTCTCC 1018  
15 AAACCTCTCAGCC 1

#### RESULT 48

BM396082 10 bp mRNA linear EST 17-JAN-2002  
LOCUS 5009-0-16-H04.c.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM396082  
VERSION BM396082.1 GI:18196135  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 10)  
Turkewitz,A.P., Karzer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
JOURNAL

#### FEATURES

source

```
1..10
  /organism="Tetrahymena thermophila"
  /mol_type="mRNA"
  /strain="CU428.1"
  /db_xref="taxon:5911"
  /clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
  /note="Vector: Bluescript SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCACGCGGCG 19

Db 10 CCACGCGGCG 1

RESULT 49 10 bp mRNA linear EST 15-AUG-2003  
CF304081/c  
LOCUS ABF1--04-A07.g1 ABF3-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--04-A07, mRNA sequence.  
ACCESSION CF304081  
VERSION CF304081.1 GI:33675842  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 10)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
JOURNAL  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

```
1..10
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="ABF1--04-A07"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli SOLR"
  /clone_1lb="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"
  /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."
```

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1012 TTCTCTCTGC 1021  
10 TTCTCTCTGC 1

#### RESULT 50

CF333615 10 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--02-J09, mRNA sequence.  
ACCESSION CF333615  
VERSION CF333615.1 GI:33815525  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 10)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 TITLE Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
 COMMENT Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
 1..10  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="JMT--02-J09"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AluMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis thaliana Carboxyl  
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 401 GGACGATGAC 410  
 Db 1 GGACGATGAC 10

RESULT 51 10 bp mRNA linear EST 18-AUG-2003  
 CF336905  
 LOCUS JMT--07-C04.g1 AluMT-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 JMT--07-C04, mRNA sequence.  
 ACCESSION CF336905  
 VERSION CF336905.1 GI:33822181  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 CONTACT Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Ehrhartoideae; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 10)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
 1..10  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="JMT--07-C04"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"

RESULT 53 10 bp mRNA linear EST 25-JUN-2005  
 CV933324/c  
 LOCUS P4pcm 0785 mating of 88069 (A1) and 618 (A2) Phycophthora infestans  
 DEFINITION cDNA, mRNA sequence.

/clone\_lib="AluMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis thaliana Carboxyl  
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AAAAGAGTGC 84  
 Db 1 AAAAGAGTTC 10

RESULT 52 10 bp mRNA linear EST 18-AUG-2003  
 CF336905/c  
 LOCUS JMT--07-C04.g1 AluMT-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 JMT--07-C04, mRNA sequence.  
 ACCESSION CF336905  
 VERSION CF336905.1 GI:33822181  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 CONTACT Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Ehrhartoideae; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 10)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source Location/Qualifiers  
 1..10  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="JMT--07-C04"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AluMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis thaliana Carboxyl  
 methyltransferase overexpression line."

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 411 GAACATTTT 420  
 Db 10 GAACCTTTT 1

RESULT 53 10 bp mRNA linear EST 25-JUN-2005  
 CV933324/c  
 LOCUS P4pcm 0785 mating of 88069 (A1) and 618 (A2) Phycophthora infestans  
 DEFINITION cDNA, mRNA sequence.

**ACCESSION** CV933324  
**VERSION** CV933324.1 GI:58122939  
**KEYWORDS** EST.  
**SOURCE** Phytophthora infestans (potato late blight agent)  
**ORGANISM** Phytophthora infestans  
**REFERENCE** 1 (bases 1 to 10)  
 Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,  
 Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,  
 Lay,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,  
 Windaas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,  
 Mauch,F., van West,P., Maugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
 Lam,S.T. and Judelson,H.S.: 2005, 'Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi'  
**TITLE** Mo1. Plant-Microbe Interact. 18 (3), 229-243 (2005)  
**JOURNAL** 15782637  
**PUBMED**  
**COMMENT** Contact: Judelson HS  
 Department of Plant Pathology  
 University of California  
 Webber Hall, Riverside, CA 92521, USA  
 Tel: 909 787 4139  
 Fax: 909 787 4234  
 Email: howard.judelson@ucr.edu.  
**FEATURES**  
 source  
 1..10  
 /organism="Phytophthora infestans"  
 /mol\_type="mRNA"  
 /strain="88069 and 618"  
 /db\_xref="taxon:4787"  
 /sex="A1 and A2"  
 /clone\_lib="mating of 88069 (A1) and 618 (A2)"  
 /note="Vector: pSPORT1"  
**Query Match** 0.5%; Score 8.4; DB 1; Length 10;  
**Best Local Similarity** 90.0%; Pred. No. 25;  
**Matches** 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**QY** 196 ACGCCTAGCT 205  
 |||||  
 10 ACGCCAGCT 1  
**Db**  
**RESULT 54**  
**CV933903** 10 bp mRNA linear EST 25-JAN-2005  
**LOCUS** PMPCm\_5366 mating of 88069 (A1) and 618 (A2) Phytophthora  
**DEFINITION** infestans cDNA, mRNA sequence.  
**ACCESSION** CV933903  
**VERSION** CV933903.1 GI:58123518  
**KEYWORDS** EST.  
**SOURCE** Phytophthora infestans (potato late blight agent)  
**ORGANISM** Phytophthora infestans  
**REFERENCE** 1 (bases 1 to 10)  
 Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,  
 Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,  
 Lay,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,  
 Windaas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,  
 Mauch,F., van West,P., Maugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
 Lam,S.T. and Judelson,H.S.: 2005, 'Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi'  
**TITLE** Mo1. Plant-Microbe Interact. 18 (3), 229-243 (2005)  
**JOURNAL** 15782637  
**PUBMED**  
**COMMENT** Contact: Judelson HS  
 Department of Plant Pathology  
 University of California  
 Webber Hall, Riverside, CA 92521, USA  
 Tel: 909 787 4139  
 Fax: 909 787 4294

**FEATURES**  
 source  
 1..10  
 /organism="Phytophthora infestans"  
 /mol\_type="mRNA"  
 /strain="88069 and 618"  
 /db\_xref="taxon:4787"  
 /sex="A1 and A2"  
 /clone\_lib="mating of 88069 (A1) and 618 (A2)"  
 /note="Vector: pSPORT1"  
**Query Match** 0.5%; Score 8.4; DB 1; Length 10;  
**Best Local Similarity** 90.0%; Pred. No. 25;  
**Matches** 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**QY** 1294 GTGGGGGCC 1303  
 |||||  
 10 GGGGGGGCC 1  
**Db**  
**RESULT 55**  
**CV998934** 10 bp mRNA linear EST 03-DEC-2004  
**LOCUS** iv47e09.bl Right Cardiac Ventricle (DOGESt6) Canis familiaris cDNA,  
**DEFINITION** mRNA sequence.  
**ACCESSION** CV998934  
**VERSION** CV998934.1 GI:56269265  
**KEYWORDS** EST.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
**REFERENCE** 1 (bases 1 to 10)  
 Balija,V.S., Nascento,L.U. and McCombie,W.R.:  
 ESTs from Canis familiaris right cardiac ventricle (dog)  
 Unpublished (2004)  
**CONTACT** W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org.  
**FEATURES**  
 source  
 1..10  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"  
 /sex="Unknown"  
 /tissue\_type="Cardiac muscle"  
 /dev\_stage="3 month old normal canine"  
 /lab\_host="XL10 Gold"  
 /clone\_lib="Right Cardiac Ventricle (DOGESt6)"  
 /note="Organ: Heart; Vector: pBluescript II SK; Site: 1;  
 ECoRI; Site 2: XhoI; Library constructed using pBluescript  
 XR kit from Stratagene. Cloned cDNA was size selected  
 between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
 Pathology and Medical Genetics, School of Veterinary  
 Medicine, University of Pennsylvania, 3800 Spruce Street,  
 Philadelphia, PA 19104-6051"

LOCUS DN953871 10 bp mRNA linear EST 04-MAY-2005  
DEFINITION it65e04.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA  
sequence.  
ACCESSION DN953871  
VERSION DN953871.1 GI:63026009  
KEYWORDS EST.  
SOURCE Gnetum gnemon  
ORGANISM Gnetum gnemon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,  
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,  
Benfey, P., Coruzzi, G., and Stevenson, D.  
Expressed tag sequences from Gnetum female cone (NYBG)  
Unpublished (2003)  
TITLE Lita Annenberg Hazen Genome Sequencing Center  
JOURNAL Cold Spring Harbor Laboratory  
COMMENT PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Seq primer: -21M3UnivRev.  
Location/Qualifiers  
1..10  
/organism="Gnetum gnemon"  
/mol\_type="mRNA"  
/db\_xref="taxon:3382"  
/sex="female"  
/clone\_id="Gnetum female cone (NYBG)"  
/note="Organ: mature, unfertilized reproductive strobili;  
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:  
Completed 02/11/02, submitted for sequencing 02/12/02.  
Library: Stratagene ZAP Express cDNA Synthesis Kit. The  
library was size-fractionated to enrich for large inserts.  
Sample: NYBG accession number #436/84"  
Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1339 CCTCGTGCC 1348  
DB 10 CCTCGTGCC 1  
RESULT 57  
DR063352 10 bp mRNA linear EST 06-JUN-2005  
LOCUS ip64b02.g2 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA  
sequence.  
ACCESSION DR063352  
VERSION DR063352.1 GI:66986920  
KEYWORDS EST.  
SOURCE Ginkgo biloba (maidenhair tree)  
ORGANISM Ginkgo biloba  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoales; Ginkgo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,  
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,  
Benfey, P., Coruzzi, G., and Stevenson, D.  
Expressed tag sequences from Ginkgo megasporophyll (NYBG)  
Unpublished (2005)  
TITLE Lita Annenberg Hazen Genome Sequencing Center  
JOURNAL Cold Spring Harbor Laboratory  
COMMENT PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Seq primer: -21M3UnivRev.

FEATURES  
source Location/Qualifiers  
1..10  
/organism="Ginkgo biloba"  
/mol\_type="mRNA"  
/db\_xref="taxon:3311"  
/sex="female"  
/clone\_id="Ginkgo megasporophyll (NYBG)"  
/note="Organ: megasporophyll; Vector: pBK-CMV; Site 1:  
XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA  
Synthesis Kit. The library was size-fractionated to enrich  
for large inserts."  
QY 1339 CCTCGTGCC 1348  
DB 10 CCTCGTGCC 1  
Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 813 TGTGCTGCTC 822  
DB 1 TGTGCTGCTC 10  
RESULT 59  
CL652677 10 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0115C.A09 - PRI0115C.B21 (10) Mixed stage foetid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
ACCESSION CL652677  
VERSION CL652677.1 GI:50131455  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/tissue\_type="liver"  
/clone\_id="Liver regeneration after partial hepatectomy"  
QY 813 TGTGCTGCTC 822  
DB 1 TGTGCTGCTC 10  
Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 813 TGTGCTGCTC 822  
DB 1 TGTGCTGCTC 10  
RESULT 58  
DW386439 10 bp mRNA linear EST 14-JAN-2006  
LOCUS LRAGE02322 Liver regeneration after partial hepatectomy Rattus  
DEFINITION norvegicus cDNA, mRNA sequence.  
ACCESSION DW386439  
VERSION DW386439.1 GI:84890561  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Xu, C.S.  
TITLE Liver regeneration after PH  
JOURNAL Unpublished (2003)  
COMMENT Contact: Cun-Shuan Xu  
Henan Bioengineering Key Lab  
Henan Normal University  
No. 148 Jianshe Road, Xinxiang City, P.R.China  
Tel: 00863733328084  
Fax: 00863733326524  
Email: xucse@263.net.  
Location/Qualifiers  
1..10  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/tissue\_type="liver"  
/clone\_id="Liver regeneration after partial hepatectomy"  
QY 813 TGTGCTGCTC 822  
DB 1 TGTGCTGCTC 10  
Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 813 TGTGCTGCTC 822  
DB 1 TGTGCTGCTC 10  
RESULT 59  
CL652677 10 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0115C.A09 - PRI0115C.B21 (10) Mixed stage foetid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
ACCESSION CL652677  
VERSION CL652677.1 GI:50131455  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

Eukaryote; Metazoa; Nematoda; Chromodorea; Diplogasterida;  
Noodiologasteridae; Pristionchus.  
1 (bases 1 to 10)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an AcceD database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
1468147  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel.: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source  
1. 10  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_1lb="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 887 GTGAGATCCC 896  
|||  
10 GTGGGATCCC 1

RESULT 60  
CL694909  
LOCUS  
DEFINITION

CL694909 10 bp DNA linear GSS 10-JUN-2004  
PFI0165C.BR (10) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL694909  
CL694909.1 GI:50216817  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;  
Noodiologasteridae; Pristionchus.  
1 (bases 1 to 10)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an AcceD database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
1468147  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel.: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source  
1. 10  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"

/db\_xref="taxon:54126"  
/clone\_1lb="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1561 TGGGTTAGCG 1570  
|||||  
1 TGGGTTAGCG 10

RESULT 61  
DX040234/c  
LOCUS  
DEFINITION

DX040234 10 bp DNA linear GSS 10-JAN-2006  
KBRB039023R KBRB, Brassica rapa BamHI BAC library Brassica rapa  
subsp. pekinensis genomic clone KBRB039023, genomic survey  
sequence.  
DX040234  
DX040234.1 GI:84734531  
GSS.  
Brassica rapa subsp. pekinensis  
Brassica rapa subsp. pekinensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 10)  
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,  
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,  
Hahn,J.H. and Park,B.S.  
End sequence of Brassica rapa BamHI (KBRB) BAC clone  
Unpublished (2005)  
Contact: Beom-Seok Park  
Brassica Genomics Team  
National Institute of Agricultural Biotechnology  
225 Seodun-Dong, Suwon, 441-707, Korea  
Tel.: +82-31-299-1670  
Fax: +82-31-299-1672  
Email: pbeom@rda.go.kr  
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone  
KBRB039023  
Seq primer: M13 Reverse  
Class: BAC ends.

FEATURES  
source  
1. 10  
/organism="Brassica rapa subsp. pekinensis"  
/mol\_type="genomic DNA"  
/cultivar="Chilifu"  
/sub\_species="pekinensis"  
/db\_xref="taxon:51351"  
/clone="KBRB039023"  
/lab\_host="E.coli DH10B"  
/clone\_1lb="KBRB, Brassica rapa BamHI BAC library"  
/note="Vector: pCUGIBAC1; Site\_1: BamHI; Brassica rapa ssp  
pekinensis var. Chilifu BAC library (KBRB BAC) is provided  
by Yong-Pyo Lim (CNU)."

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 25;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 214 GATPACGCTCC 223  
|||||  
10 GATPACGCTCC 1

RESULT 62  
AJ592517/c  
LOCUS  
DEFINITION

AJ592517 10 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
621G09, genomic survey sequence.

ACCESSION AJ592517  
 VERSION AJ592517.1 GI:37942141  
 KEYWORDS GSS; right border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL PUBLISHED 12446565  
 REFERENCE 2 (bases 1 to 10)  
 AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
 1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone\_id="621G09"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 /note="T-DNA flanking sequence  
 right border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OR 990 CTGGCTGCC 999  
 |||||  
 |||||  
 10 CTGGCGGCC 1

Db 10 CTGGCGGCC 1

RESULT 63  
 AJ593578  
 LOCUS 10 bp DNA linear GSS 15-JAN-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 383D03, genomic survey sequence.  
 ACCESSION AJ593578  
 VERSION AJ593578.1 GI:37943202  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL PUBLISHED 12446565  
 REFERENCE 2 (bases 1 to 10)  
 AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics

PUBLISHED 12446565  
 REFERENCE 2 (bases 1 to 10)  
 AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
 1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone\_id="383D03"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 /note="T-DNA flanking sequence  
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OR 496 AACGAATGCT 505  
 |||||  
 |||||  
 1 AACGAATGAT 10

Db 1 AACGAATGAT 10

RESULT 64  
 AJ594650/c  
 LOCUS 10 bp DNA linear GSS 15-JAN-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 403C10, genomic survey sequence.  
 ACCESSION AJ594650  
 VERSION AJ594650.1 GI:37944274  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL PUBLISHED 12446565  
 REFERENCE 2 (bases 1 to 10)  
 AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics



program 'Genoplatne' (<http://www.genoplatne.com> and  
<http://genoplatne-info.infobiogen.fr>).

## FEATURES

Location/Qualifiers

## SOURCE

1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="403C10"  
 /clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 1..10  
 /note="T-DNA flanking sequence  
 left border"

## misc\_feature

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1572 AAACATCCA 1581

Db 10 AAACATCGA 1

## RESULT 65

LOCUS AJ600523 10 bp DNA linear GSS 15-JAN-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
 508B03, genomic survey sequence.

## ACCESSION

AJ600523.1 GI:37950151

VERSION GSS: right border; T-DNA flanking sequence.

KEYWORDS Arabidopsis thaliana (thale cress)

## SOURCE

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

## REFERENCE

1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
 Lepoint, L., Caboche, M., and Lecharny, A.  
 T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 10)

Balzerque, S.

Direct Submission  
 Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

## COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana  
 plants from INRA (Versailles). The DNA fragment(s) resulting from  
 the PCR were directly sequenced from the left or the right border  
 to determine the genomic sequence flanking the insertion. T-DNA  
 derived sequences were removed. Information to order the  
 corresponding mutant line and a link to a database providing a  
 graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
 been generated in the framework of the French plant genomics  
 program 'Genoplatne' (<http://www.genoplatne.com> and  
<http://genoplatne-info.infobiogen.fr>).

Location/Qualifiers

## FEATURES

## SOURCE

1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="508B03"  
 /clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 1..10  
 /note="T-DNA flanking sequence  
 right border"

## misc\_feature

Query Match 0.5%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1591 CAAAATCT 1600

Db 1 CAAAATCTT 10

## RESULT 66

LOCUS ATH521087/c 10 bp DNA linear GSS 08-FEB-2006  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
 052D09, genomic survey sequence.

## ACCESSION

AJ521087.1 GI:26789323

VERSION GSS: left border; T-DNA flanking sequence.

KEYWORDS Arabidopsis thaliana (thale cress)

## SOURCE

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis

## REFERENCE

1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
 Lepoint, L., Caboche, M., and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences  
 of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 10)

Balzerque, S.

Direct Submission  
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

## COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana  
 plants from INRA (Versailles). The DNA fragment(s) resulting from  
 the PCR were directly sequenced from the left or the right border  
 to determine the genomic sequence flanking the insertion. T-DNA  
 derived sequences were removed. Information to order the  
 corresponding mutant line and a link to a database providing a  
 graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
 been generated in the framework of the French plant genomics  
 program 'Genoplatne' (<http://www.genoplatne.com> and  
<http://genoplatne-info.infobiogen.fr>).

Location/Qualifiers

## FEATURES

## SOURCE

1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /cultivar="Wassilewskija"  
 /db\_xref="taxon:3702"  
 /clone="052D09"  
 /clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 1..10  
 /note="T-DNA flanking sequence  
 left border"

## misc\_feature

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1595 AATTCAT 1604

Db 10 AAACCTCAT 1

## RESULT 67

LOCUS ATH521360 10 bp DNA linear GSS 08-FEB-2006  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
 053G10, genomic survey sequence.

## ACCESSION

AJ521360

VERSION AJ521360.1 GI:26789596  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G., Lepoint,L., Caboche,M. and Lecharny,A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)  
 PUBMED 12446565  
 REFERENCE 2 (bases 1 to 10)  
 AUTHORS Balergue,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-NOV-2002) Balergue S., UMRGV, INRA/CNRS, 2 rue

COMMENT  
 Gaetan Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
 1..10  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /culturvar="Wassilewskija"  
 /db\_xref="taxon:3702"  
 /clone="053G10"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 /note="T-DNA flanking sequence  
 left border"

misc\_feature  
 1..10  
 /note="T-DNA flanking sequence  
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 775 AACAAATTT 784  
 |||||  
 1 AACAACTTT 10

Db  
 RESULT 68  
 LOCUS AJ590935  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 577B08, genomic survey sequence.  
 ACCESSION AJ590935  
 VERSION AJ590935.1 GI:37940559  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G., Lepoint,L., Caboche,M. and Lecharny,A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565  
 REFERENCE 2 (bases 1 to 13)  
 AUTHORS Balergue,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue

COMMENT  
 Gaetan Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
 1..13  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="577B08"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 /note="T-DNA flanking sequence  
 left border"

misc\_feature  
 1..13  
 /note="T-DNA flanking sequence  
 left border"

Query Match 0.5%; Score 8.4; DB 1; Length 13;  
 Best Local Similarity 90.0%; Pred. No. 87;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 374 GGATCATCTT 383  
 |||||  
 Db 1 GAATCATCTT 10

RESULT 69  
 LOCUS AL037095  
 DEFINITION DKF2564I2064.r1.564 (synonym: hfbp2) Homo sapiens cDNA clone DKF2564I2064, mRNA sequence.  
 ACCESSION AL037095  
 VERSION AL037095.1 GI:49681937  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.  
 TITLE EST (Duesterhoeft, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS

FEATURES  
 source  
 1..8  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKF2564I2064"  
 /tissue\_type="brain"  
 /dev\_stage="fetal"  
 /lab\_host="X1-2b1ue"  
 /clone\_lib="564 (synonym: hfbp2)"  
 /note="Vector: pAMP1, Site\_1: NotI; Site\_2: SalI"

Query Match 0.5%; Score 8; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 708 CTACTACT 715  
 |||||  
 Db 1 CTACTACT 8

RESULT 70  
 CF338362/c 8 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--01-H06.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-H06,  
 mRNA sequence.

ACCESSION CF338362  
 VERSION CF338362.1 GI:33825117  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source  
 1..8  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="RCL1--01-H06"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site\_1: SctI; Site\_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696  
 |||||  
 Db 8 CCAGCTTT 1

RESULT 71  
 CF339016/c 8 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--03-111.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-111,  
 mRNA sequence.

ACCESSION CF339016  
 VERSION CF339016.1 GI:33826415  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE 1 (bases 1 to 8)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source  
 1..8  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="RCL1--05-K22"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
 /note="Vector: pBluescript SK(+); Site\_1: SctI; Site\_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696  
 |||||  
 Db 8 CCAGCTTT 1

RESULT 72  
 CF339699/c 8 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-K22,  
 mRNA sequence.

ACCESSION CF339699  
 VERSION CF339699.1 GI:33827769  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers

FEATURES  
 source  
 1..8  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="RCL1--05-K22"

/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: SctI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696  
|||||  
8 CCAGCTTT 1

RESULT 73  
CF340204/c 8 bp mRNA linear EST 18-AUG-2003  
LOCUS RCL1--07-E15.g1 Regenerated callus lambda phage cDNA library (RCL1)  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-E15,  
mRNA sequence.  
ACCESSION CF340204 GI:33828768  
VERSION CF340204.1 GI:33828768  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Eriactroideae; Oryzaceae; Oryza.  
1 (bases 1 to 8)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
SOURCE Location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="RCL1--07-E15"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: SctI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 8; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1689 CCAGCTTT 1696  
|||||  
8 CCAGCTTT 1

RESULT 74  
CO790866/c 8 bp mRNA linear EST 05-AUG-2004  
LOCUS NT010D D03 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'  
DEFINITION similar to hypothetical protein, mRNA sequence.  
ACCESSION CO790866 GI:51006837  
VERSION CO790866.1 GI:51006837  
KEYWORDS EST.  
SOURCE Ambystoma mexicanum (axolotl)  
ORGANISM Ambystoma mexicanum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;  
Ambystoma.  
1 (bases 1 to 8)  
Habermann,B., Bebin,A.G., Herklitz,S., Volkmmer,M., Eckel,K.,  
Pehlike,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.  
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352  
expressed sequence tags from embryonic and regenerating blastema  
cDNA libraries  
Genome Biol. (2004) In press  
Contact: Eilly M. Tanaka  
Tanaka Lab  
Max Planck Institute of Molecular Cell Biology and Genetics,  
Dresden  
Pfeifenhauserstrasse 108, 01307 Dresden, Germany  
Tel: 0049 351 210 2620  
Fax: 0049 351 210 1489  
Email: tanaka@mpi-cbg.de  
Plate: NT010D row: 03 column: D  
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.  
Location/Qualifiers  
1..8  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Neural Tube, Notochord, Somites"  
/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/note="Vector: pCMVSPORT6, Site 1: NotI; Site 2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was plasmid primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
EMDH10B-TONA. Average insert size is 1.5 KB.  
TAG\_LIB=NT"

JOURNAL  
COMMENT  
Tanaka Lab  
Max Planck Institute of Molecular Cell Biology and Genetics,  
Dresden  
Pfeifenhauserstrasse 108, 01307 Dresden, Germany  
Tel: 0049 351 210 2620  
Fax: 0049 351 210 1489  
Email: tanaka@mpi-cbg.de  
Plate: NT010D row: 03 column: D  
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.  
Location/Qualifiers  
1..8  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Neural Tube, Notochord, Somites"  
/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/note="Vector: pCMVSPORT6, Site 1: NotI; Site 2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was plasmid primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
EMDH10B-TONA. Average insert size is 1.5 KB.  
TAG\_LIB=NT"

FEATURES  
SOURCE Location/Qualifiers  
1..8  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Neural Tube, Notochord, Somites"  
/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/note="Vector: pCMVSPORT6, Site 1: NotI; Site 2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was plasmid primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
EMDH10B-TONA. Average insert size is 1.5 KB.  
TAG\_LIB=NT"

Query Match 0.5%; Score 8; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GGTTGTT 179  
|||||  
8 GGTTGTT 1

RESULT 75  
CL887698 8 bp DNA linear GSS 30-AUG-2004  
LOCUS abf86c02.x1 Soybean random, unfiltered genomic library Glycine max  
DEFINITION genomic, genomic survey sequence.  
ACCESSION CL887698  
VERSION CL887698.1 GI:51629775  
KEYWORDS GSS.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max (soybean)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 8)  
Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,  
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and  
Stacey,G.

REFERENCE  
AUTHORS  
Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,  
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and  
Stacey,G.

TITLE Methylation filtered genomic sequences from Glycine max  
JOURNAL Unpublished (2004)  
COMMENT Contact: Gary Stacey  
University of Missouri  
108 Waters Hall, Columbia, MO 65211, USA  
Tel: 573-884-1267  
Fax: 573-882-0588  
Email: sctacey@missouri.edu  
Lidid: 230  
Class: shotgun.

FEATURES  
source Location/Qualifiers  
1..8

/organism="Glycine max"  
/mol\_type="genomic DNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/tissue\_type="Young leaves"  
/clone\_lib="Soybean random, unfiltered genomic library"  
/note="Vector: pOT2, Site\_1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. Libid: 230"

Query Match 0.5%; Score 8; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 ATTGTGCT 1427  
|||||  
1 ATTGTGCT 8

RESULT 76 9 bp mRNA linear EST 01-AUG-2003  
CA853358 B07D03.seq CDNA Peking library 12hr SCN3 Glycine max CDNA clone  
LOCUS B07D03 5', mRNA sequence.  
DEFINITION CA853358  
ACCESSION CA853358.1 GI:33390151  
VERSION EST.  
KEYWORDS Glycine max (soybean)  
SOURCE Glycine max  
ORGANISM Glycine max (soybean)  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 9)  
Alkharouf, N., Khan, R. and Matthews, B.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean  
JOURNAL infected by the soybean cyst nematode  
PUBMED Genome 47 (2), 380-388 (2004)  
15060591  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharouf@ars.usda.gov.

FEATURES  
source Location/Qualifiers  
1..9

/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="B07D03"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="CDNA Peking library 12hr SCN3"  
/note="Vector: pBluescript SK-; CDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript

SK-phagemid. "

Query Match 0.5%; Score 8; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1688 ACCAGCTTT 1696  
|||||  
DB 9 ACNAGCTTT 1

RESULT 77 9 bp mRNA linear EST 15-AUG-2003  
CF309109 ABE--03-C20.b1 ABE3-overexpressing transgenic rice plasmid CDNA  
LOCUS library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone  
DEFINITION ABE--03-C20, mRNA sequence.  
ACCESSION CF309109.1 GI:33680870  
VERSION EST.  
KEYWORDS Oryza sativa (japonica cultivar-group)  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 9)  
Kam, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
AUTHORS Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..9

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF--03-C20"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
CDNA library (ABF)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1603 ATTCTTCC 1610  
|||||  
DB 1 ATTCTTCC 8

RESULT 78 9 bp mRNA linear EST 17-MAY-2005  
DN988509 ZBBRA\_2F\_2-11\_04\_ZBBRA\_2F\_2-11\_04 G05.ab1 Bermuda grass line Zebra  
LOCUS subcloned cold acclimated CDNA library Cynodon dactylon CDNA clone  
DEFINITION ZBBRA\_2F\_2-11\_04\_ZBBRA\_2F\_2-11\_04 G05.ab1, mRNA sequence.  
ACCESSION DN988509.1 GI:66248336  
VERSION EST.  
KEYWORDS

SOURCE Cynodon dactylon (Bermuda grass)  
ORGANISM Cynodon dactylon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.  
1 (bases 1 to 9)  
Meimaitee, K.; Elavarthi, S. and Guenzi, A.C.  
Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays  
unpublished (2005)  
Contact: Guenzi AC  
Dep. of Plant and Soil Sciences  
Oklahoma State University  
368 Agriculture Hall, Stillwater, OK 74078-6028, USA  
Tel: 405-744-6028  
Fax: 405 744 6039  
Email: acg@mail.pss.okstate.edu  
PCR primers  
FORWARD: M13 forward  
BACKWARD: M13 Reverse  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..9  
/organism="Cynodon dactylon"  
/mol\_type="mRNA"  
/cultivar="Zebra"  
/db\_xref="taxon:28909"  
/clone="ZEBRA\_2F\_2-11\_04\_ZEBRA\_2F\_2-11\_04\_G05.ab1"  
/issue\_type="Crown"  
/lab\_host="E. coli"  
/clone\_lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"  
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR-select cDNA subtraction procedure."

Query Match 0.5%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 TTCACCC 107  
Db 9 TTCACCC 2

RESULT 79  
CL659917/c 9 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0135c\_F08 - PRI0135c\_B21 (9) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL659917  
VERSION CL659917  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida; Neodiplogasterida; Pristionchus.  
1 (bases 1 to 9)  
Strinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
AppaB: an Acedb database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..9  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBf108-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 TTGTCTT 312  
Db 1 TTGTCTT 8

RESULT 80  
CL681447 9 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0131a\_G08\_2 - PRI0131a\_BR (9) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL681447  
VERSION CL681447  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida; Neodiplogasterida; Pristionchus.  
1 (bases 1 to 9)  
Strinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
AppaB: an Acedb database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..9  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBf108-5 Fosmid vector"

RESULT 81  
CL659790 10 bp DNA linear GSS 09-JUN-2004  
LOCUS PRI0135b.B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
ACCESSION CL659790  
VERSION CL659790.1 GI:50144248  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE 1 (bases 1 to 10)  
Srinivasan,V., Otto,G.W., Kahlow,U., Gelsler,R. and Sommer,R.J.  
Arapad: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
JOURNAL PUBMED  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@uebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
FEATURES  
Location/Qualifiers  
1..10  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pGpfos-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 CCGCGGGA 902  
|||||  
1 CCGCGGGA 8

RESULT 82  
CF304081 10 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF1--04-A07.g1 ABF3-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (ABF1) Oryza sativa (Japanese cultivar-group) cDNA  
clone ABF1--04-A07, mRNA sequence.  
ACCESSION CF304081  
VERSION CF304081.1 GI:33675842  
KEYWORDS EST.  
SOURCE Oryza sativa (Japanese cultivar-group)  
ORGANISM Oryza sativa (Japanese cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 10)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Yonsei University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193

Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1..10  
/organism="Oryza sativa (Japanese cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--04-A07"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E. coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="Vector: Bluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGGA 1310  
|||||  
2 CACGAGGA 9

RESULT 83  
BM393918 10 bp mRNA linear EST 17-JAN-2002  
LOCUS 50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM393918  
VERSION BM393918.1 GI:18193971  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 10)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orisz,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
FEATURES  
Location/Qualifiers  
1..10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GGGGGCCC 1303  
|||||  
10 GGGGGCCC 3

RESULT 84  
BM395575/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM395575 10 bp mRNA linear EST 17-JAN-2002  
5009-0-1-A03.c.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
BM395575  
BM395575.1 GI:18195628  
EST.  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 10)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J., and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

1. .10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 17  
|||  
10 CCACCGCG 3

Db 10 CCACCGCG 3

RESULT 85  
BM396023/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM396023 10 bp mRNA linear EST 17-JAN-2002  
5009-0-15-F12.c.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
BM396023  
BM396023.1 GI:18196076  
EST.  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 10)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J., and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

1. .10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 17  
|||  
10 CCACCGCG 3

Db 10 CCACCGCG 3

FEATURES  
source

source  
1. .10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 17  
|||  
10 CCACCGCG 3

Db 10 CCACCGCG 3

RESULT 86  
BM397885/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM397885 10 bp mRNA linear EST 17-JAN-2002  
5009-0-38-E03.c.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
BM397885  
BM397885.1 GI:18197938  
EST.  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 10)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J., and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

1. .10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCACCGCG 17  
|||  
10 CCACCGCG 3

Db 10 CCACCGCG 3

RESULT 87  
CF921234/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

CF921234 10 bp mRNA linear EST 05-NOV-2003  
gmhrwv3-07 B06\_1 046 Soybean root hair subtracted cDNA library  
gmhrwv3 Glycine max cDNA, mRNA sequence.  
CF921234  
CF921234.1 GI:38192028  
EST.  
Glycine max (soybean)  
Glycine max (soybean)



ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.  
TITLE Expressed sequence tags from soybean root hair subtractive cDNA library  
JOURNAL Unpublished (2003)  
COMMENT Contact: Gary Stacey  
University of Missouri  
108 Waters Hall, Columbia, MO 65211, USA  
Tel: 573-884-4752  
Fax: 573-882-0588  
Email: stacey@missouri.edu  
Single pass sequence  
Seq primer: T7.

FEATURES  
source  
1..10  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/tissue\_type="root hairs"  
/clone\_id="Soybean root hair subtracted cDNA library gmHRW3"  
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 891 GATCCCCG 898  
Db 9 GATCCCCG 2

RESULT 88  
LOCUS CL681384  
DEFINITION CL681384 10 bp DNA linear GSS 09-JUN-2004  
PRIO1313a.B05\_2 - PRIO1313a.BR (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL681384  
VERSION CL681384.1 GI:50188392  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Gelsler, R. and Sommer, R.J.  
TITLE Aphabds: an Acged database for the nematode satellite organism Pristionchus pacificus  
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT Contact: Sommer, R.J.  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Classes: fosmid ends.  
FEATURES  
source  
1..10  
/location/Qualifiers  
/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_id="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 CTAGCTTC 207  
Db 1 CTAGCTTC 8

RESULT 89  
LOCUS AJ587026/c  
DEFINITION AJ587026 10 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 062F10, genomic survey sequence.  
ACCESSION AJ587026  
VERSION AJ587026.1 GI:37936615  
KEYWORDS GSS; left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Crandall, C., Denose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
PUBMED 1246565  
COMMENT 2 (bases 1 to 10)  
Balzerque, S.  
Direct Submision  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
source  
1..10  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="062F10"  
/clone\_id="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
1..10  
/note="T-DNA flanking sequence  
left border"

misc\_feature  
1..10  
/note="T-DNA flanking sequence  
left border"

Query Match 0.5%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 209 AAATGAT 216  
Db 9 AAATGAT 2

RESULT 90  
AJ598138/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AJ598138  
10 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 463E04, genomic survey sequence.

AJ598138  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)  
Balzerque, S.  
Direct Submission  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
Location/Qualifiers  
1..10  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="463E04"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
1..10  
/note="T-DNA flanking sequence  
left border"

misc\_feature  
1..10  
/note="T-DNA flanking sequence  
left border"

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1514 AACCATCA 1521  
|||||  
Db 9 AACCATCA 2

RESULT 91  
ATH523869  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

ATH523869  
10 bp DNA linear GSS 08-FEB-2006  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 063E02, genomic survey sequence.

AJ523869  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
Location/Qualifiers  
1..10  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassilewskija"  
/db\_xref="taxon:3702"  
/clone="063E02"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
1..10  
/note="T-DNA flanking sequence  
left border"

misc\_feature  
1..10  
/note="T-DNA flanking sequence  
left border"

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1755 CATTTCAG 1762  
|||||  
Db 1 CATTTCAG 8

RESULT 92  
ATH526713/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

ATH526713  
10 bp DNA linear GSS 08-FEB-2006  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 125C02, genomic survey sequence.

AJ526713  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

BRUNAUD, V., BALZERQUE, S., DUBREUCQ, B., AUBOURG, S., SAMSON, F., CHAUVIN, S., BECHTOLD, N., CRUAUD, C., DEROSE, R., PELLETIER, G., LEPOINTE, L., CABOCHÉ, M. and LECHARNY, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

FEATURES  
source  
Location/Qualifiers  
1..10  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassilewskija"  
/db\_xref="taxon:3702"  
/clone="063E02"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
1..10  
/note="T-DNA flanking sequence  
left border"

misc\_feature  
1..10  
/note="T-DNA flanking sequence  
left border"

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1755 CATTTCAG 1762  
|||||  
Db 1 CATTTCAG 8

RESULT 92  
ATH526713/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

ATH526713  
10 bp DNA linear GSS 08-FEB-2006  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 125C02, genomic survey sequence.

AJ526713  
GSS; left border; T-DNA flanking sequence.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

2 (bases 1 to 10)  
Balzerque, S.  
Direct Submission  
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source

```
1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Massillewskija"
    /db_xref="taxon:3702"
    /clone="125C02"
    /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Massillewskija"
misc_feature
1. 10
    /note="T-DNA flanking sequence
    left border"
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1214 AAATGAAA 1221

Db 9 AAATGAAA 2

RESULT 93  
ATH527413 10 bp DNA linear GSS 08-FEB-2006  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
DEFINITION AJ527413 genomic survey sequence.

ACCESSION AJ527413.1 GI:26795673  
VERSION GSS; left border; T-DNA flanking sequence.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepointec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
PUBMED 12446565  
2 (bases 1 to 10)  
REFERENCE Balzerque, S.  
AUTHORS Direct Submission  
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Creteil, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

## FEATURES

source

```
1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Massillewskija"
```

```
/db_xref="taxon:3702"
/clone="139F01"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Massillewskija"
1. 10
    /note="T-DNA flanking sequence
    left border"
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 AACTATT 419

Db 3 AACTATT 10

RESULT 94  
ATH53779 10 bp DNA linear GSS 08-FEB-2006  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
DEFINITION 382B01, genomic survey sequence.

ACCESSION AJ53779.1 GI:29370246  
VERSION GSS; left border; T-DNA flanking sequence.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepointec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
PUBMED 12446565  
2 (bases 1 to 10)  
REFERENCE Balzerque, S.  
AUTHORS Direct Submission  
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Creteil, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

## FEATURES

source

```
1. 10
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /cultivar="Massillewskija"
    /db_xref="taxon:3702"
    /clone="382B01"
    /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Massillewskija"
misc_feature
1. 10
    /note="T-DNA flanking sequence
    left border"
```

Query Match  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 TGTACAGA 184

|||||||

Db 2 TGTACAGA 9

RESULT 95  
LOCUS AJ681839/c 11 bp mRNA linear EST 29-JUN-2004  
DEFINITION AJ681839 CSEQRAN04 Sus scrofa cDNA clone C0001797\_P06, mRNA sequence.  
ACCESSION AJ681839  
VERSION AJ681839.1 GI:49414429  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE  
AUTHORS 1 (bases 1 to 11)  
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
JOURNAL Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
COMMENT Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arxgenomics.org.  
Location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001797\_P06"  
/issue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pb1uescriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

FEATURES  
source

Query Match 0.5%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCGCGG 18  
Db 11 CACCGCGG 4

RESULT 96  
LOCUS AJ682947/c 11 bp mRNA linear EST 29-JUN-2004  
DEFINITION AJ682947 CSEQRAN04 Sus scrofa cDNA clone C0001800\_K12, mRNA sequence.  
ACCESSION AJ682947  
VERSION AJ682947.1 GI:49415537  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE  
AUTHORS 1 (bases 1 to 11)  
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
JOURNAL Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
COMMENT Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics

FEATURES  
source

Query Match 0.5%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCGCGG 18  
Db 11 CACCGCGG 4

RESULT 97  
LOCUS AJ685455/c 11 bp mRNA linear EST 29-JUN-2004  
DEFINITION AJ685455 CSEQRAN04 Sus scrofa cDNA clone C0001800\_P05, mRNA sequence.  
ACCESSION AJ685455  
VERSION AJ685455.1 GI:49418045  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE  
AUTHORS 1 (bases 1 to 11)  
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
JOURNAL Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
COMMENT Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pb1uescriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arxgenomics.org.  
Location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001800\_P05"  
/issue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pb1uescriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."

FEATURES  
source

Query Match 0.5%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CACGCGG 18  
| | | | |  
Db 11 CACGCGG 4

RESULT 98  
AJ686546 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686546 CSEORAN04 Sus scrofa cDNA clone C0001812\_C13, mRNA  
DEFINITION sequence.  
AJ686546  
ACCESSION AJ686546.1 GI:49419136  
VERSION EST.  
KEYWORDS Sus scrofa (pig)  
SOURCE Sus scrofa  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;  
Sus.  
REFERENCE 1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
unpublished (2004)  
JOURNAL Contact: Anderson SI  
COMMENT Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options. Vector:PBHescriptII(KS+). R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001812\_C13"  
/tissue\_type="uterus"  
/clone\_id="CSEORAN04"  
/note="Vector: pbHescriptII(KS+); Site\_1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.4%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 69;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 580 ACGGCTGGC 590  
| | | | |  
Db 1 ACCGCGTGGC 11

RESULT 99  
AJ686590 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686590 CSEORAN04 Sus scrofa cDNA clone C0001812\_E11, mRNA  
DEFINITION sequence.  
AJ686590  
ACCESSION AJ686590.1 GI:49419180  
VERSION EST.  
KEYWORDS Sus scrofa (pig)  
SOURCE Sus scrofa  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;  
Sus.  
REFERENCE 1 (bases 1 to 11)  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
Development of cDNA and EST resources for studying reproduction and

JOURNAL unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options. Vector:PBHescriptII(KS+). R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
location/Qualifiers  
1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001812\_E11"  
/tissue\_type="uterus"  
/clone\_id="CSEORAN04"  
/note="Vector: pbHescriptII(KS+); Site\_1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.4%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 69;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 580 ACGGCTGGC 590  
| | | | |  
Db 1 ACCGCGTGGC 11

RESULT 100  
DU733106 11 bp DNA linear GSS 27-JAN-2006  
LOCUS DU733106  
DEFINITION AFK12073.g3 HF70\_10-07-02 uncultured marine microorganism  
HF70\_10-07-02 genomic clone HF0070\_029A08, genomic survey sequence.  
ACCESSION DU733106  
VERSION DU733106.1 GI:85742940  
KEYWORDS GSS.  
SOURCE uncultured marine microorganism HF70\_10-07-02  
ORANISM unclassified sequences; environmental samples.  
REFERENCE 1 (bases 1 to 11)  
DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,  
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.  
and Karl,D.M.  
Comparative genomics reveals ecological trends in stratified  
microbial communities in the ocean's interior  
Science (2006) in press  
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,  
Kerrie Barry, Tijana Glavanadelrio, David Bruce, Paul Richardson  
and Edward Delong  
US DOE Joint Genome Institute  
US DOE Joint Genome Institute  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA  
Tel: 617-253-5271  
Fax: 617-253-2679  
Email: PRichardson@lbl.gov; delong@mit.edu  
Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m  
Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/kg  
Class: formla ends.  
location/Qualifiers  
1..11  
/organism="uncultured marine microorganism HF70\_10-07-02"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:361144"  
/clone="HF0070\_029A08"  
/cell\_type="marine picoplankton, less than 1.8 um, greater  
than 0.22 um fraction"  
/clone\_id="HF70\_10-07-02"

/note="Vector: pCC1FOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 70 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth 70 m Temperature: 24.93 C Salinity: 35.21 psu Oxygen: 217.4 umol/kg"

Query Match 0.4%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 69;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1469 CCTTGACCTG 1479  
Db 1 CTTTGACCG 11

RESULT 101  
AJ655540

LOCUS 12 bp mRNA linear EST 28-JUN-2004  
DEFINITION AJ655540 KN277 Sus scrofa cDNA clone C0005190\_G13, mRNA sequence.  
ACCESSION AJ655540  
VERSION AJ655540.1 GI:49339572  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options. Vector:PB1uescriptII(SK+). R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13p Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES  
SOURCE Location/Qualifiers  
1..12

/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005190\_G13"  
/tissue\_type="embryo"  
/clone\_id="KN277"  
/note="Vector: PB1uescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.4%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 94;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 466 ACAGTGTGAA 476  
Db 1 ACTGTGAGAA 11

RESULT 102  
BM395918 12 bp mRNA linear EST 17-JAN-2002  
LOCUS BM395918  
DEFINITION 5009-0-14-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION Tetrahymena thermophila cDNA, mRNA sequence.  
BM395918

VERSION BM395918.1 GI:18195971

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Turkewitz,A.P., Karer,K.M., Jahn,C., Orías,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
SOURCE Location/Qualifiers  
1..12

/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.8; DB 1; Length 12;  
Best Local Similarity 81.8%; Pred. No. 94;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 438 CGCGAGGCGCT 448  
Db 2 CGCGGTGGCTT 12

RESULT 103

LOCUS CNS06E5N

DEFINITION 9 bp DNA linear GSS 17-JUN-2001

T3 end of clone A80A018H04 of library A80A from strain CBS 732 of Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL394689

VERSION AL394689.1 GI:12145788

KEYWORDS GSS.

SOURCE Zygosaccharomyces rouxii

ORGANISM Zygosaccharomyces rouxii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE 1 (bases 1 to 9)  
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolojin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Iepingie,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozeri-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Webołowski-Louvel,M., Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)  
PUBMED 11152876

REFERENCE 2 (bases 1 to 9)

AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 8. Zygosaccharomyces rouxii

JOURNAL FEBS Lett. 487 (1), 52-55 (2000)  
PUBMED 11152883

REFERENCE 3 (bases 1 to 9)  
AUTHORS Genoscope.

**TITLE** Direct Submission  
**JOURNAL** Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
**COMMENT** This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. uvarum, *Saccharomyces exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.  
**FEATURES**  
 source  
 1..9  
 /organism="Zygosaccharomyces rouxii"  
 /mol\_type="genomic DNA"  
 /strain="CBS 732"  
 /db\_xref="taxon:4956"  
 /clone="AR0A018H04"  
 /clone\_lib="AR0AA"  
 /note="end : T3"

**Query Match** 0.4%; Score 7.6; DB 1; Length 9;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**Db** 951 CAAATGA 958  
 1 CAAATGA 8

**RESULT 104**  
**LOCUS** DN988509  
**DEFINITION** DN988509 9 bp mRNA linear EST 17-MAY-2005  
 ZEBRA\_2F\_2-II\_04\_ZEBRA\_2F\_2-II\_04\_G05.ab1 Bermuda grass line zebra  
 substracted cold acclimated cDNA library Cynodon dactylon cDNA clone  
 ZEBRA\_2F\_2-II\_04\_ZEBRA\_2F\_2-II\_04\_G05.ab1, mRNA sequence.  
**ACCESSION** DN988509  
**VERSION** DN988509.1 GI:66248336  
**KEYWORDS** EST.  
**SOURCE** Cynodon dactylon (Bermuda grass)  
**ORGANISM** Cynodon dactylon  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Chloridoideae; Cynodonteae; Cynodon.  
**REFERENCE** 1 (bases 1 to 9)  
 Melmaitee, K., Elavarachi, S. and Guenzi, A.C.  
 Identification of differentially expressed genes associated with  
 cold acclimation using suppression subtraction hybridization (SSH)  
 and cDNA microarrays  
 Unpublished (2005)  
**CONTACT** Guenzi, AC  
 Dep. of Plant and Soil Sciences  
 Oklahoma State University  
 368 Agriculture Hall, Stillwater, OK 74078-6028, USA  
 Tel: 405-744-6028  
 Fax: 405-744-6039  
 Email: acg@mail.pss.okstate.edu  
**PCR PRIMERs**  
 FORWARD: M13 forward  
 BACKWARD: M13 Reverse  
**Seq primer:** M13 Forward.  
**FEATURES**  
 source  
 1..9  
 /organism="Cynodon dactylon"  
 /mol\_type="mRNA"  
 /culturvar="Zedira"  
 /db\_xref="taxon:28909"  
 /clone="ZEBRA\_2F\_2-II\_04\_ZEBRA\_2F\_2-II\_04\_G05.ab1"  
 /issue\_type="crown"  
 /lab\_host="B. coli"

**Query Match** 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Db** 1207 GGGCTGGAA 1215  
 1 GGGCTGGAA 9

**RESULT 105**  
**LOCUS** BU101621  
**DEFINITION** BU101621 9 bp mRNA linear EST 25-MAR-2004  
 PRODIGID193F1 Compugen\_targeted\_mRNA\_sequencing Homo sapiens cDNA,  
 mRNA sequence.  
**ACCESSION** BU101621  
**VERSION** BU101621.1 GI:45737021  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
**REFERENCE** 1 (bases 1 to 9)  
 Xie, H., Diber, A., Pollack, S., Nemzer, S., Safer, H., Melson, B.,  
 Olson, A., Hwang, J.-J., Endress, G.A., Savitsky, K. and Gill-More, R.  
 Bridging expressed sequence alignments through targeted cDNA  
 sequencing  
**COMMENT** Genomics 83 (4), 572-576 (2004)  
 Contact: Xie H  
 Compugen  
 7 Center Drive, Suite 9, Jamesburg, NJ 08831, USA  
 Tel: 609-655-5105 X 26  
 Fax: 609-655-5114  
 Email: han@compugen.com.  
**FEATURES**  
 source  
 1..9  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Compugen\_targeted\_mRNA\_sequencing"  
 /note="These sequences resulted from single pass  
 sequencing of PCR products from Compugen targeted mRNA  
 sequencing project. PCR primers and nested primers were  
 designed to join two neighboring expressed sequence  
 contigs based on Compugen LEADS expressed sequence cluster  
 and assembly platform. Reverse transcriptase PCR and  
 nested PCR reactions were performed by Prodyne Inc.  
 (Windser, CT 06095, USA) on normal human heart, brain,  
 lung, liver, placenta, and testis poly mRNA preparations  
 from Origin (Rockville, MD 20850, USA) with reagents from  
 Invitrogen (Carlsbad, California 92008). PCR products were  
 sequenced by Qiagen (Valencia, CA 91355)."

**Query Match** 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Db** 501 ATGCTACTA 509  
 1 ATGCTACTA 9

**RESULT 106**  
 CF307008/c

LOCUS CF307008 9 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HDAl--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
 clone library 1 (HDAl) Oryza sativa (japonica cultivar-group) cDNA  
 ACCESSION CF307008  
 VERSION CF307008.1 GI:33678769  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 9)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 LOCATION/Qualifiers  
 1..9  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HDAl--05-H11"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOUR"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
 phage cDNA library 1 (HDAl)"  
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1339 CCCTGTCG 1347  
 Db 9 CCCTGTCG 1

RESULT 107  
 LOCUS CF312817/c 9 bp mRNA linear EST 15-AUG-2003  
 DEFINITION ABR--08-L15.b1 ABR3-overexpressing transgenic rice plasmid cDNA  
 library (ABR) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABR--08-L15, mRNA sequence.  
 ACCESSION CF312817  
 VERSION CF312817.1 GI:33684578  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 9)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY

Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 LOCATION/Qualifiers  
 1..9  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABR--08-L15"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABR3-overexpressing transgenic rice plasmid  
 cDNA library (ABR)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1673 AAAATATA 1681  
 Db 9 AAAAAAAAA 1

RESULT 108  
 LOCUS CF313414/c 9 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--01-115.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--01-115, mRNA sequence.  
 ACCESSION CF313414  
 VERSION CF313414.1 GI:33685175  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
 clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 9)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 LOCATION/Qualifiers  
 1..9  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HD--01-115"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression



line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 107 CTCCTGCT 115  
Db 9 CTCGAGCT 1

RESULT 109  
CF318771/c 9 bp mRNA linear EST 15-AUG-2003  
LOCUS CF318771  
DEFINITION HD--09-A13.g1 OshDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-A13, mRNA sequence.  
CF318771  
ACCESSION CF318771.1 GI:33690532  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euhartioideae; Oryzaceae; Oryza.  
1 (bases 1 to 9)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
Source  
1..9  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiyar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HD--09-A13"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDACL-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1673 AAAATAAA 1681  
Db 9 AAAAAAAAAA 1

RESULT 110  
CF330649/c 9 bp mRNA linear EST 18-AUG-2003  
LOCUS CF330649  
DEFINITION NACL--06-H06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-H06, mRNA sequence.  
CF330649  
ACCESSION CF330649.1 GI:33809535  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euhartioideae; Oryzaceae; Oryza.  
1 (bases 1 to 9)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
Source  
1..9  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiyar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="NACL--06-H06"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1673 AAAATAAA 1681  
Db 9 AAAAAAAAAA 1

RESULT 111  
CO818814 9 bp mRNA linear EST 09-AUG-2004  
LOCUS CO818814  
DEFINITION CSECS120A07.PREN0028 Cabsau Normalised Berry Fruit Set Stage 28 (PREN0028) Vitis vinifera cDNA clone CSECS120A07 3', mRNA sequence.  
CO818814  
ACCESSION CO818814.1 GI:51050957  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; Vitaceae; Vitis.  
1 (bases 1 to 9)  
Iocco,P., Davies,C. and Thomas,M.R.  
Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon (2004)  
Unpublished (2004)  
Contact: Mark R. Thomas  
CSIRO Plant Industry  
CSIRO  
PO Box 350, Glen Osmond, SA, 5064, Australia  
Tel: 61 8 83038600  
Fax: 61 8 83038601  
Email: Mark.R.Thomas@csiro.au  
Seq primer: CCCGTCACGACGCTTGAACG (M13 forward)  
POLY-A=yes  
Location/Qualifiers

FEATURES  
Source  
1..9  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultiyar="Cabernet Sauvignon"

```

/db_xref="taxon:29760"
/clone="CSECS120A07"
/sex="Hermaphrodite"
/dev_stage="28 - modified E-L system"
/clone_1ib="CabSau Normalised Berry Fruit Set Stage 28
(PRE0028)"
/note="Organ: Fruit; Vector: pBL; A cDNA library from
preveraison fruit, 1-2 weeks post anthesis, at stage 28 of
the modified E-L system. Tissue collected from field grown
plants. A description of the modified E-L system can be
found in the paper by B. G. Coombe 'Adoption of a system
for identifying grapevine growth stages' (1995) Aust. J.
Grape and Wine Res. 1: 104-110."

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1508 ATCTGAGAC 1516
Db      1 ATCTGAGAC 9

RESULT 112
LOCUS      CV933314      9 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION      PMOcm_0671 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
ACCESSION      CV933314
VERSION      CV933314.1 GI:58122929
KEYWORDS      EST.
SOURCE      Phytophthora infestans (potato late blight agent)
ORGANISM      Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora.
REFERENCE      1 (bases 1 to 9)
AUTHORS      Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatkan,B., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windas,J., Binder,A., Birch,P.R.U., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Maugh,M.E., Yu,D., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson,H.S.
TITLE      Large-scale gene discovery in the oomycete Phytophthora infestans
reveals likely components of phytopathogenicity shared with true
fungi
JOURNAL      Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED      15782637
COMMENT      Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
FEATURES
source
1..9
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="A1 and A2"
/clone_1ib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPOR1"

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1651 CACTGAACT 1659
Db      1 CACCGAACT 9

RESULT 113

```

```

CX005921
LOCUS      CX005921      9 bp      mRNA      linear      EST 03-DEC-2004
DEFINITION      iv22h10.g1 Brain - Cerebellum Library (DOGEST8) Canis familiaris
cDNA, mRNA sequence.
ACCESSION      CX005921
VERSION      CX005921.1 GI:56277337
KEYWORDS      EST.
SOURCE      Canis familiaris (dog)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE      1 (bases 1 to 9)
AUTHORS      Balija,V., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris cerebellum (dog)
Unpublished (2004)
JOURNAL      Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
FEATURES
source
1..9
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cerebellum"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_1ib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site 1:
ECORI; Site 2: XhoI; Library constructed using plasmid
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      0.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      293 CAGCTGGC 301
Db      1 CAGCTGAC 9

RESULT 114
LOCUS      DT904968/c      9 bp      mRNA      linear      EST 19-SEP-2005
DEFINITION      BMSB16761 Hematopoietic stem cells Mus musculus cDNA, mRNA
sequence.
ACCESSION      DT904968
VERSION      DT904968.1 GI:75865454
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 9)
AUTHORS      Pritsker,M., Doniger,T.T., Kramer,L.C., Westcott,S.E. and
Lemischka,I.R.
Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
Proc. Natl. Acad. Sci. U.S.A. (2005) In press
JOURNAL      Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA

```

Tel: 609 258 5657  
Fax: 609 258 1704  
Email: pritsker@molbio.princeton.edu.  
Location/Qualifiers

## FEATURES

source

1..9  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="Hematopoietic stem cells"  
/cell\_type="Hematopoietic stem cells"  
/clone\_lib="Hematopoietic stem cells"  
/note="cDNA library was made from FACS-purified hematopoietic stem cells"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 TACCTGAAG 1050  
|||||  
Db 9 TACCTGCAG 1

RESULT 115  
DT909435 9 bp mRNA linear EST 19-SEP-2005  
LOCUS BMSB17098 Hematopoietic stem cells Mus musculus cDNA, mRNA  
DEFINITION  
Sequence.

ACCESSION DT909435  
VERSION DT909435  
KEYWORDS EST.  
SOURCE GI:75889921

ORGANISM Mus musculus (house mouse)  
Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 9)

AUTHORS Pritsker, M., Doniger, T. T., Kramer, L. C., Westcott, S. E. and Lemischka, I. R.  
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative Splicing

JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press  
COMMENT Contact: Pritsker M  
Lab of Ihor Lemischka, Department of Molecular Biology  
Princeton University  
Princeton, NJ 08544, USA  
Tel: 609 258 5657  
Fax: 609 258 1704  
Email: pritsker@molbio.princeton.edu.

FEATURES  
Location/Qualifiers

1..9  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="Hematopoietic stem cells"  
/cell\_type="Hematopoietic stem cells"  
/clone\_lib="Hematopoietic stem cells"  
/note="cDNA library was made from FACS-purified hematopoietic stem cells"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 428 ACCTGGCCT 436  
|||||  
Db 1 ACCGGGCCT 9

RESULT 116  
DV571332 9 bp mRNA linear EST 04-NOV-2005  
LOCUS DV571332  
DEFINITION 0058P0010A01\_3' library 58 - normalized (50 mix pooled juveniles +

adults) - female Taeniopygia guttata cDNA clone 0058P0010A01 3'

similar to unknown 0058P0010A01, mRNA sequence.

ACCESSION DV571332  
VERSION DV571332.1  
KEYWORDS GI:78432685  
EST.

SOURCE

ORGANISM

Taeniopygia guttata  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Estrildinae; Taeniopygia.  
1 (bases 1 to 9)

REFERENCE

Wada, K., Howard, J. T., McConnell, P., Lints, T., Rivas, M. V., Whitney, O., Horita, H., Patterson, M. A., White, S., Zhao, S., Sakaguchi, H., Hagihara, M., Shiraki, T., Hirozane-Kishikawa, T., Skene, P., Hayashizaki, Y., Carninci, P. and Jarvis, E. D.  
A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes  
Unpublished (2005)

JOURNAL

COMMENT

Other ESTs: 0058P00102.x0 A01  
Contact: Kazuhito Wada and Erich Jarvis  
Erich D. Jarvis Lab  
Duke University Medical Center - Department of Neurobiology  
Box 3209 Bryan Research Building, Durham, NC 27710, USA  
Tel: 919 681-1681  
Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu  
Plate: 0058P0010 row: A column: 01  
POLYA=NO.

FEATURES  
source

Location/Qualifiers  
1..9  
/organism="Taeniopygia guttata"  
/mol\_type="mRNA"  
/db\_xref="taxon:59729"  
/clone="0058P0010A01"  
/sex="female"  
/tissue\_type="brain"  
/dev\_stage="adult and juvenile"  
/clone\_lib="library 58 - normalized (50 mix pooled juveniles + adults) - female"  
/note="Organ: brain; Vector: pFLC-1; Site: 1; EcoRI; Site 2: BamHI; The library was constructed as described by Carninci, P. (2003) in DNA Microarrays: A Molecular Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.  
TAG\_TISSUE=whole brain  
TAG\_SEQ=gatccaacatagctnnnnnnnnnn"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 826 TTCTCTCCC 834  
|||||  
Db 1 TTGCTCCCC 9

RESULT 117  
CW95814 9 bp DNA linear GSS 29-DEC-2004  
LOCUS KBH011P15R KBHr, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBH011P15, genomic survey  
DEFINITION  
Sequence.

ACCESSION CW95814  
VERSION CW95814.1  
KEYWORDS GI:56851838  
GSS.

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 9)

REFERENCE Yang, T. J., Kwon, S. J., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M., Park, J. Y., Lim, M. H., Kim, H. I., Lim, Y. P. and Park, B. S.  
TITLE End sequence of Brassica rapa HindIII BAC library (KBHr)

JOURNAL Unpublished (2004)  
 COMMENT Contact: Beom-Seok Park  
 Brassica Genomics Team  
 National Institute of Agricultural Biotechnology  
 225 Seodun-Dong, Suwon, 441-707, Korea  
 Tel: +82-31-299-1670  
 Fax: +82-31-299-1672  
 Email: pbeom@rda.go.kr  
 BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone  
 KBrH011P15  
 Seq primer: M13 Reverse  
 Class: BAC ends.

FEATURES  
 source Location/Qualifiers  
 1..9  
 /organism="Brassica rapa subsp. pekinensis"  
 /mol\_type="genomic DNA"  
 /cultivar="Chifu"  
 /sub\_species="pekinensis"  
 /db\_xref="taxon:51351"  
 /clone="KBrH011P15"  
 /tissue\_type="Young leaves"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="KBrH, Brassica rapa HindIII BAC library"  
 /note="Vector: pCUGIBac1; Site 1: HindIII; Brassica rapa  
 ssp. pekinensis inbred line Chifu BAC library (KBrH BAC)  
 is provided by Yong-Pyo Lim."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1035 AGATCTCTA 1043  
 |||||  
 1 AGATCTATA 9

RESULT 118  
 CL663701 9 bp DNA linear GSS 09-JUL-2004  
 LOCUS PR10145a\_F06 - PR10145a.B21.1 (9) Mixed stage fosmid library of P.  
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.  
 ACCESSION CL663701  
 VERSION CL663701.1 GI:50153095  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 9)  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppaDB: an Acedb database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 JOURNAL 14681447  
 COMMENT Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 source Location/Qualifiers  
 1..9  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pDpfos-5 Fosmid vector"

var. California"  
 /note="Vector: pDpfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1422 TGTGCTCTC 1430  
 |||||  
 1 TGTGCTTTC 9

RESULT 119  
 CL672804 9 bp DNA linear GSS 09-JUL-2004  
 LOCUS PR1017d\_E02 - PR1017d.B21 (9) Mixed stage fosmid library of P.  
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.  
 ACCESSION CL672804  
 VERSION CL672804.1 GI:50173549  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 9)  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppaDB: an Acedb database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 JOURNAL 14681447  
 COMMENT Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 source Location/Qualifiers  
 1..9  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pDpfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 264 CACCTCGGA 272  
 |||||  
 1 CACCTCCGA 9

RESULT 120  
 CL682372 9 bp DNA linear GSS 09-JUL-2004  
 LOCUS PR10133d\_D05\_2 - PR10133d.BR (9) Mixed stage fosmid library of P.  
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.  
 ACCESSION CL682372  
 VERSION CL682372.1 GI:50189761  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

REFERENCE 1 Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 9)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
Apapadi: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447

JOURNAL PUBMED  
COMMENT  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@uebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES  
source  
1..9  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pGPIfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1681 AGTCGGAC 1689  
|||  
1 AGATCGGAC 9

Db 1

RESULT 121 9 bp DNA linear GSS 10-JAN-2006  
DX058225 KBRB063119 KBRB, Brassica rapa BamHI BAC library Brassica rapa  
LOCUS KBRB063119 KBRB, Brassica rapa BamHI BAC library Brassica rapa  
DEFINITION KBRB063119, genomic survey  
sequence.  
ACCESSION DX058225  
VERSION DX058225.1 GI:84752521  
KEYWORDS GSS.  
SOURCE Brassica rapa subsp. pekinensis  
ORGANISM Brassica rapa subsp. pekinensis  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 9)  
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,  
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,  
Hahn,J.H. and Park,B.S.  
End sequence of Brassica rapa BamHI (KBRB) BAC clone  
Unpublished (2005)  
Contact: Beom-Seok Park  
Brassica Genomics Team  
National Institute of Agricultural Biotechnology  
225 Seodun-Dong, Suwon, 441-707, Korea  
Tel.: +82-31-299-1670  
Fax: +82-31-299-1672  
Email: pbeom@da.go.kr  
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone  
KBRB063119  
Seq primer: M13 Reverse  
Class: BAC ends.

FEATURES  
source  
1..9  
/organism="Brassica rapa subsp. pekinensis"  
/mol\_type="genomic DNA"  
/culturivar="Chifu"

REFERENCE 1 /sub\_species="pekinensis"  
/db\_xref="taxon:51351"  
/clone="KBRB063119"  
/lab\_host="E.coli DH10B"  
/clone\_lib="KBRB, Brassica rapa BamHI BAC library"  
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp  
pekinensis var. Chifu BAC library (KBRB BAC) is provided  
by Yong-Pyo Lim (CNU)."

Query Match 0.4%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 733 CCACGACGA 741  
|||||  
9 CCACACAGA 1

Db 9

RESULT 122 10 bp mRNA linear EST 17-JAN-2002  
BM396011  
LOCUS 5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM396011  
VERSION BM396011.1 GI:18196064  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.  
1 (bases 1 to 10)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1..10  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 59;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGGAGGC 446  
|||||  
2 CGCGGTGGC 10

Db 2

RESULT 123 10 bp mRNA linear EST 17-JAN-2002  
BM398849  
LOCUS 5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM398849  
VERSION BM398849.1 GI:18198902  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
 1 (bases 1 to 10)  
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Oriae, E., Kirk, K.E.,  
 Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
 1..10  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript SK<sup>+</sup>; Details on library  
 preparation can be found in Chilcoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 59;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 438 CGCGGAGGC 446  
 |||||  
 2 CGCGGTGAC 10

RESULT 124  
 CF311011 10 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF-06-B02.D1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF-06-B02, mRNA sequence.  
 CF311011  
 CF311011.1 GI:33682772  
 EST.  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 10)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..10  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF-06-B02"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 59;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1410 CTCTCTCTC 1418  
 |||||  
 2 CTCTCTCTC 10

RESULT 125  
 CL694909/c 10 bp DNA linear GSS 10-JUL-2004  
 LOCUS PRI0165C\_A04.2 - PRI0165C.BR (10) Mixed stage fosmid library of P.  
 DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
 survey sequence.  
 CL694909  
 CL694909.1 GI:50216817  
 GSS.  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 10)  
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
 AppADB: an Acedb database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 14681447  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.  
 Location/Qualifiers  
 1..10  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pBplfos-5 Fosmid vector"

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 59;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 269 CGGACCCA 277  
 |||||  
 9 CGTACCCA 1

RESULT 126  
 AJ592517 10 bp DNA linear GSS 15-JAN-2004  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
 DEFINITION 621G09, genomic survey sequence.  
 AJ592517  
 AJ592517.1 GI:37942141  
 GSS.  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.  
 1 (bases 1 to 10)  
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
 AppADB: an Acedb database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 14681447  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.  
 Location/Qualifiers  
 1..10  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pBplfos-5 Fosmid vector"

ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
 Brunaud V., Balergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Cruaud C., Derose R., Pelletier G., Lepoint J., Caboche M. and Lecharny A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL 12446565  
 PUBMED 2 (bases 1 to 10)  
 REFERENCE Balergue S.  
 AUTHORS Direct Submission  
 TITLE Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomes program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>). Location/Qualifiers

FEATURES 1..10  
 source /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="621G09"  
 /clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 1..10  
 /note="T-DNA flanking sequence  
 right border"

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 59;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 22 GCGCGGCAG 30  
 |||||  
 Db 2 GCGCGGCAG 10

RESULT 127  
 AJ587026 10 bp DNA linear GSS 15-JAN-2004  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone 062F10, genomic survey sequence.  
 ACCESSION AJ587026  
 VERSION AJ587026.1 GI:37936615  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
 Brunaud V., Balergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Cruaud C., Derose R., Pelletier G., Lepoint J., Caboche M. and Lecharny A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL 12446565  
 PUBMED 2 (bases 1 to 10)  
 REFERENCE Balergue S.  
 AUTHORS Direct Submission  
 TITLE

JOURNAL Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomes program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>). Location/Qualifiers

FEATURES 1..10  
 source /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="062F10"  
 /clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Wassilewskija"  
 1..10  
 /note="T-DNA flanking sequence  
 left border"

Query Match 0.4%; Score 7.4; DB 1; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 59;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1715 ATTGCATT 1723  
 |||||  
 Db 1 AATCATT 9

RESULT 128  
 AJ679435 11 bp mRNA linear EST 29-JUN-2004  
 LOCUS AJ679435 CSEORAN04 Sus scrofa cDNA clone C0001779\_B18, mRNA sequence.  
 ACCESSION AJ679435  
 VERSION AJ679435.1 GI:49412022  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa (pig)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 11)  
 Anderson S.I., Finlayson H.A. and Archibald A.L.  
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 Unpublished (2004)  
 CONTACT: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options. Vector:pbuescriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, [www.arkgenomics.org](http://www.arkgenomics.org). Location/Qualifiers

FEATURES 1..11  
 source /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0001779\_B18"  
 /issue\_type="uterus"  
 /clone\_1lb="CSEORAN04"  
 /note="Vector: pbuescriptII(KS+); site 1: EcoRI; site 2: NotI; single pass sequencing. Normalised library

constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
AUTHORS  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446  
|||||  
Db 3 CGCGGTGSC 11

## RESULT 129

AJ681247 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ681247  
DEFINITION AJ681247 CSEQRAN04 Sus scrofa cDNA clone C001795\_I24, mRNA  
SEQUENCE  
ACCESSION AJ681247  
VERSION AJ681247.1 GI:49413837  
KEYWORDS  
SOURCE EST.  
ORGANISM Sus scrofa (pig)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:PBHuescriptII(KS+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
FEATURES  
source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001795\_I24"  
/issue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pBHuescriptII(KS+); Site\_1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446  
|||||  
Db 3 CGCGGTGSC 11

## RESULT 130

AJ683713 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ683713  
DEFINITION AJ683713 CSEQRAN04 Sus scrofa cDNA clone C001802\_O06, mRNA  
SEQUENCE  
ACCESSION AJ683713  
VERSION AJ683713.1 GI:49416303  
KEYWORDS  
SOURCE EST.  
ORGANISM Sus scrofa (pig)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:PBHuescriptII(KS+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
FEATURES  
source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001802\_O06"  
/issue\_type="uterus"  
/clone\_lib="CSEQRAN04"  
/note="Vector: pBHuescriptII(KS+); Site\_1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 438 CGCGAGGC 446  
|||||  
Db 3 CGCGGTGSC 11

## RESULT 131

AJ686459 11 bp mRNA linear EST 29-JUN-2004  
LOCUS AJ686459  
DEFINITION AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811\_K23, mRNA  
SEQUENCE  
ACCESSION AJ686459  
VERSION AJ686459.1 GI:49419049  
KEYWORDS  
SOURCE EST.  
ORGANISM Sus scrofa (pig)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
Sus.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:PBHuescriptII(KS+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
FEATURES  
source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001811\_K23"



/tissue\_type="uterus"  
/clone\_id="CSEORAN04"  
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGGAGGC 446  
|||||  
Db 3 CGCGGTGGC 11

RESULT 132  
BM396384 11 bp mRNA linear EST 17-JAN-2002  
LOCUS  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM396384  
VERSION BM396384.1 GI:18196422  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,V. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1..11  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGGAGGC 446  
|||||  
Db 3 CGCGGTGGC 11

RESULT 133  
BM397892 11 bp mRNA linear EST 17-JAN-2002  
LOCUS  
DEFINITION 5009-0-38-F04.c.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM397892  
VERSION BM397892.1 GI:18197945  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 11)  
Query Match 0.4%; Score 7.4; DB 1; Length 12;  
Best Local Similarity 88.9%; Pred. No. 11e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,V. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1..11  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 11;  
Best Local Similarity 88.9%; Pred. No. 89;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 438 CGCGGAGGC 446  
|||||  
Db 3 CGCGGTGGC 11

RESULT 134  
BM398341 12 bp mRNA linear EST 17-JAN-2002  
LOCUS  
DEFINITION 5009-0-44-D05.c.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM398341  
VERSION BM398341.1 GI:18198394  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenida; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,V. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1..12  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.4; DB 1; Length 12;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 CGCGTGGC 10

RESULT 135  
AJ666341/c  
LOCUS  
DEFINITION AJ666341 CSEQRAN09 Sus scrofa cDNA clone C0000033\_C09, mRNA  
SEQUENCE.  
AJ666341 GI:49350792  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Sus scrofa (pig)  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
TITLE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
JOURNAL Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
COMMENT Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -mismscore 20 and -mismatch 12 options. Vector:pbLuescriptII(KS+). R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.atkgenomics.org.

FEATURES  
source location/Qualifiers  
1..13  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0000033\_C09"  
/tissue\_type="placenta"  
/clone\_lib="CSEQRAN09"  
/note="Vector: pbLuescriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.4%; Score 7.4; DB 1; Length 13;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1496 GAAATTCCTC 1504  
|||||  
9 GAATTTCCC 1

Db

RESULT 136  
CF297970/c  
LOCUS  
DEFINITION CF297970 8 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-Cl6.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-Cl6, mRNA  
SEQUENCE.  
CF297970 GI:33669731  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Eihartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 8)  
TITLE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiyar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--06-009"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 633 GCTGTCA 639  
|||||  
8 GCTGTCA 2

Db

RESULT 137  
CF305141  
LOCUS  
DEFINITION CF305141 8 bp mRNA linear EST 15-AUG-2003  
ABF1--06-009.g1 ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--06-009, mRNA sequence.  
CF305141  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM CF305141.1 GI:33676902  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Eihartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 8)  
TITLE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
JOURNAL Large-scale Sequencing Analysis of Rice ESTs  
COMMENT Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultiyar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--06-009"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)"  
/note="Vector: pLuescript SK(+); Site 1: EcoRI; Site\_2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression  
line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309  
Db 2 CACGAGG 8

## RESULT 138

CF306116 8 bp mRNA linear EST 15-AUG-2003  
LOCUS HDAL1--02-L22.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA  
clone HDAL1--02-L22, mRNA sequence.

ACCESSION CF306116 GI:33677877

## VERSION

EST.

## KEYWORDS

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

## JOURNAL

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

## SOURCE

1. .8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDAL1--02-L22"  
/cissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
was inserted into lambda Uni-ZAP XR vector at 5' end with  
EcoRI and 3' end with XhoI site. mRNA was derived from  
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309  
Db 2 CACGAGG 8

## RESULT 139

CF306762 8 bp mRNA linear EST 15-AUG-2003  
LOCUS HDAL1--04-M13.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA  
clone HDAL1--04-M13, mRNA sequence.

ACCESSION CF306762 GI:33678523

KEYWORDS EST.

## SOURCE

## ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

## JOURNAL

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

## SOURCE

1. .8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDAL1--04-M13"  
/cissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
was inserted into lambda Uni-ZAP XR vector at 5' end with  
EcoRI and 3' end with XhoI site. mRNA was derived from  
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309  
Db 2 CACGAGG 8

## RESULT 140

CF322514 8 bp mRNA linear EST 18-AUG-2003  
LOCUS HDN--01-E13.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
clone HDN--01-E13, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

## JOURNAL

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

## SOURCE

1. .8

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0.4%; Score 7; DB 1; Length 8;

Qy 1303 CACGAGG 1309  
 Db 2 CACGAGG 8

## RESULT 141

LOCUS CF322653 8 bp mRNA linear EST 18-AUG-2003  
 DEFINITION HDN--01-K24.g1 OsHDA1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN--01-K24, mRNA sequence.

ACCESSION CF322653  
 VERSION CF322653.1 GI:33793540  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
 source location/Qualifiers

1..8  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HDN--01-K24"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OsHDA1-overexpressing transgenic rice lambda phage CDNA library II (HDN)"  
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309  
 Db 2 CACGAGG 8

## RESULT 142

LOCUS CF323889 8 bp mRNA linear EST 18-AUG-2003  
 DEFINITION HDN--05-A16.g1 OsHDA1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN--05-A16, mRNA sequence.

ACCESSION CF323889  
 VERSION CF323889.1 GI:33796043  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
 source location/Qualifiers

1..8  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HDN--05-A16"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OsHDA1-overexpressing transgenic rice lambda phage CDNA library II (HDN)"  
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1303 CACGAGG 1309  
 Db 2 CACGAGG 8

## RESULT 143

LOCUS CF324406 8 bp mRNA linear EST 18-AUG-2003  
 DEFINITION HDN--06-H05.g1 OsHDA1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN--06-H05, mRNA sequence.

ACCESSION CF324406  
 VERSION CF324406.1 GI:33797080  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN-06-H05"  
/issue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDA1-overexpressing transgenic rice lambda  
phage cDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309  
|||||  
2 CACGAGG 8

Db

RESULT 144  
CF325379  
LOCUS JMT1--03-B08.g1 AtUMT-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA  
clone JMT1--03-B08, mRNA sequence.  
ACCESSION CF325379  
VERSION CF325379.1 GI:33799039  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 8)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Contact: Nahm B.H.  
Unpublished (2003)  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT1--03-B08"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="AtUMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

/lab\_host="E.coli SOLR"  
/clone\_lib="AtUMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309  
|||||  
2 CACGAGG 8

Db

RESULT 145  
CF325469  
LOCUS JMT1--03-F06.g1 AtUMT-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA  
clone JMT1--03-F06, mRNA sequence.  
ACCESSION CF325469  
VERSION CF325469.1 GI:33799223  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 8)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Contact: Nahm B.H.  
Unpublished (2003)  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT1--03-F06"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="AtUMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309  
|||||  
2 CACGAGG 8

Db

RESULT 146  
CF325485

LOCUS CF325485 8 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT1--03-F22.g1 ActMT-overexpressing transgenic rice lambda phage  
cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA  
clone JMT1--03-F22, mRNA sequence.  
ACCESSION CF325485  
VERSION CF325485.1 GI:33799255  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Euhartioideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 8)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT1--03-F22"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ActMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis thaliana Carboxyl  
methyltransferase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAG 1309  
Db 2 CACGAG 8

RESULT 147  
LOCUS CF330558/c 8 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--06-F04.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA  
sequence.  
ACCESSION CF330558  
VERSION CF330558.1 GI:33809354  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Euhartioideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 8)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="NACL--06-F04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 GCTGTCA 639  
Db 8 GCTGTCA 2

RESULT 148  
LOCUS CF339091/c 8 bp mRNA linear EST 18-AUG-2003  
DEFINITION RCL1--03-M05.g1 Regenerated callus lambda phage cDNA library (RCL1)  
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-M05,  
mRNA sequence.  
ACCESSION CF339091  
VERSION CF339091.1 GI:33826564  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep  
clade; Euhartioideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 8)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers  
1..8  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="RCL1--03-M05"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library  
(RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with SstI and 3' end with XhoI site. Callus was  
induced on 2N6 media for 30 days and cultured for 36hrs on  
regenerated media"

Query Match 0.4%; Score 7; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 AGCTCCA 1102  
8 AGCTCCA 2

## RESULT 149

CV933258 8 bp mRNA linear EST 25-JAN-2005  
LOCUS CV933258  
DEFINITION PMCM 0140 mating of 88069 (A1) and 618 (A2) Phytophthora infestans  
cDNA, mRNA sequence.

ACCESSION CV933258  
VERSION CV933258.1 GI:58122873  
KEYWORDS EST.

SOURCE Phytophthora infestans (potato late blight agent)  
ORGANISM Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (bases 1 to 8)  
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,  
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatikan,E., Gaffney,T.,  
Lam,S.T., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,  
Mindas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,  
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
Lam,S.T. and Udelsdon, H.S.

TITLE Large-scale gene discovery in the oomycete Phytophthora infestans  
reveals likely components of phytopathogenicity shared with true  
fungi  
Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

JOURNAL PUBMED 15782637  
COMMENT Contact: Judelson HS  
Department of Plant Pathology  
University of California  
Webber Hall, Riverside, CA 92521, USA  
Tel: 909 787 4199  
Fax: 909 787 4294  
Email: howard.judelson@ucr.edu.

FEATURES  
source Location/Qualifiers

1..8  
/organism="Phytophthora infestans"  
/mol\_type="mRNA"  
/strain="88069 and 618"  
/db\_xref="taxon:4787"  
/sex="A1 and A2"  
/clone\_lib="mating of 88069 (A1) and 618 (A2)"  
/note="Vector: pSPORT1"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 ACCAGCT 1694  
2 ACCAGCT 8

## RESULT 150

CV933304 8 bp mRNA linear EST 25-JAN-2005  
LOCUS CV933304  
DEFINITION PMCM 0589 mating of 88069 (A1) and 618 (A2) Phytophthora infestans  
cDNA, mRNA sequence.

ACCESSION CV933304  
VERSION CV933304.1 GI:58122919  
KEYWORDS EST.

SOURCE Phytophthora infestans (potato late blight agent)  
ORGANISM Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (bases 1 to 8)  
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,  
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatikan,E., Gaffney,T.,  
Lam,S.T., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,  
Mindas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,  
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
Lam,S.T. and Udelsdon, H.S.

Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
Lam,S.T. and Udelsdon, H.S.

TITLE Large-scale gene discovery in the oomycete Phytophthora infestans  
reveals likely components of phytopathogenicity shared with true  
fungi  
Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)

JOURNAL PUBMED 15782637  
COMMENT Contact: Judelson HS  
Department of Plant Pathology  
University of California  
Webber Hall, Riverside, CA 92521, USA  
Tel: 909 787 4199  
Fax: 909 787 4294  
Email: howard.judelson@ucr.edu.

FEATURES  
source Location/Qualifiers

1..8  
/organism="Phytophthora infestans"  
/mol\_type="mRNA"  
/strain="88069 and 618"  
/db\_xref="taxon:4787"  
/sex="A1 and A2"  
/clone\_lib="mating of 88069 (A1) and 618 (A2)"  
/note="Vector: pSPORT1"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 ACCAGCT 1694  
2 ACCAGCT 8

## RESULT 151

CV933304 8 bp mRNA linear EST 03-DEC-2004  
LOCUS CV933304  
DEFINITION PMCM 0589 mating of 88069 (A1) and 618 (A2) Phytophthora infestans  
cDNA, mRNA sequence.

ACCESSION CV933304  
VERSION CV933304.1 GI:58122919  
KEYWORDS EST.

SOURCE Phytophthora infestans (potato late blight agent)  
ORGANISM Eukaryota; Stramenopiles; Oomycetes; Peronosporales; Phytophthora.

REFERENCE 1 (bases 1 to 8)  
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,  
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatikan,E., Gaffney,T.,  
Lam,S.T., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,  
Mindas,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,  
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
Lam,S.T. and Udelsdon, H.S.

Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,  
Lam,S.T. and Udelsdon, H.S.

FEATURES  
source Location/Qualifiers

1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XJ10 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOGS77)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Tissue supplied by Mark Haakins VMD, PhD,  
Pathology and Medical Genetics, School of Veterinary  
Medicine, University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGC 1309  
|||||  
7 CACGAGC 1

Db

RESULT 152  
CX001172/c 8 bp mRNA linear EST 03-DEC-2004  
LOCUS  
DEFINITION i439e06.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX001172  
VERSION CX001172.1 GI:56272588  
KEYWORDS EST.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Bajaja,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.

FEATURES  
source Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOGEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site\_1:  
EcoRI; Site\_2: XhoI; Library constructed using pBluescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
Pathology and Medical Genetics, School of Veterinary  
Medicine, University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GGGGGGCC 1302  
|||||  
7 GGGGGGCC 1

Db

RESULT 153  
CX001200 8 bp mRNA linear EST 03-DEC-2004  
LOCUS  
DEFINITION i439f09.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX001200  
VERSION CX001200.1 GI:56272616  
KEYWORDS EST.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Bajaja,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.

FEATURES  
source Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

RESULT 154  
CX001601/c 8 bp mRNA linear EST 03-DEC-2004  
LOCUS  
DEFINITION i442a05.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX001601  
VERSION CX001601.1 GI:56273017  
KEYWORDS EST.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Bajaja,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.

FEATURES  
source Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"



/clone.lib="Left Cardiac Ventricle (DOGE5T7)"  
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
 EcoRI; Site 2: XhoI; Library constructed using pBluescript  
 XR kit from Stratagene. Cloned cDNA was size selected  
 between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
 Pathology and Medical Genetics, School of Veterinary  
 Medicine, University of Pennsylvania, 3800 Spruce Street,  
 Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1296 GGGGGCC 1302  
 |||||  
 Db 7 GGGGGCC 1

# RESULT 155

LOCUS CX001811 8 bp mRNA linear EST 03-DEC-2004  
 DEFINITION iV43b11.g1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,  
 mRNA sequence.

ACCESSION CX001811 GI:56273227  
 VERSION CX001811.1 GI:56273227  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 8)  
 AUTHORS Ballig, V.S., Nascimento, L.U. and McCombie, W.R.  
 TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mccombie@cshl.org.

FEATURES  
 source Location/Qualifiers

1..8  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"  
 /sex="Unknown"  
 /tissue\_type="Cardiac muscle"  
 /dev\_stage="3 month old normal canine"  
 /lab\_host="XL10 Gold"  
 /clone.lib="Left Cardiac Ventricle (DOGE5T7)"  
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
 EcoRI; Site 2: XhoI; Library constructed using pBluescript  
 XR kit from Stratagene. Cloned cDNA was size selected  
 between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
 Pathology and Medical Genetics, School of Veterinary  
 Medicine, University of Pennsylvania, 3800 Spruce Street,  
 Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309  
 |||||  
 Db 2 CACGAGG 8

RESULT 156  
 LOCUS CX001864/C 8 bp mRNA linear EST 03-DEC-2004  
 DEFINITION iV43e04.b1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,

mRNA sequence.  
 ACCESSION CX001864  
 VERSION CX001864.1 GI:56273280  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 8)  
 AUTHORS Ballig, V.S., Nascimento, L.U. and McCombie, W.R.  
 TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mccombie@cshl.org.

FEATURES  
 source Location/Qualifiers

1..8  
 /organism="Canis familiaris"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9615"  
 /sex="Unknown"  
 /tissue\_type="Cardiac muscle"  
 /dev\_stage="3 month old normal canine"  
 /lab\_host="XL10 Gold"  
 /clone.lib="Left Cardiac Ventricle (DOGE5T7)"  
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
 EcoRI; Site 2: XhoI; Library constructed using pBluescript  
 XR kit from Stratagene. Cloned cDNA was size selected  
 between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
 Pathology and Medical Genetics, School of Veterinary  
 Medicine, University of Pennsylvania, 3800 Spruce Street,  
 Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAGG 1309  
 |||||  
 Db 7 CACGAGG 1

# RESULT 157

LOCUS CX001954 8 bp mRNA linear EST 03-DEC-2004  
 DEFINITION iV44a06.g1 Left Cardiac Ventricle (DOGE5T7) Canis familiaris cDNA,  
 mRNA sequence.

ACCESSION CX001954  
 VERSION CX001954.1 GI:56273370  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 8)  
 AUTHORS Ballig, V.S., Nascimento, L.U. and McCombie, W.R.  
 TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mccombie@cshl.org.

FEATURES  
 source Location/Qualifiers

1..8

/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="X110 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site\_1: EcORI; Site\_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309  
|||||

Db 2 CACGAG 8

RESULT 158  
LOCUS CX001980 8 bp mRNA linear EST 03-DEC-2004  
DEFINITION i144b07.g1 Left Cardiac Ventricle (DOEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX001980  
VERSION CX001980.1 GI:56273396  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.  
Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="X110 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site\_1: EcORI; Site\_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309  
|||||

Db 2 CACGAG 8

REFERENCE  
AUTHORS Baliya,V.S., Nascimento,L.U. and McCombie,W.R.  
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)  
JOURNAL Unpublished (2004)  
COMMENT Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.  
Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="X110 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site\_1: EcORI; Site\_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Db 2 CACGAG 8

RESULT 159  
LOCUS CX002359 8 bp mRNA linear EST 03-DEC-2004  
DEFINITION i131d02.g1 Left Cardiac Ventricle (DOEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX002359  
VERSION CX002359.1 GI:56273775  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org.  
Location/Qualifiers  
1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="X110 Gold"  
/clone\_lib="Left Cardiac Ventricle (DOEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site\_1: EcORI; Site\_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 CACGAG 1309  
|||||

Db 2 CACGAG 8

RESULT 160  
LOCUS CX002747 8 bp mRNA linear EST 03-DEC-2004  
DEFINITION i1331d0.g1 Left Cardiac Ventricle (DOEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX002747  
VERSION CX002747.1 GI:56274163  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 8)  
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcconbie@cshl.org

FEATURES  
source  
Location/Qualifiers

1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_id="Left Cardiac Ventricle (DOGEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
EcoRI; Site 2: XhoI; Library constructed using pBluescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
Pathology and Medical Genetics, School of Veterinary  
Medicine, University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309  
|||||  
2 CACGAGG 8

RESULT 161  
LOCUS CX003296 8 bp mRNA linear EST 03-DEC-2004  
DEFINITION i366f10.g1 left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX003296  
VERSION CX003296.1 GI:56274712  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 8)  
Balija,V.S., Nascimbeno,L.U. and McCombie,W.R.  
ESTs from Canis familiaris left cardiac ventricle (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcconbie@cshl.org

FEATURES  
source  
Location/Qualifiers

1..8  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/tissue\_type="Cardiac muscle"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_id="Left Cardiac Ventricle (DOGEST7)"  
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:  
EcoRI; Site 2: XhoI; Library constructed using pBluescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,  
Pathology and Medical Genetics, School of Veterinary  
Medicine, University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1303 CACGAGG 1309  
|||||  
2 CACGAGG 8

RESULT 162  
LOCUS DR025726 8 bp mRNA linear EST 26-MAY-2005  
DEFINITION Osmo00576 F. cylindrus osmotic stress library Fragiliariopsis  
cylindrus cDNA clone Fcyl187a23h01.sl, mRNA sequence.  
ACCESSION DR025726  
VERSION DR025726.1 GI:66748089  
KEYWORDS EST.

SOURCE Fragiliariopsis cylindrus  
Fragiliariopsis cylindrus

ORGANISM Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;  
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragiliariopsis.

REFERENCE 1 (bases 1 to 8)  
Krell,A. and Gloeckner,G.  
Analysis of an osmotic stress induced cDNA library of the  
psychrophilic diatom Fragiliariopsis cylindrus  
Unpublished (2004)  
Contact: Krell, Andreas; Gloeckner, Gernot  
Biological Oceanography, Sea ice research; Genome Analysis  
Alfred-Wegener-Institute for Polar and Marine Research; Institute  
for Molecular Biotechnology  
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr.  
11, D-07745 Jena, Germany  
Tel: ++49 471 48311812; ++49 3641 656440  
Fax: ++49 471 48311425; ++49 3641 656255  
Email: skrell@wi-bremenhaven.de; gernot@imb-jena.de

PCR Primers  
FORWARD: 5'M13  
BACKWARD: 3'M13  
Seq primer: 5'GTAAACGACGCGCCAG 3'.  
Location/Qualifiers

1..8  
/organism="Fragiliariopsis cylindrus"  
/mol\_type="mRNA"  
/db\_xref="taxon:186039"  
/clone="Fcyl187a23h01.sl"  
/clone\_id="F. cylindrus osmotic stress library"  
/note="Samples for total RNA isolation were taken  
continuous for 5 days after a salt shock treatment  
increasing salinity from 34 to 60 PSU. Total RNA  
extraction was performed with RNAqueous (Ambion) and mRNA  
purification with polyA Purist (Ambion). Further steps  
were carried out as described in the Clontecher Kit. cDNA  
size fractionation was carried out with CHROMA Spin-400  
columns and additionally on a gel."

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 AAAAATC 1599  
|||||  
1 AAAAATC 7

RESULT 163  
LOCUS DT909735 8 bp mRNA linear EST 19-SEP-2005  
DEFINITION BMSB16597 Hematopoietic stem cells Mus musculus cDNA, mRNA  
sequence.  
ACCESSION DT909735  
VERSION DT909735.1 GI:75890216  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 8)  
Pritsker M., Doniger, T.T., Kramer, L.C., Westcott, S.E. and  
Lemischka, I.R.  
Diversification of Stem Cell Molecular Repertoire by Alternative  
Splicing  
Proc. Natl. Acad. Sci. U.S.A. (2005) In press

JOURNAL Contact: Pritsker M  
Lab of Ihor Lemischka, Department of Molecular Biology  
Princeton University  
Princeton, NJ 08544, USA  
Tel: 609 258 5657  
Fax: 609 258 1704  
Email: pritsker@molbio.princeton.edu.

COMMENT Location/Qualifiers

FEATURES

source

1..8  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="Hematopoietic stem cells"  
/cell\_type="Hematopoietic stem cells"  
/clone\_lib="Hematopoietic stem cells"  
/note="cDNA library was made from FACS-purified  
hematopoietic stem cells"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 GCTGCAG 166  
|||||  
1 GCTGCAG 7

Db

RESULT 164  
CL659535  
LOCUS  
DEFINITION  
CL659535 8 bp DNA linear GSS 09-JUL-2004  
PRI0134b.G05 - PRI0134b.B21 (8) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL659535  
CL659535.1 GI:50143739  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.  
Apdab: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES

source

1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpiFos-5 Fosmid vector"

REFERENCE

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.  
TITLE Apdab: an Acedb database for the nematode satellite organism  
JOURNAL Pristionchus pacificus  
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES

source

1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpiFos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 CTCCCGG 229  
|||||  
1 CTCCCGG 7

Db

RESULT 166  
CL676755  
LOCUS  
DEFINITION  
CL676755 8 bp DNA linear GSS 09-JUL-2004  
PRI0119c.A08\_2 - PRI0119c.BR (8) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL676755  
CL676755.1 GI:50182472  
GSS.  
Pristionchus pacificus

/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpiFos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 TGCTGAT 821  
|||||  
2 TGCTGAT 8

Db

RESULT 165  
CL675700  
LOCUS  
DEFINITION  
CL675700 8 bp DNA linear GSS 09-JUL-2004  
PRI0115c.E10\_2 - PRI0115c.BR (8) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL675700  
CL675700.1 GI:50180435  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.  
Apdab: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES

source

1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpiFos-5 Fosmid vector"

REFERENCE

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.U.  
TITLE Apdab: an Acedb database for the nematode satellite organism  
JOURNAL Pristionchus pacificus  
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

FEATURES

source

1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pEpiFos-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 CTCCCGG 229  
|||||  
1 CTCCCGG 7

Db

RESULT 166  
CL676755  
LOCUS  
DEFINITION  
CL676755 8 bp DNA linear GSS 09-JUL-2004  
PRI0119c.A08\_2 - PRI0119c.BR (8) Mixed stage fosmid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.  
CL676755  
CL676755.1 GI:50182472  
GSS.  
Pristionchus pacificus

ORGANISM *Pristionchus pacificus*  
Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;  
Nemodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an Acedb database for the nematode satelellite organism  
*Pristionchus pacificus*  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_1b="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 CCTCCT 1486  
Db 2 CCTCCT 8

RESULT 167  
CL677992 8 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0121d\_B07\_2 - PRI0121d.BR (8) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California *Pristionchus pacificus* genomic, genomic  
survey sequence.  
CL677992  
ACCESSION CL677992.1 GI:50184054  
VERSION  
KEYWORDS GSS.  
SOURCE *Pristionchus pacificus*  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;  
Nemodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an Acedb database for the nematode satelellite organism  
*Pristionchus pacificus*  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"

FEATURES  
source

/strain="California"  
/db\_xref="taxon:54126"  
/clone\_1b="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 975 CACCTTC 981  
Db 1 CACCTTC 7

RESULT 168  
CL681141/c 8 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0130b\_C04\_2 - PRI0130b.BR (8) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California *Pristionchus pacificus* genomic, genomic  
survey sequence.  
CL681141  
ACCESSION CL681141.1 GI:50188149  
VERSION  
KEYWORDS GSS.  
SOURCE *Pristionchus pacificus*  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromodorea; Diplogasterida;  
Nemodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an Acedb database for the nematode satelellite organism  
*Pristionchus pacificus*  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..8  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_1b="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBf105-5 Fosmid vector"

Query Match 0.4%; Score 7; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1397 CAGAGAG 1403  
Db 7 CAGAGAG 1

RESULT 169  
CL682011/c 8 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0133c\_H05\_2 - PRI0133c.BR (8) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California *Pristionchus pacificus* genomic, genomic  
survey sequence.  
CL682011  
ACCESSION CL682011.1 GI:50189203  
VERSION  
KEYWORDS GSS.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Nemodiplogasteridae; Pristionchus.  
1 (bases 1 to 8)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
Appadri: an Acceda database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: 77  
Class: fosmid ends.

FEATURES  
source  
1..8  
Location/Qualifiers  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pGP1fos-5 Fosmid vector"

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 AAAAAA 80  
|||||  
7 AAAAAA 1

RESULT 170  
DUT53265 8 bp DNA linear GSS 27-JAN-2006  
LOCUS  
DEFINITION  
ASNP3048.b2 HF130\_10-06-02 uncultured marine microorganism  
HF130\_10-06-02 genomic clone HF0130\_044H09, genomic survey  
sequence.  
DUT53265  
DUT53265.1 GI:85763101  
GSS.  
uncultured marine microorganism HF130\_10-06-02  
uncultured marine microorganism HF130\_10-06-02  
unclassified sequences; environmental samples.  
1 (bases 1 to 8)  
DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,  
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.  
and Karl,D.M.  
Comparative genomics reveals the ocean's interior  
microbial communities in the ocean's interior  
Science (2006) In press  
Contact: Susan Lucas, Alex Copeland, Sam Pittluck, Alla Lapidus,  
Kerrie Barry, Tijana Glavinadiliro, David Bruce, Paul Richardson  
and Edward DeLong  
US DOE Joint Genome Institute  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA  
Tel: 617-253-5271  
Fax: 617-253-2679  
Email: pwrichardson@lbl.gov; delong@mit.edu  
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid  
DNA library prepared from marine picoplankton in the less than 1.6  
um, greater than 0.22 um fraction. Sample Date: 10/6/2002  
Coordinates: 22.45 N, 158 W Depth 130 m Temperature: 22.19 C  
Salinity: 35.31 psu Oxygen: 204.9 umol/kg

Class: fosmid ends.  
Location/Qualifiers  
1..8  
/organism="uncultured marine microorganism HF130\_10-06-02"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:361146"  
/clone="HF0130\_044H09"  
/cell\_type="marine picoplankton, less than 1.8 um, greater  
than 0.22 um fraction"  
/clone\_lib="HF130\_10-06-02"  
/note="Vector: pCC1PROS; North Pacific Subtropical Gyre  
(Hawaii) picoplankton genomic fosmid DNA library prepared  
from marine picoplankton in the less than 1.6 um, greater  
than 0.22 um fraction. Picoplankton collected at 130 m  
depth on 10/6/2002. Coordinates: 22.45 N, 158 W. Sample  
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 130 m  
Temperature: 22.19 C Salinity: 35.31 psu Oxygen: 204.9  
umol/kg"

FEATURES  
source  
1..8  
Location/Qualifiers  
/organism="Brassica rapa subsp. pekinensis"  
/mol\_type="genomic DNA"  
/cultivar="Chifu"  
/sub\_species="pekinensis"  
/db\_xref="taxon:51351"  
/clone="KBR015G08"  
/lab\_host="R.coli DH10B"  
/clone\_lib="KBR, Brassica rapa BamHI BAC library"  
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp  
pekinensis var. Chifu BAC library (KBR BAC) is provided  
by Yong-Pyo Lim (CNU)."

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 CCCCCA 251  
|||||  
2 CCCCCA 8

RESULT 171  
DX021589/c 8 bp DNA linear GSS 10-JAN-2006  
LOCUS  
DEFINITION  
KBR015G08 KBR, Brassica rapa BamHI BAC library Brassica rapa  
subsp. pekinensis genomic clone KBR015G08, genomic survey  
sequence.  
DX021589  
DX021589.1 GI:84712826  
GSS.  
Brassica rapa subsp. pekinensis  
Brassica rapa subsp. pekinensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 8)  
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,  
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,  
Hahn,J.H. and Park,B.S.  
End sequence of Brassica rapa BamHI (KBR) BAC clone  
Unpublished (2005)  
Contact: Beom-Seok Park  
Brassica Genomics Team  
National Institute of Agricultural Biotechnology  
225 Seodun-dong, Suwon, 441-707, Korea  
Tel: +82-31-298-1670  
Fax: +82-31-299-1672  
Email: pbeom@da.go.kr  
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone  
KBR015G08  
Seq primer: M13 Reverse  
Class: BAC ends.

Query Match 0.4%; Score 7; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 941 GCACAGT 947  
 |||||  
 Db 7 GCACAGT 1

RESULT 172  
 CDS06E5N 9 bp DNA linear GSS 17-JUN-2001  
 LOCUS  
 DEFINITION T3 end of clone AR0A018H04 of library AR0A from strain CBS 732 of  
 Zygosaccharomyces rouxii, genomic survey sequence.  
 ACCESSION AL394689  
 VERSION AL394689.1 GI:12145788  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Zygosaccharomyces rouxii  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

REFERENCE  
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,  
 1 (bases 1 to 9)  
 Bolotin-Fukuhara,M., Bon,E., Broctier,P., Casaregola,S.,  
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Morente,B.,  
 Maupertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,  
 Saurin,W., Tekaya,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,  
 Winkler,P. and Weissenbach,J.  
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
 yeast species for molecular evolution studies  
 FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL  
 PUBMED 11152876  
 REFERENCE  
 AUTHORS de Montigny,J., Straub,M., Potier,S., Tekaya,F., Dujon,B.,  
 Winkler,P., Artiguenave,F. and Souciet,J.  
 Genomic exploration of the hemiascomycetous yeasts: 8.

TITLE Zygosaccharomyces rouxii  
 FEBS Lett. 487 (1), 52-55 (2000)

JOURNAL  
 PUBMED 11152883  
 REFERENCE  
 AUTHORS 3 (bases 1 to 9)

TITLE Direct Submission  
 Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,  
 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
 seqret@genoscope.cns.fr - Web : www.genoscope.cns.fr)

## COMMENT

This GSS is part of a random genomic sequencing program of thirteen  
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
 ecklinus, Saccharomyces servazzii, Zygosaccharomyces rouxii,  
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia  
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
 5 kb were prepared and both extremities were sequenced. See  
 keywords for description of this sequence and for the sequence of  
 the other extremity of this insert.

## FEATURES

source  
 1..9  
 /organism="Zygosaccharomyces rouxii"  
 /mol\_type="genomic DNA"  
 /strain="CBS 732"  
 /db\_xref="taxon:4956"  
 /clone="AR0A018H04"  
 /clone\_11b="AR0A"  
 /note="end : T3"

Query Match 0.4%; Score 7; DB 1; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 331 GTCAATTGTG 339  
 |||||  
 Db 9 GTCAATTGTG 1

RESULT 173  
 CF307008 9 bp mRNA linear EST 15-AUG-2003  
 LOCUS  
 DEFINITION HDAL--05-H11.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
 cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA  
 clone HDAL--05-H11, mRNA sequence.

ACCESSION CF307008.1 GI:33678769  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
 1..9  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HDAL--05-H11"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E. coli SOLR"  
 /clone\_11b="OSHDA1-overexpressing transgenic rice lambda  
 phage cDNA library I (HDAL)"  
 /note="Vector: pBluescript SK(+), site\_1: EcoRI; site\_2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice histone Deacetylase overexpression line."

Query Match 0.4%; Score 7; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1303 CACGAGG 1309  
 |||||  
 Db 2 CACGAGG 8

Search completed: June 12, 2006, 06:13:47  
 Job time : 3 secs

**THIS PAGE BLANK (USPTO)**